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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:02:01 ; Search time 142.194 Seconds
(without alignments)
49.440 Million cell updates/sec

Title: US-10-735-916A-2

Perfect score: 81

Sequence: 1 RSSQSIVHSGNTYLQ 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_21.*

1: Geneseqp1980s.*

2: Geneseqp1980s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81	100.0	16	7	ADJ76836 CDR seque
2	81	100.0	16	9	ADZ67006 Murine in
3	81	100.0	112	7	ADJ76888 Anti-IGF-
4	81	100.0	112	7	ADJ76899 Anti-IGF-
5	81	100.0	112	7	ADJ76895 Anti-IGF-
6	81	100.0	112	9	ADZ67058 Murine im
7	81	100.0	112	9	ADZ67069 Human ant
8	81	100.0	112	9	ADZ67065 Human ant
9	81	100.0	114	9	AEb21358 Mouse ant
10	81	100.0	114	9	AEb31116 Antibody
11	81	100.0	122	7	ADJ76883 Anti-IGF-
12	81	100.0	122	9	ADZ67053 Murine im
13	81	100.0	131	7	ADJ76901 Anti-IGF-
14	81	100.0	131	7	ADJ76897 Anti-IGF-
15	81	100.0	131	9	ADZ67071 Human ant
16	81	100.0	131	9	ADZ67067 Human ant
17	79	97.5	238	2	AAW14937 Murine an
18	79	97.5	238	2	AAW14942 3F4 Human
19	79	97.5	251	3	AAy53587 Anti-HPV1
20	78	96.3	16	2	AAr70451 VL sequen
21	78	96.3	16	5	ABP52343 Fv region
22	78	96.3	16	7	ADc03151 Colon spe
23	78	96.3	16	7	ADd94147 Mouse HUI
24	78	96.3	16	7	ADh61992 Mouse ant

25	78	96.3	16	8	ADL27487
26	78	96.3	16	8	ADM78123
27	78	96.3	16	8	ADM78129 Human SJB
28	78	96.3	16	8	ADM78081 Human SJB
29	78	96.3	16	8	ADP84865 Complemen
30	78	96.3	16	8	ADRI19270 Glycosyla
31	78	96.3	16	8	ADs87339 Humanised
32	78	96.3	92	2	AAr27009 Hypercalc
33	78	96.3	100	4	AAe06963 Mouse ger
34	78	96.3	100	4	AAE06965 Mouse ger
35	78	96.3	100	8	ADh17816 Antibody
36	78	96.3	100	8	ADq89248 Mouse imm
37	78	96.3	100	8	ADQ89250 Mouse imm
38	78	96.3	100	9	ADW11447 House mou
39	78	96.3	100	9	AEb09521 Murine ge
40	78	96.3	100	9	AEb09523 Murine ge
41	78	96.3	105	6	ABG74916 Murine NM
42	78	96.3	109	5	ABP52310 Fv region
43	78	96.3	110	6	ABG72733 Mouse U4
44	78	96.3	111	7	ADc03138 Colon spe
45	78	96.3	112	2	AAr32239 Humanised

ALIGNMENTS

RESULT 1

ADJ76836	ADJ76836 standard; peptide; 16 AA.
XX	XX
AC	ADJ76836;
XX	XX
DT	06-MAY-2004 (first entry)
XX	XX
DE	CDR sequence for anti-IGF-1R antibody.
XX	XX
KW	cytostatic; antipsoriatic; antibody;
KW	insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;
KW	or epidermal growth factor receptor; EGFR; signal transduction pathway;
KW	ligand; tumor; cancer; osteosarcoma; complementarity determining region;
KW	CDR.
XX	XX
OS	Mus musculus.
XX	XX
PN	WO2003059951-A2.
XX	XX
PD	24-JUL-2003.
XX	XX
PF	20-JAN-2003; 2003WO-FR000178.
XX	XX
PR	18-JAN-2002; 2002FR-00000653.
PR	18-JAN-2002; 2002FR-00000654.
XX	XX
PR	07-MAY-2002; 2002FR-00005753.
XX	XX
PA	(FABR) FABRE MEDICAMENT SA PIERRE.
XX	XX
FI	Goetsch L, Corvaia N, Leger O;
XX	XX
DR	WPI; 2003-569653/53.
XX	XX
DR	N-PSDB; ADJ76835.
XX	XX
PT	New antibodies that bind to human insulin-like growth factor receptor,
PT	useful for treatment, prevention and diagnosis of cancers.
XX	XX
PS	Claim 1; SEQ ID NO 2; 164pp; French.
XX	XX
CC	The invention relates to an isolated antibody (Ab), and its functional
CC	fragments, that bind to human insulin-like growth factor-1 receptor (IGF-
CC	1R) and optionally: (i) inhibit natural binding of insulin-like growth
CC	factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine
CC	kinase activity of IGF-1R. Ab and its fragments are used to prevent or
CC	treat diseases associated with overexpression and/or abnormal activity of
CC	IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with

CC hyperactivity of signal transduction pathways mediated by interaction of
 CC these receptors with their ligands. Especially they inhibit
 CC transformation of normal cells to tumor cells, inhibit growth and/or
 CC proliferation of tumor cells, so are useful against cancers of the
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused
 CC by abnormal expression of IGF-IR and/or EGFR. This sequence represents an
 CC CDR sequence used to generate the Ab of the invention.
 XX
 SQ Sequence 16 AA;
 Query Match 100.0%; Score 81; DB 7; Length 16;
 Best Local Similarity 100.0%; Pred. No. 4.8e-07; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 0;
 QY 1 RSSQSIHSHNGNTYLQ 16
 Db 1 RSSQSIHSHNGNTYLQ 16
 RESULT 2
 ADZ67006
 ID ADZ67006 standard; peptide; 16 AA.
 AC ADZ67006;
 XX
 DT 30-JUN-2005 (first entry)
 XX
 DE Murine insulin-like growth factor T receptor IGF-IR CDR SEQ ID NO:2.
 XX
 KW Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
 KW neoplasia; prostate tumor; andrology; genitourinary disease; osteosarcoma;
 KW musculoskeletal disease; respiratory disease; lung tumor;
 KW endocrine disease; gynecology and obstetrics; breast tumor;
 KW endometrial carcinoma; gastrointestinal disease; colon tumor;
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder.
 XX
 OS Mus musculus.
 XX
 PN US2005084906-A1.
 XX
 PD 21-APR-2005.
 XX
 PF 16-DEC-2003; 2003US-00735916.
 XX
 PR 18-JAN-2002; 2002FR-00000653.
 PR 18-JAN-2002; 2002FR-00000654.
 PR 07-MAY-2002; 2002FR-00005753.
 PR 20-JAN-2003; 2003WO-FR000178.
 PR 11-JUL-2003; 2003FR-00008538.
 XX
 PA (GOET/) GOETSCH L.
 PA (CORV/) CORVAIA N.
 PA (LEGE/) LEGER O.
 PA (DUFEL/) DUFLOS A.
 PA (HAEU/) HAEUW J.
 PA (BECK/) BECK A.
 XX
 PI Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;
 XX
 DR WPI; 2005-321968/33.
 DR N-PSDB; ADZ67005.
 XX
 PT Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)
 PT antibody or its functional fragment, being capable of binding human IGF-
 PT IR and specifically inhibiting tyrosine kinase activity of receptor,
 PT useful for treating cancer.
 XX
 PS Claim 1; SEQ ID NO 2; 125pp; English.
 XX
 CC The invention relates to a novel isolated anti-insulin-like growth factor
 CC I receptor (IGF-IR) antibody (I) or its functional fragment, being
 CC capable of binding to human IGF-IR and, if necessary, capable of

CC specifically inhibiting tyrosine kinase activity of the receptor,
 CC comprising a light or heavy chain having at least one complementary
 CC determining region (CDR) consisting of one of two fully defined 16 amino
 CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in
 CC the preparation of a medicament intended for the prevention or treatment
 CC of an illness connected with an overexpression and/or an abnormal
 CC activation of the IGF-IR and/or EGFR, and/or connected with a
 CC hyperactivation of the transduction pathway of the signal mediated by the
 CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where
 CC the administration of the medicament does not induce or only slightly
 CC induces secondary effects connected with inhibition of the insulin
 CC receptor. The antibody is useful for preparation of a medicament intended
 CC to inhibit the transformation of normal cells into cells with tumoral
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is
 CC useful for preparation of a medicament intended to inhibit the growth
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a
 CC medicament intended for prevention or for the treatment of cancer, where
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the
 CC preparation of a medicament intended for the prevention or for the
 CC treatment of psoriasis. (I) is useful in preparation of a medicament
 CC intended for the specific targeting of a biologically active compound to
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)
 CC is useful for in vitro diagnosis of illnesses induced by an
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor
 CC starting from a biological sample in which the abnormal presence, of IGF-
 CC IR and/or EGFR receptor is suspected, which involves contacting the
 CC biological sample with (I), which is optionally labeled. The present
 CC sequence is used in the exemplification of the invention.
 XX
 SQ Sequence 16 AA;
 Query Match 100.0%; Score 81; DB 9; Length 16;
 Best Local Similarity 100.0%; Pred. No. 4.8e-07; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 0;
 QY 1 RSSQSIHSHNGNTYLQ 16
 Db 1 RSSQSIHSHNGNTYLQ 16
 RESULT 3
 ADJ76888
 ID ADJ76888 standard; protein; 112 AA.
 XX
 AC ADJ76888;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Anti-IGF-IR related protein #5.
 XX
 KW cytostatic; antipsoriatic; antibody;
 KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;
 KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;
 KW CDR.
 XX
 OS Mus musculus.
 XX
 PN WO2003059951-A2.
 XX
 PD 24-JUL-2003.
 XX
 PF 20-JAN-2003; 2003WO-FR000178.
 XX
 PR 18-JAN-2002; 2002FR-00000653.
 PR 18-JAN-2002; 2002FR-00000654.
 PR 07-MAY-2002; 2002FR-00005753.
 XX
 PA (FABR) FABRE MEDICAMENT SA PIERRE.

XX PI Goetsch L, Corvaia N, Leger O;
 XX DR WPI; 2003-569653/53.
 XX PT New antibodies that bind to human insulin-like growth factor receptor,
 XX PT useful for treatment, prevention and diagnosis of cancers.
 XX PS Disclosure; SEQ ID NO 54; 164pp; French.
 XX CC The invention relates to an isolated antibody (Ab), and its functional
 CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-
 CC 1R) and optionally: (i) inhibit natural binding of insulin-like growth
 CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine
 CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or
 CC treat diseases associated with overexpression and/or abnormal activity of
 CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with
 CC hyperactivity of signal transduction pathways mediated by interaction of
 CC these receptors with their ligands. Especially they inhibit
 CC transformation of normal cells to tumor cells, inhibit growth and/or
 CC proliferation of tumor cells, so are useful against cancers of the
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a
 CC protein sequence used to generate the Ab of the invention.
 XX CC
 XX SQ Sequence 112 AA;
 Query Match 100.0%; Score 81; DB 7; Length 112;
 Best Local Similarity 100.0%; Pred. No. 5e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RSSQSIVHSNGNTYLQ 16
 Db 24 RSSQSIVHSNGNTYLQ 39
 RESULT 4
 ID ADJ76899 standard; protein; 112 AA.
 XX AC ADJ76899;
 XX DT 06-MAY-2004 (first entry)
 XX DE Anti-IGF-1R related protein #14.
 XX KW Cytostatic; antipsoriatic; antibody;
 XX KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;
 KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;
 KW CDR.
 XX OS Homo sapiens.
 XX PN WO2003059951-A2.
 XX PD 24-JUL-2003.
 XX PF 20-JAN-2003; 2003WO-FR000178.
 XX PR 18-JAN-2002; 2002FR-00000653.
 PR 18-JAN-2002; 2002FR-00000654.
 PR 07-MAY-2002; 2002FR-000005753.
 XX PA (FABR) FABRE MEDICAMENT SA PIERRE.
 XX PI Goetsch L, Corvaia N, Leger O;
 XX DR WPI; 2003-569653/53.
 XX PT New antibodies that bind to human insulin-like growth factor receptor,
 PT useful for treatment, prevention and diagnosis of cancers.

XX PS Disclosure; SEQ ID NO 65; 164pp; French.
 XX CC The invention relates to an isolated antibody (Ab), and its functional
 CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-
 CC 1R) and optionally: (i) inhibit natural binding of insulin-like growth
 CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine
 CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or
 CC treat diseases associated with overexpression and/or abnormal activity of
 CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with
 CC hyperactivity of signal transduction pathways mediated by interaction of
 CC these receptors with their ligands. Especially they inhibit
 CC transformation of normal cells to tumor cells, inhibit growth and/or
 CC proliferation of tumor cells, so are useful against cancers of the
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a
 CC protein sequence used to generate the Ab of the invention.
 XX CC
 XX SQ Sequence 112 AA;
 Query Match 100.0%; Score 81; DB 7; Length 112;
 Best Local Similarity 100.0%; Pred. No. 5e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RSSQSIVHSNGNTYLQ 16
 Db 24 RSSQSIVHSNGNTYLQ 39
 RESULT 5
 ID ADJ76895 standard; protein; 112 AA.
 XX AC ADJ76895;
 XX DT 06-MAY-2004 (first entry)
 XX DE Anti-IGF-1R related protein #12.
 XX KW Cytostatic; antipsoriatic; antibody;
 KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;
 KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;
 KW CDR.
 XX OS Homo sapiens.
 XX PN WO2003059951-A2.
 XX PD 24-JUL-2003.
 XX PF 20-JAN-2003; 2003WO-FR000178.
 XX PR 18-JAN-2002; 2002FR-00000653.
 PR 18-JAN-2002; 2002FR-00000654.
 PR 07-MAY-2002; 2002FR-000005753.
 XX PA (FABR) FABRE MEDICAMENT SA PIERRE.
 XX PI Goetsch L, Corvaia N, Leger O;
 XX DR WPI; 2003-569653/53.
 XX PT New antibodies that bind to human insulin-like growth factor receptor,
 PT useful for treatment, prevention and diagnosis of cancers.
 XX PS Disclosure; SEQ ID NO 61; 164pp; French.
 XX CC The invention relates to an isolated antibody (Ab), and its functional
 CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-
 CC 1R) and optionally: (i) inhibit natural binding of insulin-like growth
 CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine
 CC kinase activity of IGF-1R and/or EGFR. This sequence represents a
 CC protein sequence used to generate the Ab of the invention.

CC kinase activity of IGF-IR. Ab and its fragments are used to prevent or
 CC treat diseases associated with overexpression and/or abnormal activity of
 CC IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with
 CC hyperactivity of signal transduction pathways mediated by interaction of
 CC these receptors with their ligands. Especially they inhibit
 CC transformation of normal cells to tumor cells, inhibit growth and/or
 CC proliferation of tumor cells, so are useful against cancers of the
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused
 CC by abnormal expression of IGF-IR and/or EGFR. This sequence represents a
 CC protein sequence used to generate the Ab of the invention.
 XX
 SQ Sequence 112 AA;

Query Match 100.0%; Score 81; DB 7; Length 112;
 Best Local Similarity 100.0%; Pred. No. 5e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSNGNTYLQ 16
 |||||
 Db 24 RSSQSIVHSNGNTYLQ 39

RESULT 6
 ADZ67058
 ID ADZ67058 standard; protein; 112 AA.
 AC ADZ67058;

DT 30-JUN-2005 (first entry)

DE Murine immunoglobulin light chain variable region 7C10 VL SEQ ID NO:54.

KW Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
 KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;
 KW musculoskeletal disease; respiratory disease; lung tumor;
 KW endocrine disease; gynecology and obstetrics; breast tumor;
 KW endometrial carcinoma; gastrointestinal disease; colon tumor;
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder;
 KW immunoglobulin; light chain variable region.
 XX Mus musculus.

XX US2005084906-A1.

XX 21-APR-2005.

XX 16-DEC-2003; 2003US-00735916.

XX 18-JAN-2002; 2002FR-00000653.

XX 18-JAN-2002; 2002FR-00000654.

XX 07-MAY-2002; 2002FR-00005753.

XX 20-JAN-2003; 2003WO-FR000178.

XX 11-JUL-2003; 2003FR-00008538.

XX (GOET/) GOETSCH L.

PA (CORV/) CORVAIA N.

PA (LEGE/) LEGER O.

PA (DUFL/) DUFLOS A.

PA (HAEU/) HAEUW J.

PA (BECK/) BECK A.

XX Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;
 XX WPI; 2005-321968/33.

XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)
 PT antibody or its functional fragment, being capable of binding human IGF-
 PT IR and specifically inhibiting tyrosine kinase activity of receptor,
 PT useful for treating cancer.

XX Example 12; SEQ ID NO 54; 125pp; English.

CC The invention relates to a novel isolated anti-insulin-like growth factor
 CC I receptor (IGF-IR) antibody (I) or its functional fragment, being
 CC capable of binding to human IGF-IR and, if necessary, capable of
 CC specifically inhibiting tyrosine kinase activity of the receptor,
 CC comprising a light or heavy chain having at least one complementary
 CC determining region (CDR) consisting of one of two fully defined 16 amino
 CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in
 CC the preparation of a medicament intended for the prevention or treatment
 CC of an illness connected with an overexpression and/or an abnormal
 CC activation of the IGF-IR and/or EGFR, and/or connected with a
 CC hyperactivation of the transduction pathway of the signal mediated by the
 CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where
 CC the administration of the medicament does not induce or only slightly
 CC induces secondary effects connected with inhibition of the insulin
 CC receptor. The antibody is useful for preparation of a medicament intended
 CC to inhibit the transformation of normal cells into cells with tumoral
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is
 CC useful for preparation of a medicament intended to inhibit the growth
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a
 CC medicament intended for prevention or for the treatment of cancer, where
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the
 CC preparation of a medicament intended for the prevention or for the
 CC treatment of psoriasis. (I) is useful in preparation of a medicament
 CC intended for the specific targeting of a biologically active compound to
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)
 CC is useful for in vitro diagnosis of illnesses induced by an
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor
 CC starting from a biological sample in which the abnormal presence, of IGF-
 CC IR and/or EGFR receptor is suspected, which involves contacting the
 CC biological sample with (I), which is optionally labeled. The present
 CC sequence is used in the exemplification of the invention.
 XX

SQ Sequence 112 AA;

Query Match 100.0%; Score 81; DB 9; Length 112;
 Best Local Similarity 100.0%; Pred. No. 5e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSNGNTYLQ 16

Db 24 RSSQSIVHSNGNTYLQ 39

RESULT 7
 ADZ67069

ID ADZ67069 standard; protein; 112 AA.

AC ADZ67069;

DT 30-JUN-2005 (first entry)

XX Human antibody 7C10 2 light chain variable region SEQ ID NO:65.

XX Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
 KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;
 KW musculoskeletal disease; respiratory disease; lung tumor;
 KW endocrine disease; gynecology and obstetrics; breast tumor;
 KW endometrial carcinoma; gastrointestinal disease; colon tumor;
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder;
 KW light chain variable region.

XX Homo sapiens.

XX US2005084906-A1.

XX 21-APR-2005.

XX 16-DEC-2003; 2003US-00735916.

PR 18-JAN-2002; 2002FR-00000653.
 PR 18-JAN-2002; 2002FR-00000654.
 PR 07-MAY-2002; 2002FR-00005753.
 PR 20-JAN-2003; 2003WO-FR000178.
 PR 11-JUL-2003; 2003FR-00008538.
 XX
 XX (GOET/) GOETSCH L.
 PA (CORV/) CORVAIA N.
 PA (LEGE/) LEGER O.
 PA (DUFL/) DUFLOS A.
 PA (HAEU/) HAEUW J.
 PA (BECK/) BECK A.
 XX
 XX Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;
 XX WPI; 2005-321968/33.
 DR
 XX
 XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)
 PT antibody or its functional fragment, being capable of binding human IGF-
 PT IR and specifically inhibiting tyrosine kinase activity of receptor,
 PT useful for treating cancer.
 XX
 XX Example 12; SEQ ID NO 65; 125pp; English.
 PS
 XX The invention relates to a novel isolated anti-insulin-like growth factor
 CC I receptor (IGF-IR) antibody (I) or its functional fragment, being
 CC capable of binding to human IGF-IR and, if necessary, capable of
 CC specifically inhibiting tyrosine kinase activity of the receptor,
 CC comprising a light or heavy chain having at least one complementary
 CC determining region (CDR) consisting of one of two fully defined 16 amino
 CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in
 CC the preparation of a medicament intended for the prevention or treatment
 CC of an illness connected with an overexpression and/or an abnormal
 CC activation of the IGF-IR and/or EGFR, and/or connected with a
 CC hyperactivation of the transduction pathway of the signal mediated by the
 CC interaction of IGf1 or IGf2 with IGF-IR and/or of EGF with EGFR, where
 CC the administration of the medicament does not induce or only slightly
 CC induces secondary effects connected with inhibition of the insulin
 CC receptor. The antibody is useful for preparation of a medicament intended
 CC to inhibit the transformation of normal cells into cells with tumoral
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is
 CC useful for preparation of a medicament intended to inhibit the growth
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a
 CC medicament intended for prevention or for the treatment of cancer, where
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the
 CC preparation of a medicament intended for the prevention or for the
 CC treatment of psoriasis. (I) is useful in preparation of a medicament
 CC intended for the specific targeting of a biologically active compound to
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)
 CC is useful for in vitro diagnosis of illnesses induced by an
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor
 CC starting from a biological sample in which the abnormal presence, of IGF-
 CC IR and/or EGFR receptor is suspected, which involves contacting the
 CC biological sample with (I), which is optionally labeled. The present
 CC sequence is used in the exemplification of the invention.
 XX
 SQ Sequence 112 AA;
 Query Match 100.0%; Score 81; DB 9; Length 112;
 Best Local Similarity 100.0%; Pred. No. 5e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RSSQSIVHSNGNTYLIQ 16
 Db 24 RSSQSIVHSNGNTYLIQ 39
 RESULT 8
 ADZ67065

ID ADZ67065 standard; protein; 112 AA.
 XX
 AC ADZ67065;
 XX
 XX 30-JUN-2005 (first entry)
 DT
 XX Human antibody 7C10 1 light chain variable region SEQ ID NO:61.
 DE
 XX Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
 KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;
 KW musculoskeletal disease; respiratory disease; lung tumor;
 KW endocrine disease; gynecology and obstetrics; breast tumor;
 KW endometrial carcinoma; gastrointestinal disease; colon tumor;
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder;
 KW light chain variable region.
 XX
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FH 24..39
 FT /note= "CDR1"
 FT Region
 FT 55..61
 FT /note= "CDR2"
 FT Region
 FT 94..102
 FT /note= "CDR3"
 FT Region
 XX US2005084906-A1.
 XX 21-APR-2005.
 XX 16-DEC-2003; 2003US-00735916.
 XX 18-JAN-2002; 2002FR-00000653.
 XX 18-JAN-2002; 2002FR-00000654.
 PR 07-MAY-2002; 2002FR-00005753.
 PR 20-JAN-2003; 2003WO-FR000178.
 PR 11-JUL-2003; 2003FR-00008538.
 XX (GOET/) GOETSCH L.
 PA (CORV/) CORVAIA N.
 PA (LEGE/) LEGER O.
 PA (DUFL/) DUFLOS A.
 PA (HAEU/) HAEUW J.
 PA (BECK/) BECK A.
 XX Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;
 WPI; 2005-321968/33.
 N-PSDB; ADZ67065.
 Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)
 antibody or its functional fragment, being capable of binding human IGF-
 IR and specifically inhibiting tyrosine kinase activity of receptor,
 useful for treating cancer.
 Example 12; SEQ ID NO 61; 125pp; English.
 The invention relates to a novel isolated anti-insulin-like growth factor
 I receptor (IGF-IR) antibody (I) or its functional fragment, being
 capable of binding to human IGF-IR and, if necessary, capable of
 specifically inhibiting tyrosine kinase activity of the receptor,
 comprising a light or heavy chain having at least one complementary
 determining region (CDR) consisting of one of two fully defined 16 amino
 acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in
 the preparation of a medicament intended for the prevention or treatment
 of an illness connected with an overexpression and/or an abnormal
 activation of the IGF-IR and/or EGFR, and/or connected with a
 hyperactivation of the transduction pathway of the signal mediated by the
 interaction of IGf1 or IGf2 with IGF-IR and/or of EGF with EGFR, where
 the administration of the medicament does not induce or only slightly
 induces secondary effects connected with inhibition of the insulin
 receptor. The antibody is useful for preparation of a medicament intended
 to inhibit the transformation of normal cells into cells with tumoral
 character, preferably IGF-dependent, especially IGF1 and/or IGF2-
 dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is
 useful for preparation of a medicament intended to inhibit the growth
 and/or the proliferation of tumor cells, preferably IGF-dependent,
 especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or
 HER2/neu-dependent cells. (I) is useful in the preparation of a
 medicament intended for prevention or for the treatment of cancer, where
 the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,
 breast cancer, endometrial cancer or colon cancer. (I) is useful in the
 preparation of a medicament intended for the prevention or for the
 treatment of psoriasis. (I) is useful in preparation of a medicament
 intended for the specific targeting of a biologically active compound to
 cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)
 is useful for in vitro diagnosis of illnesses induced by an
 overexpression or an underexpression of the IGF-IR and/or EGFR receptor
 starting from a biological sample in which the abnormal presence, of IGF-
 IR and/or EGFR receptor is suspected, which involves contacting the
 biological sample with (I), which is optionally labeled. The present
 sequence is used in the exemplification of the invention.

CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is
 CC useful for preparation of a medicament intended to inhibit the growth
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a
 CC medicament intended for prevention or for the treatment of cancer, where
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the
 CC preparation of a medicament intended for the prevention or for the
 CC treatment of psoriasis. (I) is useful in preparation of a medicament
 CC intended for the specific targeting of a biologically active compound to
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)
 CC is useful for in vitro diagnosis of illnesses induced by an
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor
 CC starting from a biological sample in which the abnormal presence, of IGF-
 CC IR and/or EGFR receptor is suspected, which involves contacting the
 CC biological sample with (I), which is optionally labeled. The present
 CC sequence is used in the exemplification of the invention.
 XX
 SQ Sequence 112 AA;

Query Match 100.0%; Score 81; DB 9; Length 112;
 Best Local Similarity 100.0%; Pred. No. 58-06; Mismatches 0; Indels 0; Gaps 0;
 Matches 16; Conservative 0;

QY 1 RSSQSVHSGNGNTYLQ 16
 |||||
 DB 24 RSSQSVHSGNGNTYLQ 39

RESULT 9
 AEB21358
 ID AEB21358 standard; protein; 114 AA.

XX AEB21358;
 AC AEB21358;
 DT 22-SEP-2005 (first entry)
 XX Mouse anti-IL-13 antibody 227-26 light chain variable region (VK).
 DE
 XX Interleukin-13; IL-13; antibody engineering; humanized antibody;
 KW Antiasthmatic; Antiinflammatory; Dermatological; Antiallergic;
 KW Respiratory-Gen.; Antiulcer; Gastrointestinal-Gen.; Ophthalmological;
 KW Osteopathic; Virucide; asthma; allergic rhinitis; atopic dermatitis;
 KW allergic conjunctivitis; eczema; urticaria; allergy;
 KW chronic obstructive pulmonary disease; ulcerative colitis;
 KW respiratory syncytial virus infection; uveitis; scleroderma;
 KW osteoporosis; monoclonal antibody; light chain variable region.
 XX

OS Mus sp.
 XX
 XX WO2005062967-A2.
 PN
 XX
 PD 14-JUL-2005.
 XX

XX 23-DEC-2004; 2004WO-US043501.
 XX
 XX 23-DEC-2003; 2003US-0532130P.
 XX
 XX (TANO-) TANOX INC.
 XX

XX Fung SC, Moyle M, Lu M, Yan C, Singh S, Huang D;
 XX WPI; 2005-506603/51.
 XX

XX New antibody or its antigen-binding fragment that binds specifically and
 PT with high affinity to glycosylated and non-glycosylated human interleukin
 PT -13 (IL-13), useful for treating IL-13-mediated disorders, such as asthma
 PT and eczema.
 XX

PS Claim 10; SEQ ID NO 7; 129pp; English.

CC The invention relates to an antibody or its antigen-binding fragment that
 CC binds specifically and with high affinity to glycosylated and non-
 CC glycosylated human interleukin-13 (IL-13), does not bind mouse IL-13, and
 CC neutralizes human IL-13 activity at an approximate molar ratio of 1:2
 CC (Mab:IL13). Also included are an antibody that binds to the same epitope
 CC as the antibody cited above, an antibody comprising antigen binding
 CC regions derived from the light and heavy chain variable regions of the
 CC novel antibody, a hybridoma cell line that produces a monoclonal antibody
 CC (selected from 228B/C-1, 228A-4, 227-26, and 227-43 and designated with
 CC the ATCC deposit number PTA-5657, PTA-5656, PTA-5654, and PTA-5655,
 CC respectively), a cell line comprising a nucleic acid encoding the
 CC antibody, a vector comprising the nucleic acid encoding the antibody, a
 CC composition (comprising the antibody and a physiologically acceptable
 CC carrier, diluent, excipient, or stabilizer), a variable light chain
 CC region (comprising an amino acid sequence having the formula: FR11-CDRL1-
 CC FR12-CDRL2-FR13-CDRL3-FRL4) a variable heavy chain region (comprising an
 CC amino acid sequence having the formula: FRH1-CDRH1-FRH2-CDRH2-FRH3-CDRH3-
 CC FRH4), an antibody (or its antigen binding fragment, comprising the
 CC variable light or heavy chain region, where the antibody binds
 CC specifically to IL-13), treating a subject suffering from asthmatic
 CC symptoms (comprising administering an antibody to reduce the asthmatic
 CC symptoms), an inhalation device that delivers the antibody to a patient,
 CC detecting interleukin-13 protein in a sample, diagnosing overexpression
 CC of IL-13 in a subject, producing the antibody, a recombinant antibody
 CC molecule (or an IL-13-binding fragment, comprising at least one antibody
 CC heavy chain, or an IL-13-binding fragment, comprising non-human CDRs at
 CC positions 31-35 (CDR1), 50-65 (CDR2) and 95-102 (CDR3) (Kabat numbering)
 CC from a mouse anti-IL-13 antibody, where positions 27-30 have the amino
 CC acid Gly 26, Phe 27, Ser 28, Leu 29, Asn 30), and at least one antibody
 CC light chain (or an IL-13-binding fragment, comprising non-human CDRs at
 CC positions 24-34 (CDR1), 50-56 (CDR2) and 89-97 (CDR3) from a mouse anti-
 CC IL13 antibody and framework regions from a monoclonal antibody), a vector
 CC comprising the DNA sequence, a host cell comprising the vector,
 CC inhibiting IGE antibody production in a patient, treating an IL-13-
 CC mediated disorder in a patient, reducing the severity of asthma in a
 CC mammal, and an IL-13 epitope peptide appearing as AEB21369 or AEB21370.
 CC The antibody and methods are useful for treating IL-13-mediated
 CC disorders, such as allergic asthma, non-allergic (intrinsic) asthma,
 CC allergic rhinitis, atopic dermatitis, allergic conjunctivitis, eczema,
 CC urticaria, food allergies, chronic obstructive pulmonary disease,
 CC ulcerative colitis, RSV infection, uveitis, scleroderma, or osteoporosis.
 CC The present sequence represents a the light chain variable region of a
 CC mouse anti-IL-13 monoclonal antibody.

Sequence 114 AA;

Query Match 100.0%; Score 81; DB 9; Length 114;
 Best Local Similarity 100.0%; Pred. No. 5.1e-06; Mismatches 0; Indels 0; Gaps 0;
 Matches 16; Conservative 0;

QY 1 RSSQSVHSGNGNTYLQ 16
 |||||
 DB 24 RSSQSVHSGNGNTYLQ 39

RESULT 10
 AEB31116
 ID AEB31116 standard; protein; 114 AA.

XX AEB31116;
 AC AEB31116;
 XX

DT 22-SEP-2005 (first entry)
 XX

DE Antibody 227-26/227-26.1 variable light chain.

XX cytostatic; antibody therapy; neoplasm; interleukin 13; IL-13; cancer;
 KW diagnosis; tumor; humanized antibody; cell proliferation;
 KW Hodgkins disease; cytotoxin; chemotherapy; lymphoma; skin tumor;
 KW stomach tumor; colon tumor; breast tumor; pancreatic tumor; liver tumor;
 KW prostate tumor; lung tumor; head and neck tumor; renal tumor;
 KW squamous cell carcinoma; brain tumor; Kaposi's carcinoma; solid tumor;
 KW monoclonal antibody; 227-26; 227-26-1, light chain variable region.

OS Mus sp.
XX Synthetic.
XX WO2005062972-A2.
XX 14-JUL-2005.
XX 23-DEC-2004; 2004WO-US043541.
XX 23-DEC-2003; 2003US-0532130P.
XX (TANO-) TANOX INC.
XX Fung SC, Moyle M;
XX WPI; 2005-506604/51.
XX Treating a neoplasm, e.g. Hodgkin's disease, that expresses and/or binds
PT interleukin-13 (IL-13) comprises administering an anti-IL-13 antibody or
PT its binding fragment that binds to both glycosylated and non-glycosylated
PT human IL-13.
XX Claim 13; SEQ ID NO 7; 98pp; English.
XX This invention describes a novel method for treating a neoplasm that
CC expresses and/or binds interleukin-13 (IL-13). The method comprises
CC administering an anti-IL-13 antibody or its binding fragment that binds
CC specifically and with high affinity to both glycosylated and non-
CC glycosylated human IL-13, and neutralizes human IL-13 activity at an
CC approximate molar ratio of 1:2 (MAB:IL-13). The method also describes 1)
CC a method for treating Hodgkin's disease comprising administering a
CC humanized or chimeric antibody or binding fragment to a patient; 2)
CC inhibiting IL-13 dependent proliferation of neoplastic cells in a mammal
CC comprising administering the antibody, or a binding fragment that
CC inhibits the biological activity of IL-13 and 3) diagnosing a cancer or
CC tumor overexpressing IL-13 comprising the use of the anti-IL-13 antibody
CC to detect overexpression of IL-13 in the biological sample taken from a
CC patient suspected of having the cancer or tumor. The antibodies used in
CC the method of the invention are 228B/C produced by the hybridoma
CC designated PTA-5657, 228A-4 and produced by the hybridoma designated PTA-
CC 5656; 227-26, produced by the hybridoma designated PTA-5654; or 227-43
CC produced by the hybridoma designated PTA-5655. The antibody is a human
CC antibody, a chimeric antibody, a single domain antibody or a humanized
CC antibody. The antibody is a fragment, such as Fv, Fab, and F(ab')₂
CC fragments, single-chain antibodies such as scFv, and various chain
CC combinations. The antibody further comprises a physiologically acceptable
CC carrier, diluent, excipient, or stabilizer. The antibody mediates killing
CC by antibody dependent cell-mediated cytotoxicity and/or complement
CC mediated cytotoxicity. The antibody comprises at least a variable light
CC chain region comprising an amino acid sequence having the formula: FRL1-
CC CDRL1-FRL2-CDRL2-FRL3-CDRL3-FRL4. The antibody comprises at least a
CC variable light or heavy chain region. The variable light or heavy chain
CC region further comprises a constant region. The constant region is from
CC an Igg antibody. The Igg antibody is an Igg1, Igg2, Igg3 or an Igg4
CC antibody. The antibody further comprises the heavy chain. The antibody is
CC associated with a cytotoxic agent, such as a radioisotope or a
CC chemotherapeutic agent. The methods and antibodies are useful for
CC treating neoplasms such as Hodgkin's lymphoma, skin cancer, stomach
CC cancer, colon cancer, breast cancer, pancreatic cancer, liver cancer,
CC prostate cancer, lung cancer, head-and-neck cancer, renal cell cancer,
CC squamous cell carcinoma, AIDS-associated Kaposi's carcinoma and brain
CC cancer. This sequence represents the humanized mouse monoclonal antibody
CC 227-26 and 227-26-1 variable light chain.
XX Sequence 114 AA;
SQ
Query Match 100.0%; Score 81; DB 9; Length 114;
Best Local Similarity 100.0%; Pred. No. 5.1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RSSQSIVHSNGNTYLIQ 16
DB 24 RSSQSIVHSNGNTYLIQ 39

RESULT 11
ADJ76883
ID ADJ76883 standard; protein; 122 AA.
XX
AC ADJ76883;
XX
DT 06-MAY-2004 (first entry)
XX
DE Anti-IGF-1R related protein #3.
XX
DE cytostatic; antiproliferative; antibody;
KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;
KW or epidermal growth factor receptor; EGFR; signal transduction pathway;
KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;
KW CDR.
XX
OS Mus musculus.
XX
XX WO2003059951-A2.
XX
XX 24-JUL-2003.
XX
XX 20-JAN-2003; 2003WO-FR000178.
XX
XX 18-JAN-2002; 2002FR-00000653.
XX
XX 18-JAN-2002; 2002FR-00000654.
XX
XX 07-MAY-2002; 2002FR-00005753.
XX
XX (FABR) PABRE MEDICAMENT SA PIERRE.
XX
XX Goetsch L, Corvaia N, Leger O;
XX WPI; 2003-569653/53.
XX
XX New antibodies that bind to human insulin-like growth factor receptor,
PT useful for treatment, prevention and diagnosis of cancers.
XX
XX Disclosure; SEQ ID NO 49; 164pp; French.
XX
XX The invention relates to an isolated antibody (Ab), and its functional
CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-
CC 1R) and optionally: (i) inhibit natural binding of insulin-like growth
CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine
CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or
CC treat diseases associated with overexpression and/or abnormal activity of
CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with
CC hyperactivity of signal transduction pathways mediated by interaction of
CC these receptors with their ligands. Especially they inhibit
CC transformation of normal cells to tumor cells, inhibit growth and/or
CC proliferation of tumor cells, so are useful against cancers of the
CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
CC also for treating psoriasis. Ab are also used to diagnose diseases caused
CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a
CC protein sequence used to generate the Ab of the invention.
XX
XX Sequence 122 AA;
SQ
Query Match 100.0%; Score 81; DB 7; Length 122;
Best Local Similarity 100.0%; Pred. No. 5.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RSSQSIVHSNGNTYLIQ 16
DB 34 RSSQSIVHSNGNTYLIQ 49

RESULT 12
ADZ67053
ID ADZ67053 standard; protein; 122 AA.
XX
XX
AC ADZ67053;

XX 30-JUN-2005 (first entry)
 DE Murine immunoglobulin light chain variable region 7C10 VL SEQ ID NO:49.
 XX
 XX Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
 KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;
 KW musculoskeletal disease; respiratory disease; lung tumor;
 KW endocrine disease; gynecology and obstetrics; breast tumor;
 KW endometroid carcinoma; gastrointestinal disease; colon tumor;
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder;
 KW immunoglobulin, light chain variable region.
 XX
 OS Mus musculus.
 FH
 FH Key Location/Qualifiers
 FT Peptide 1..10
 FT /note= "leader peptide"
 FT Region 34..49
 FT /note= "CDR1"
 FT Region 65..71
 FT /note= "CDR2"
 FT Region 104..111
 FT /note= "CDR3"
 XX
 PN US2005084906-A1.
 XX
 XX 21-APR-2005.
 XX
 XX 16-DEC-2003; 2003US-00735916.
 XX
 XX 18-JAN-2002; 2002FR-00000653.
 PR 18-JAN-2002; 2002FR-00000654.
 PR 07-MAY-2002; 2002FR-00005753.
 PR 20-JAN-2003; 2003WO-FR000178.
 PR 11-JUL-2003; 2003FR-00008538.
 XX
 XX (GOET/) GOETSCH L.
 PA (CORV/) CORVAIA N.
 PA (LEGE/) LEGER O.
 PA (DUFL/) DUFLOS A.
 PA (HAEU/) HAEUW J.
 PA (BECK/) BECK A.
 XX
 XX Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;
 XX
 XX WPI; 2005-321968/33.
 DR N-PSDB; AD267052.
 XX
 XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)
 PT antibody or its functional fragment, being capable of binding human IGF-
 PT IR and specifically inhibiting tyrosine kinase activity of receptor,
 PT useful for treating cancer.
 XX
 PS Example 8; SEQ ID NO 49; 125pp; English.
 XX
 XX The invention relates to a novel isolated anti-insulin-like growth factor
 CC I receptor (IGF-IR) antibody (I) or its functional fragment, being
 CC capable of binding to human IGF-IR and, if necessary, capable of
 CC specifically inhibiting tyrosine kinase activity of the receptor,
 CC comprising a light or heavy chain having at least one complementary
 CC determining region (CDR) consisting of one of two fully defined 16 amino
 CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in
 CC the preparation of a medicament intended for the prevention or treatment
 CC of an illness connected with an overexpression and/or an abnormal
 CC activation of the IGF-IR and/or EGFR, and/or connected with a
 CC hyperactivation of the transduction pathway of the signal mediated by the
 CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where
 CC the administration of the medicament does not induce or only slightly
 CC induces secondary effects connected with inhibition of the insulin
 CC receptor. The antibody is useful for preparation of a medicament intended
 CC to inhibit the transformation of normal cells into cells with tumoral
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-

CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is
 CC useful for preparation of a medicament intended to inhibit the growth
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a
 CC medicament intended for prevention or for the treatment of cancer, where
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the
 CC preparation of a medicament intended for the prevention or for the
 CC treatment of psoriasis. (I) is useful in preparation of a medicament
 CC intended for the specific targeting of a biologically active compound to
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)
 CC is useful for in vitro diagnosis of illnesses induced by an
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor
 CC starting from a biological sample in which the abnormal presence, of IGF-
 CC IR and/or EGFR receptor is suspected, which involves contacting the
 CC biological sample with (I), which is optionally labeled. The present
 CC sequence is used in the exemplification of the invention.
 XX

SQ Sequence 122 AA;

Query Match 100.0%; Score 81; DB 9; Length 122;
 Best Local Similarity 100.0%; Pred. No. 5.6e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGTYLQ 16
 |||||
 Db 34 RSSQSIVHSGNGTYLQ 49

RESULT 13

ADJ76901

ID ADJ76901 standard; protein; 131 AA.

AC ADJ76901;

DT 06-MAY-2004 (first entry)

DE Anti-IGF-IR related protein #15.

KW cytostatic; antipsoriatic; antibody;
 KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;
 KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;
 KW CDR.

OS Homo sapiens.

XX WO2003059951-A2.

XX 24-JUL-2003.

XX 20-JAN-2003; 2003WO-FR000178.

PR 18-JAN-2002; 2002FR-00000653.

PR 18-JAN-2002; 2002FR-00000654.

PR 07-MAY-2002; 2002FR-00005753.

XX (FABR) FABRE MEDICAMENT SA PIERRE.

XX Goetsch L, Corvaia N, Leger O;

XX WPI; 2003-569653/53.

XX New antibodies that bind to human insulin-like growth factor receptor,
 PT useful for treatment, prevention and diagnosis of cancers.

XX Disclosure; SEQ ID NO 67; 164pp; French.

XX The invention relates to an isolated antibody (Ab), and its functional
 CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-
 CC IR) and optionally: (i) inhibit natural binding of insulin-like growth
 CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine

CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or
 CC treat diseases associated with overexpression and/or abnormal activity of
 CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with
 CC hyperactivity of signal transduction pathways mediated by interaction of
 CC these receptors with their ligands. Especially they inhibit
 CC transformation of normal cells to tumor cells, inhibit growth and/or
 CC proliferation of tumor cells, so are useful against cancers of the
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a
 CC protein sequence used to generate the Ab of the invention.
 XX
 SQ Sequence 131 AA;

Query Match 100.0%; Score 81; DB 7; Length 131;
 Best Local Similarity 100.0%; Pred. No. 6.1e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIHVSNGNTYLQ 16
 DB 43 RSSQSIHVSNGNTYLQ 58
 |||||

RESULT 14
 ADJ76897
 ID ADJ76897 standard; protein; 131 AA.

AC ADJ76897;

XX 06-MAY-2004 (first entry)

XX Anti-IGF-1R related protein #13.

XX cytostatic; antipsoriatic; antibody;
 KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;
 KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;
 KW CDR.

XX Homo sapiens.

XX WO2003059951-A2.

XX 24-JUL-2003.

XX 20-JAN-2003; 2003WO-FR000178.

XX 18-JAN-2002; 2002FR-00000653.

XX 18-JAN-2002; 2002FR-00000654.

XX 07-MAY-2002; 2002FR-00005753.

XX (FABR) FABRE MEDICAMENT SA PIERRE.

XX Goetsch L, Corvaia N, Leger O;

XX WPI; 2003-569653/53.

XX New antibodies that bind to human insulin-like growth factor receptor,

XX useful for treatment, prevention and diagnosis of cancers.

XX Disclosure; SEQ ID NO 63; 164pp; French.

XX The invention relates to an isolated antibody (Ab), and its functional
 CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-
 CC 1R) and optionally: (i) inhibit natural binding of insulin-like growth
 CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine
 CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or
 CC treat diseases associated with overexpression and/or abnormal activity of
 CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with
 CC hyperactivity of signal transduction pathways mediated by interaction of
 CC these receptors with their ligands. Especially they inhibit
 CC transformation of normal cells to tumor cells, inhibit growth and/or
 CC proliferation of tumor cells, so are useful against cancers of the

CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a
 CC protein sequence used to generate the Ab of the invention.
 XX
 SQ Sequence 131 AA;

Query Match 100.0%; Score 81; DB 7; Length 131;
 Best Local Similarity 100.0%; Pred. No. 6.1e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIHVSNGNTYLQ 16
 DB 43 RSSQSIHVSNGNTYLQ 58
 |||||

RESULT 15
 ADZ67071
 ID ADZ67071 standard; protein; 131 AA.

XX AC ADZ67071;

XX 30-JUN-2005 (first entry)

XX Human antibody 7C10 2 light chain variable region SEQ ID NO:67.

XX Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
 KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;
 KW musculoskeletal disease; respiratory disease; lung tumor;
 KW endocrine disease; gynecology and obstetrics; breast tumor;
 KW endometrial carcinoma; gastrointestinal disease; colon tumor;
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder;
 KW light chain variable region.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT Peptide 1..19
 /note= "leader peptide"

FT Region 43..58
 /note= "CDR1"

FT Region 74..80
 /note= "CDR2"

FT Region 113..121
 /note= "CDR3"

XX US2005084906-A1.

XX 21-APR-2005.

XX 16-DEC-2003; 2003US-00735916.

XX 18-JAN-2002; 2002FR-00000653.

XX 18-JAN-2002; 2002FR-00000654.

XX 07-MAY-2002; 2002FR-00005753.

XX 20-JAN-2003; 2003WO-FR000178.

XX 11-JUL-2003; 2003FR-00008538.

XX (GOET/) GOETSCH L.

XX (CORV/) CORVAIA N.

XX (LEGE/) LEGER O.

XX (DUFL/) DUFLOS A.

XX (HAEU/) HAEUW J.

XX (BECK/) BECK A.

XX Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;

XX WPI; 2005-321968/33.

XX N-ESDB; ADZ67070.

Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)
 antibody or its functional fragment, being capable of binding human IGF-
 IR and specifically inhibiting tyrosine kinase activity of receptor,

PT useful for treating cancer.
XX
PS
XX Example 12; SEQ ID NO 67; 125pp; English.
CC
CC The invention relates to a novel isolated anti-insulin-like growth factor
CC I receptor (IGF-IR) antibody (I) or its functional fragment, being
CC capable of binding to human IGF-IR and, if necessary, capable of
CC specifically inhibiting tyrosine kinase activity of the receptor,
CC comprising a light or heavy chain having at least one complementary
CC determining region (CDR) consisting of one of two fully defined 16 amino
CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in
CC the preparation of a medicament intended for the prevention or treatment
CC of an illness connected with an overexpression and/or an abnormal
CC activation of the IGF-IR and/or EGFR, and/or connected with a
CC hyperactivation of the transduction pathway of the signal mediated by the
CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where
CC the administration of the medicament does not induce or only slightly
CC induces secondary effects connected with inhibition of the insulin
CC receptor. The antibody is useful for preparation of a medicament intended
CC to inhibit the transformation of normal cells into cells with tumoral
CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-
CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is
CC useful for preparation of a medicament intended to inhibit the growth
CC and/or the proliferation of tumor cells, preferably IGF-dependent,
CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or
CC HER2/neu-dependent cells. (I) is useful in the preparation of a
CC medicament intended for prevention or for the treatment of cancer, where
CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,
CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the
CC preparation of a medicament intended for the prevention or for the
CC treatment of psoriasis. (I) is useful in preparation of a medicament
CC intended for the specific targeting of a biologically active compound to
CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)
CC is useful for in vitro diagnosis of illnesses induced by an
CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor
CC starting from a biological sample in which the abnormal presence, of IGF-
CC IR and/or EGFR receptor is suspected, which involves contacting the
CC biological sample with (I), which is optionally labeled. The present
XX sequence is used in the exemplification of the invention.
SQ Sequence 131 AA;

Query Match 100.0%; Score 81; DB 9; Length 131;
Best Local Similarity 100.0%; Pred. No. 6.1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RSSQSIVHNGNTYLQ 16
Db 43 RSSQSIVHNGNTYLQ 58

Search completed: December 30, 2005, 13:23:55
Job time : 144.194 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:11:41 ; Search time 22.7097 Seconds
(without alignments)
67.789 Million cell updates/sec

Title: US-10-735-916A-2
Perfect score: 81
Sequence: 1 RSSQSIVHSNGNTYIQ 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	79	97.5	130	2 C29380	Ig kappa chain pre
2	79	97.5	131	2 D29380	Ig kappa chain pre
3	78	96.3	46	2 S07456	Ig kappa chain v r
4	78	96.3	91	2 S25463	Ig kappa chain v r
5	78	96.3	93	2 S24502	Ig kappa chain v r
6	78	96.3	99	2 S24504	Ig kappa chain v r
7	78	96.3	99	2 S24501	Ig kappa chain v r
8	78	96.3	101	2 S11126	Ig kappa chain v r
9	78	96.3	102	2 S14590	Ig kappa chain v r
10	78	96.3	103	2 PH1042	Ig light chain v r
11	78	96.3	103	2 PH1043	Ig light chain v r
12	78	96.3	110	2 S26335	Ig kappa chain v r
13	78	96.3	112	2 P27887	Ig kappa chain v r
14	78	96.3	112	2 A31807	Ig kappa chain v r
15	78	96.3	113	2 P10203	anti-DNA autoantib
16	78	96.3	113	2 S24538	Ig kappa chain v r
17	78	96.3	118	2 S24536	Ig kappa chain v r
18	78	96.3	118	2 S24503	Ig kappa chain v r
19	78	96.3	118	2 S24531	Ig kappa chain v r
20	78	96.3	118	2 S24533	Ig kappa chain v r
21	78	96.3	118	2 S24535	Ig kappa chain v r
22	78	96.3	118	2 S24500	Ig kappa chain v r
23	78	96.3	118	2 S24508	Ig kappa chain v r
24	78	96.3	118	2 S24506	Ig kappa chain v r
25	78	96.3	118	2 S24532	Ig kappa chain v r
26	78	96.3	118	2 S24507	Ig kappa chain v r
27	78	96.3	118	2 S24537	Ig kappa chain v r
28	78	96.3	118	2 S24539	Ig kappa chain v r
29	78	96.3	119	2 A45032	Ig kappa chain v r

Ig light chain pre
Ig kappa chain - m
Ig kappa chain v r
Ig kappa chain v r
Ig kappa chain v r
Ig kappa chain pre
Ig kappa chain (mo
Ig light chain v r
Ig heavy chain v r
Ig light chain v r
Ig light chain v r
Ig light chain v r
Ig light chain v r
Ig light chain v r
Ig light chain v r
Ig kappa chain v r

ALIGNMENTS

RESULT 1

C29380
Ig kappa chain precursor V region (BC-1004) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 21-Jul-2000
C;Accession: C29380
R;Chen, H.T.; Kabat, E.A.; Lundblad, A.; Ratcliffe, R.M.
J. Biol. Chem. 262, 13579-13583, 1987
A;Title: Nucleotide and translated amino acid sequences of cDNA coding for the variable
A;Reference number: A92612; MUID:88007582; PMID:3115981
A;Accession: C29380
A;Molecule type: mRNA
A;Residues: 1-130 <CHE>
A;Cross-references: UNIPARC:UPI000011677D; GB:M17162; GB:J02815; NID:g196899; PIDN:AAA38
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-113/Domain: immunoglobulin homology <IMM>

Query Match 97.5%; Score 79; DB 2; Length 130;
Best Local Similarity 93.8%; Pred. No. 3.4e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSNGNTYIQ 16
|||:|||||
Db 42 RSSQSLVHSNGNTYIQ 57

RESULT 2

D29380
Ig kappa chain precursor V region (B003 46/2D7) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C;Accession: D29380
R;Chen, H.T.; Kabat, E.A.; Lundblad, A.; Ratcliffe, R.M.
J. Biol. Chem. 262, 13579-13583, 1987
A;Title: Nucleotide and translated amino acid sequences of cDNA coding for the variable
A;Reference number: A92612; MUID:88007582; PMID:3115981
A;Accession: D29380
A;Molecule type: mRNA
A;Residues: 1-131 <CHE>
A;Cross-references: UNIPROT:Q8VC16; UNIPARC:UPI000017678A
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-113/Domain: immunoglobulin homology <IMM>

Query Match 97.5%; Score 79; DB 2; Length 131;
Best Local Similarity 93.8%; Pred. No. 3.5e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSNGNTYIQ 16
|||:|||||
Db 42 RSSQSLVHSNGNTYIQ 57

```
RESULT 3
S07456
IG kappa chain V region (hybridoma G8 Ad 3.8) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-May-1997
C:Accession: S07456
R:Rocca-Serra, J.; Mazie, J.C.; Moinier, D.; Leclercq, L.; Somme, G.; Theze, J.; Fougere
J. Immunol. 129, 2554-2558, 1982
A:Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not se
A:Reference number: S07453; MUID:83058021; PMID:6815271
A:Accession: S07456
A:Molecule type: protein
A:Residues: 1-46 <ROC>
A:Cross-references: UNIPARC:UPI0000176D8D
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match          96.3%; Score 78; DB 2; Length 46;
Best Local Similarity 93.8%; Pred. No. 1.7e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSNGNTYLQ 16
Db 24 RSSQSIVHSNGNTYLE 39

RESULT 4
S25463
IG kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S25463
R:Monestier, M.; Fasy, T.M.; Losman, M.J.; Novick, K.E.; Muller, S.
submitted to the EMBL Data Library, July 1992
A:Description: Structure and binding properties of monoclonal antibodies to core histone
A:Reference number: S25174
A:Accession: S25463
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-91 <MON>
A:Cross-references: UNIPARC:UPI00001160C6; EMBL:X67624; NID:952189; PIDN:CAA47882.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match          96.3%; Score 78; DB 2; Length 91;
Best Local Similarity 93.8%; Pred. No. 3.5e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSNGNTYLQ 16
Db 24 RSSQSIVHSNGNTYLE 39

RESULT 5
S24502
IG kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S24502
R:Kaartinen, M.
submitted to the EMBL Data Library, October 1991
A:Reference number: S24490
A:Accession: S24502
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-93 <KAA>
A:Cross-references: UNIPROT:Q99M37; UNIPARC:UPI0000176B20; EMBL:X66639
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:10-89/Domain: immunoglobulin homology <IMM>
```

```
Query Match          96.3%; Score 78; DB 2; Length 93;
Best Local Similarity 93.8%; Pred. No. 3.5e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSNGNTYLQ 16
Db 18 RSSQSIVHSNGNTYLE 33

RESULT 6
S24504
IG kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S24504
R:Kaartinen, M.
submitted to the EMBL Data Library, October 1991
A:Reference number: S24490
A:Accession: S24504
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-99 <KAA>
A:Cross-references: UNIPROT:Q99M37; UNIPARC:UPI0000176B19; EMBL:X66641
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>
```

```
Query Match          96.3%; Score 78; DB 2; Length 99;
Best Local Similarity 93.8%; Pred. No. 3.8e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSNGNTYLQ 16
Db 24 RSSQSIVHSNGNTYLE 39

RESULT 7
S24501
IG kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S24501
R:Kaartinen, M.
submitted to the EMBL Data Library, October 1991
A:Reference number: S24490
A:Accession: S24501
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-99 <KAA>
A:Cross-references: UNIPROT:Q99M37; UNIPARC:UPI0000176B17; EMBL:X66638
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>
```

```
Query Match          96.3%; Score 78; DB 2; Length 99;
Best Local Similarity 93.8%; Pred. No. 3.8e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSNGNTYLQ 16
Db 24 RSSQSIVHSNGNTYLE 39

RESULT 8
S11126
IG kappa chain V region (clone NQ2-45.1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 19-Mar-1997 #sequence_revision 23-Aug-1997 #text_change 23-Aug-1997
C:Accession: S11126
R:Kaartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.
Nature 304, 320-324, 1983
A:Title: mRNA sequences define an unusually restricted IgG response to 2-phenylloxazolone
A:Reference number: S07331; MUID:83271467; PMID:6877353
```

A;Accession: S1126
A;Molecule type: mRNA
A;Residues: 1-101 <NAT>
A;Cross-References: UNIPARC:UPI000017658F
C;Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 96.3%; Score 78; DB 2; Length 101;
Best Local Similarity 93.8%; Pred. No. 3.9e-06;
Matches 15; Conservative 1; Mismatches 0; Indels

Qy 1 RSSQSI VHSNGNTYLQ 16
|||
Dp 24 RSSQSI VHSNGNTYLE 39
|||

RESULT 9

I14590
 Ig kappa chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
 C:Accession: S14590 #S14589
 R:Chen, Q.; Stenzel-Poore, M.; Rittenberg, M.B.
 Submitted to the EMBL Data Library, March, 1991.
 A:Description: Natural polyreactive antibodies differ from Ag-induced antibodies in VH Q
 A:Reference number: S14484
 A:Accession: S14590
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-102 <CHE>
 A:Cross-references: UNIPARC:UPT0000115F40; EMBL:X58662; NID:g52927; PIDN:CAA41519.1; PID
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 96.3%; Score 78; DB 2; Length 102;
Best Local Similarity 93.8%; Pred. No. 3.9e-06;
Matches 15; Conservative 1; Mismatches 0; Indels

Qy 1 RSSQSIVHSNGNTYLQ 16
|||
Db 24 RSSQSIVHSNGNTYLE 39
|||

RESIST 10

PH1042
IG light chain V region (clone 202.s38) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: PH1042
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marlon, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and Igg anti-DNA antibodies are the products of clonally selective B C
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH1042
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-103 <TIL>
A:Cross-references: UNIPROT:Q9NM37; UNIPARC:UPI0000176AA4
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 96.3%; Score 78; DB 2; Length 103;
Best Local Similarity 93.8%; Pred. No. 4e-06;
Matches 15; Conservative 1; Mismatches 0; Indels

Qy 1 RSSQSIVHSNGNTYLQ 16
24 RSSQSIVHSNGNTYLE 39
Db

DEBIT 11

PH1043
Ig light chain V region (clone 111.68) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: PH1043
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH1043
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-103 <TIL>
A:Cross-references: UNIPROT:Q99M37; UNIPARC:UPI0000176AA5
A:Experimental source: B cell, strain [NZB x NZW] F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
P:16-95/Domain: immunoglobulin homology <IMM>

Query Match 96.3%; Score 78; DB 2; Length 103;
Best Local Similarity 93.8%; Pred. No. 4e-06;
Matches 15: Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSNGNTYLQ 16
|||
Db 24 RSSQSIVHSNGNTYLE 39

RESIT.T 12

S26335
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C:Accession: S26335
R:Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protein e
A:Reference number: S26309; MUID:91341421; PMID:1908510
A:Accession: S26335
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-110 <STA>
A:Cross-references: UNIPARC:UPI0000115F78; EMBL:X59183; NID:G52314; PIDN:CAA41893.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
P:16-95/Domain: immunoglobulin homology <IMM>

Query Match	96.3%	Score 78;	DB 2;	Length 110;
Best Local Similarity	93.8%	Pred. No. 4.2e-06;		
Matches 15:	Conservative	1;	Mismatches 0;	Indels 0;
				Gaps 0;

Qy 1 RSSQSIVHSNGNTYLQ 16
|||
24 RSSQSIVHSNGNTYLQ 39
|||

REC'D T 13

F27887
 Ig kappa chain V region (HIC5-4D1) - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
 C:Accession: F27887
 R:Caton, A. J.; Brownlee, G. G.; Staudt, L. M.; Gerhard, W.
 EMBO J. 5, 1577-1587, 1986
 A>Title: Structural and functional implications of a restricted antibody response to a c
 A:Reference number: A91043; MUID:86300658; PMID:2427335
 A:Accession: F27887

C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 96.3%; Score 78; DB 2; Length 112;
Best Local Similarity 93.8%; Pred. No. 4.3e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSNGNTYLQ 16
|||
Db 24 RSSQSIVHSNGNTYLE 39

RESULT 14

A31807
IG kappa chain V region (PAC1) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Jul-1989 #sequence_revision 20-Jul-1989 #text_change 09-Jul-2004
C;Accession: A31807
R;Taub, R.; Gould, R.J.; Garsky, V.M.; Ciccarone, T.M.; Hoxie, J.; Friedman, P.A.; Shatt
J. Biol. Chem. 264, 259-265, 1989
A;Title: A monoclonal antibody against the platelet fibrinogen receptor contains a sequ
A;Reference number: A31807; MUID:89079661; PMID:2909518
A;Accession: A31807
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-112 <TAU>
A;Cross-references: UNIPROT:Q99M37; UNIPARC:UPI00001424F9
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 96.3%; Score 78; DB 2; Length 112;
Best Local Similarity 93.8%; Pred. No. 4.3e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSNGNTYLQ 16
|||
Db 24 RSSQSIVHSNGNTYLE 39

RESULT 15

PL0203
anti-DNA autoantibody BV17-31, kappa chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C;Accession: PL0203
R;Smith, R.G.; Voss Jr., E.W.
Mol. Immunol. 27, 463-470, 1990
A;Title: Variable region primary structures of monoclonal anti-DNA autoantibodies from N
A;Reference number: PL0198; MUID:90309768; PMID:2114528
A;Accession: PL0203
A;Molecule type: mRNA
A;Residues: 1-113 <SMI>
A;Cross-references: UNIPARC:UPI0000113786; GB:X53643; NID:G50196; PIDN:CRAA37694.1; PID:G
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-95/Domain: immunoglobulin homology <IMM>
F;24-39/Region: complementarity-determining 1
F;55-61/Region: complementarity-determining 2
F;94-102/Region: complementarity-determining 3
F;101-113/Region: D region

Query Match 96.3%; Score 78; DB 2; Length 113;
Best Local Similarity 93.8%; Pred. No. 4.4e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSNGNTYLQ 16
|||
Db 24 RSSQSIVHSNGNTYLE 39

Search completed: December 30, 2005, 13:34:52
Job time : 23.7097 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:11:26 ; Search time 144 Seconds
(without alignments)

78.392 Million cell updates/sec

Title: US-10-735-916A-2

Perfect score: 81

Sequence: 1 RSSQSIHNGNTVLQ 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	91.4	113	1 KV2G MOUSE	P01631 mus musculus
2	74	91.4	115	2 QSF2IO MOUSE	Q5f2i0 mus musculus
3	72	88.9	248	2 Q5ZQ7 9MURI	Q5zq7 mus sp. b3(
4	71	87.7	219	2 Q5ZC0 MOUSE	Q5zco mus musculus
5	68	84.0	239	2 Q6P491 HUMAN	Q6p491 homo sapien
6	67	82.7	113	1 KV2F MOUSE	P01630 mus musculus
7	63	77.8	86	2 Q7Z3V5 HUMAN	Q7z3v5 homo sapien
8	63	77.8	133	1 KV2F HUMAN	P06310 homo sapien
9	62	76.5	239	2 Q38E08 MOUSE	Q38e08 mus musculus
10	61	75.3	112	2 Q5LEM8 MOUSE	Q5lem8 mus musculus
11	60	74.1	239	2 Q8TCD0 HUMAN	Q8tcd0 homo sapien
12	58	71.6	112	2 Q53VP8 MOUSE	Q53vp8 mus musculus
13	58	71.6	113	1 KV2E MOUSE	P03976 mus musculus
14	58	71.6	114	2 Q9UL80 HUMAN	Q9ul80 homo sapien
15	58	71.6	117	1 KV2B HUMAN	P06309 homo sapien
16	57	70.4	113	1 KV2B HUMAN	P01615 homo sapien
17	56	69.1	234	2 Q5XKG4 MOUSE	Q5xkg4 mus musculus
18	54	66.7	240	2 Q6PIH6 HUMAN	Q6pih6 homo sapien
19	53	65.4	239	2 Q8NEK0 HUMAN	Q8nek0 homo sapien
20	52	64.2	113	1 KV2D HUMAN	P01617 homo sapien
21	49	60.5	202	2 Q86IX8 DICDI	Q86ix8 dictyosteli
22	46.5	57.4	115	1 KV2A HUMAN	P01614 homo sapien
23	46	56.8	112	1 KV2A MOUSE	P01626 mus musculus
24	46	56.8	113	1 KV2C MOUSE	P01628 mus musculus
25	46	56.8	120	1 KV2B MOUSE	P01627 mus musculus
26	46	56.8	172	2 Q8PR28 XANAC	Q8pr28 xanthomonas
27	46	56.8	2738	2 Q5EN26 DEBHA	Q5en26 debaryomyce
28	45	55.6	393	2 Q4PDR3 USTMA	Q4pdr3 ustilago ma
29	45	55.6	771	2 Q5AVM5 DICDI	Q5avm5 dictyosteli
30	45	55.6	1976	2 Q7NAT4 MYCGLA	Q7nat4 mycoplasma
31	44	54.3	302	2 Q7Y106 9LAMI	Q7y106 antirrhinum

32	44	54.3	448	2	Q8A7N7 BACTN	Q8a7n7 bacteroides
33	44	54.3	480	2	Q9LRN2 ARATH	Q9lrn2 arabidopsis
34	44	54.3	2399	2	Q9ZKS9 HELPJ	Q9zks9 helicobacte
35	44	54.3	2529	2	Q25579 HELPY	Q25579 helicobacte
36	43.5	53.7	647	2	Q68895 CHDEL	Q68895 chlorella e
37	43	53.1	118	2	Q08922 MOUSE	Q08922 mus musculu
38	43	53.1	283	2	Q8EHQ2 SHEON	Q8ehq2 shewanella
39	43	53.1	318	2	Q6V4Z7 SCHMA	Q6v4z7 schistosoma
40	43	53.1	327	2	Q26703 TRYBR	Q26703 trypanosoma
41	43	53.1	438	2	Q4W58 ASPFU	Q4w58 aspergillus
42	43	53.1	873	2	Q95V81 DROME	Q95v81 drosophila
43	43	53.1	882	2	Q7YU02 DROME	Q7yu02 drosophila
44	43	53.1	1409	2	Q4QGZ6 LEIMA	Q4qgz6 leishmania
45	43	53.1	1643	2	Q96244 PLAF7	Q96244 plasmodium

ALIGNMENTS

RESULT 1

KV2G MOUSE ID KV2G MOUSE STANDARD; PRT; 113 AA.

AC P01631;
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-II region 26-10.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=83178921; PubMed=6404298;
RA Novotny J., Margolies M.N.;
RT "Amino acid sequence of the light chain variable region from a mouse
anti-digoxin hybridoma antibody."
RL Biochemistry 22:1153-1158(1983).
CC -1- MISCELLANEOUS: This chain was isolated from an IgG2a hybridoma
protein that binds digoxin.

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the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.

CC PIR: A01914; KWS26.
DR HSP; Q99M37; 1191.
DR Ensembl; ENSMUSG0000055315; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Hybridoma; Immunoglobulin domain;
KW Immunoglobulin v region; Monoclonal antibody.
FT REGION 1 23
FT REGION 24 39
FT REGION 40 54
FT REGION 55 61
FT REGION 62 93
FT REGION 94 102
FT REGION 103 112
FT DISULFID 23 93
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12273 MW; F9F39CE949A84C2A CRC64;

Query Match 91.4%; Score 74; DB 1; Length 113;
Best Local Similarity 93.3%; Pred. No. 5.2e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIHVHNGNTYL 15
 |||||:|||||||
 Db 24 RSSQSLVHNGNTYL 38

RESULT 2

Q5F210 MOUSE
 ID Q5F210 MOUSE PRELIMINARY; PRT; 115 AA.
 AC Q5F210;
 DT 10-MAY-2005 (T-EMBLrel. 30, Created)
 DT 10-MAY-2005 (T-EMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (T-EMBLrel. 30, Last annotation update)
 DE Kappa light chain variable region (Fragment).
 GN Name=IgG1 anti-TS1 VL;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Erlandsson A., Holm P., Ullen A., Stigbrand T., Sundstrom B.E.;
 RT "Studies of the interactions between the anticytokerin 8 monoclonal
 antibody TS1, its antigen and its anti-idiotypic antibody alphats1.";
 RL J. Mol. Recognit. 16:157-163 (2003).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Erlandsson A.;
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
 DR ENBL; AJ884575; CA156337.1; -; mRNA.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR Pfam; PF07686; V-set; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 FT NON_TER 1
 FT NON_TER 115
 SQ SEQUENCE 115 AA; 12560 MW; E4D3BF3D63E88007 CRC64;

Query Match 91.4%; Score 74; DB 2; Length 115;
 Best Local Similarity 93.3%; Pred. No. 5.3e-05;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIHVHNGNTYL 15
 |||||:|||||||
 Db 24 RSSQSLVHNGNTYL 38

RESULT 3

Q65ZQ7_9MURI
 ID Q65ZQ7_9MURI PRELIMINARY; PRT; 248 AA.
 AC Q65ZQ7;
 DT 25-OCT-2004 (T-EMBLrel. 28, Created)
 DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
 DE B3(Fv)-PE40 (Fragment).
 GN Name=B3(Fv)-PE40;
 OS Mus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10095;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA MEDLINE=92020904; PubMed=1924323;
 RA Brinkmann U., Pai L.H., FitzGerald D.J., Willingham M., Pastan I.;
 RT "B3(Fv)-PE38KDEL, a single-chain immunotoxin that causes complete
 regression of a human carcinoma in mice."
 RL Proc. Natl. Acad. Sci. U.S.A. 88:8616-8620 (1991).
 DR ENBL; S57990; BAB19971.2; -; mRNA.
 DR SNR; Q65ZQ7; 4-247.

DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00406; IGV; 2.
 DR PROSITE; PSS0835; IG_LIKE; 2.
 FT NON_TER 248
 SQ SEQUENCE 248 AA; 26634 MW; 7A3759B43E570950 CRC64;

Query Match 88.9%; Score 72; DB 2; Length 248;
 Best Local Similarity 87.5%; Pred. No. 0.0003;
 Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSSQSIHVHNGNTYLQ 16
 |||||:|||||||
 Db 159 RSSQIIVHNGNTYLE 174

RESULT 4

Q65ZC0 MOUSE
 ID Q65ZC0 MOUSE PRELIMINARY; PRT; 219 AA.
 AC Q65ZC0;
 DT 25-OCT-2004 (T-EMBLrel. 28, Created)
 DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
 DE Kappa light chain C region (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Balb/c; TISSUE=Spleen;
 RX MEDLINE=96319505; PubMed=8768802;
 RA Kipp B., Schlaak M., Becker W.M.;
 RT "Cloning and expression of a recombinant mouse Fab-fragment
 recognizing a defined linear epitope of Chironomus thummi major
 allergen Chi t 1.";
 RL Int. Arch. Allergy Immunol. 110:348-353 (1996).
 DR ENBL; Z37459; CA385724.1; -; mRNA.
 DR SMR; Q65ZC0; 1-219.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; IG_c1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IGV.
 DR Pfam; PF07654; C1-set; 1.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGV; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 2.
 DR PROSITE; PSS0290; IG_MHC; 1.
 FT NON_TER 1
 FT NON_TER 219
 SQ SEQUENCE 219 AA; 23944 MW; 7E1B82A14EAF8445 CRC64;

Query Match 87.7%; Score 71; DB 2; Length 219;
 Best Local Similarity 86.7%; Pred. No. 0.00039;
 Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIHVHNGNTYL 15
 |||||:|||||||
 Db 24 RSSQSLVHNGNTYL 38

RESULT 5

Q6P491 HUMAN
 ID Q6P491 HUMAN PRELIMINARY; PRT; 239 AA.
 AC Q6P491;
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)

DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skin;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haie F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences".
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC063599; AAH63599.1; -, mRNA.
DR HSSP; P01837; 1KCU.
DR SMR; Q6P491; 21-237.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; Ig-2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE. 239 AA; 26245 MW; CD7313DDPFD358B3 CRC64;

Query Match 84.0%; Score 68; DB 2; Length 239;
Best Local Similarity 80.0%; Pred. No. 0.0015;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Oy 1 RSSQSIVHSNGNTYL 15
|||:|:|||||
Db 44 RSSESLLHSNGNTYL 58

RESULT 6
KV2F MOUSE STANDARD; PRT; 113 AA.
AC P01630;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-II region 7S34.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=83256427; PubMed=6409088;
RA Chang J.-Y., Herbst H., Aebersold R., Braun D.G.;
RT "A new isotype sequence (V kappa 27) of the variable region of kappa-
RT light chains from a mouse hybridoma-derived anti-(streptococcal group
RT A polysaccharide) antibody containing an additional cysteine residue.
RT Application of the dimethylaminobenzene isothiocyanate technique
RT for the isolation of peptides".
RL Biochem. J. 211:173-180 (1983).
CC -1- MISCELLANEOUS: This chain is from a hybridoma-derived monoclonal
CC antibody against the streptococcal group A polysaccharide.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC removed.
CC -----
CC PIR; A01913; KWS7S.
DR HSSP; Q99M37; 1191.
DR SMR; P01630; 1-113.
DR Ensembl; ENSMUSG0000061260; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
DR Direct protein sequencing; Hybridoma; Immunoglobulin domain;
KW Immunoglobulin V region; Monoclonal antibody.
FT REGION 1 23 Framework-1.
FT REGION 24 39 Complementarity-determining-1.
FT REGION 40 54 Framework-2.
FT REGION 55 61 Complementarity-determining-2.
FT REGION 62 93 Framework-3.
FT REGION 94 102 Complementarity-determining-3.
FT REGION 103 112 Framework-4.
FT DISULFID 23 93 By similarity.
FT NON TER 113 113
SQ SEQUENCE 113 AA; 12496 MW; 42C019D10ADA3C91 CRC64;
Query Match 82.7%; Score 67; DB 1; Length 113;
Best Local Similarity 80.0%; Pred. No. 0.00092;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Oy 1 RSSQSIVHSNGNTYL 15
|||:|:|||||
Db 24 RSSKSLLHSNGNTYL 38

RESULT 7
Q7Z3Y5 HUMAN PRELIMINARY; PRT; 86 AA.
ID Q7Z3Y5 HUMAN PRELIMINARY; PRT; 86 AA.
AC Q7Z3Y5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Rearranged VKA17 V gene segment (Fragment).
GN Name=VKAL17;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Hodgkin lymphoma;
RA Tinguely M., Rosenquist R., Sundstroem C., Amini R.M., Kuppers R.,
RA Hansmann M.L., Brauning A.,
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ564426; CAD92033.1; -, Genomic DNA.
DR HSSP; P01625; 1EEQ.
DR SMR; Q7Z3Y5; 1-80.

DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1 86
FT NON_TER 86
SQ SEQUENCE 86 AA; 9764 MW; D198FC04FE0C78FD CRC64;

Query Match 77.8%; Score 63; DB 2; Length 86;
Best Local Similarity 80.0%; Pred. No. 0.0034;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSVHSGNGNTYL 15
Db 3 RSSQSLVSDGNTYL 17
|||||:|:|:|

RESULT 8
KV2F_HUMAN STANDARD; PRT; 133 AA.
AC P06310;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-II region RPMI 6410 precursor.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86041852; PubMed=2997711;
RA Klobbeck H.G., Weindl A., Combratio G., Solomon A., Zachau H.G.;
RT "Human immunoglobulin kappa light chain genes of subgroups II and III";
RL Nucleic Acids Res. 13:6499-6513 (1985).
CC -----
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CC removed.

CC -----
CC EMBL; Z00020; CAA77315.1; -; Genomic_DNA.
DR PIR; A01890; K2HURP.
DR HSSP; Q99M37; 1191.
DR SMR; P06310; 21-133.
DR Ensembl; ENSG00000173758; Homo sapiens.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 133 Ig kappa chain V-II region RPMI 6410.
FT REGION 21 43 Framework-1.
FT REGION 44 59 Complementarity-determining-1.
FT REGION 60 74 Framework-2.
FT REGION 75 81 Complementarity-determining-2.
FT REGION 82 113 Framework-3.
FT REGION 114 122 Complementarity-determining-3.
FT REGION 123 132 Framework-4.
FT DISULFID 43 113 By similarity.
FT NON_TER 133
SQ SEQUENCE 133 AA; 14707 MW; 513CCAF3673009EE CRC64;

Query Match 77.8%; Score 63; DB 1; Length 133;
Best Local Similarity 80.0%; Pred. No. 0.0057;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSVHSGNGNTYL 15
Db 44 RSSQSLVSDGNTYL 58
|||||:|:|:|

RESULT 9
Q58EUB_MOUSE PRELIMINARY; PRT; 239 AA.
AC Q58EUB;
DT 10-MAY-2005 (TREMBlrel. 30, Created)
DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
DE Igk-C protein.
GN Name=Igk-C;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
RC Expression driven by an MMTV-LTR enhancer.;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.

RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
RC Expression driven by an MMTV-LTR enhancer.;
RG NIH MGC Project;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC091750; AAH91750.1; -; mRNA.
DR SMR; Q58EUB; 21-239.
DR GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 239 AA; 26302 MW; 98FC4BA8EB404215 CRC64;

Query Match 76.5%; Score 62; DB 2; Length 239;
Best Local Similarity 73.3%; Pred. No. 0.017;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;


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Qy 1 RSSQSIHVHNGNTYL 15
Db 44 KSSQSLHNSGNTYL 58

RESULT 10
O6LEMB_MOUSE PRELIMINARY; PRT; 112 AA.
AC O6LEMB;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22267451; PubMed=12379368; DOI=10.1016/S0022-1759(02)00242-9;
RA Hifumi E., Mitsuda Y., Ohara K., Uda T.;
RT "Targeted destruction of the HIV-1 coat protein gp41 by a catalytic
RT antibody light chain."
RL J. Immunol. Methods 269:283-298(2002).
DR EMBL; D85104; BAD00151.1; -; mRNA.
DR HSSP; P01820; IAYO.
DR SMR; O6LEMB; 1-112.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Hypothetical protein.
FT NON_TER 1
FT NON_TER 112
FT NON_TER 112
SQ SEQUENCE 112 AA; 12443 MW; BAD3E14B90BCF122 CRC64;

Query Match 75.3%; Score 61; DB 2; Length 112;
Best Local Similarity 73.3%; Pred. No. 0.011;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIHVHNGNTYL 15
Db 24 RSSKSLHNSGNTYL 38

RESULT 11
Q8TCD0_HUMAN PRELIMINARY; PRT; 239 AA.
AC Q8TCD0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
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RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Heiton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX TISSUE=Lung;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1598223;
RA Hirabayashi Y., Munakata Y., Sasaki T., Sano H.;
RT "Variable regions of a human anti-DNA antibody O-81 possessing lupus
RT nephritis-associated idiotype."
RL Nucleic Acids Res. 20:2601-0(1992).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1551402;
RA Lautner-Rieske A., Huber C., Meindl A., Pargent W., Schable K.F.,
RA Thiele R., Zocher I., Zachau H.G.;
RT "The human immunoglobulin kappa locus. Characterization of the
RT duplicated A regions."
RL Eur. J. Immunol. 22:1023-1029(1992).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=8258341;
RA Klein R., Jaenichen R., Zachau H.G.;
RT "Expressed human immunoglobulin kappa genes and their hypermutation."
RL Eur. J. Immunol. 23:3248-3262(1993).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=8436174;
RA Wagner S.D., Luzzatto L.;
RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are
RT distributed over a large portion of the V kappa locus and do not show
RT somatic mutation."
RL Eur. J. Immunol. 23:391-397(1993).
DR EMBL; BC022362; AAH22362.1; -; mRNA.
DR PIR; S22658; S22658.
DR PIR; S34095; S34095.
DR PIR; S40324; S40324.
DR PIR; S40374; S40374.
DR PIR; S42267; S42267.
DR PIR; S42268; S42268.
DR HSSP; P01834; I172.
DR SMR; Q8TCD0; 21-237.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_ch.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 239 AA; 26235 MW; FAGEDC3A3B03871D CRC64;

Query Match 74.1%; Score 60; DB 2; Length 239;
Best Local Similarity 73.3%; Pred. No. 0.039;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIHVHNGNTYL 15
Db 44 RSTQSLVSDGNTYL 58
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RESULT 12
Q53VP8 MOUSE
ID Q53VP8_MOUSE PRELIMINARY; PRT; 112 AA.
AC Q53VP8_MOUSE
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DE Kappa chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86136012; PubMed=3937730;
RA Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
RT "The idiotypic network and the internal image: possible regulation of
RT a germ-line network by paucigenic encoded Ab2 (anti-idiotypic)
RT antibodies in the GAT system.";
RL EMBO J. 4:3681-3688(1985).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 108-109.
RA Fougereau M.;
RL Submitted (NOV-1986) to the EMBL/GenBank/DBJ databases.
DR EMBL; X03386; CAA27113.1; -; mRNA.
FT NON_TER 1 1
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 12266 MW; C844B7881A99C18A CRC64;

Query Match 71.6%; Score 58; DB 2; Length 112;
Best Local Similarity 81.2%; Pred. No. 0.036;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGTYLQ 16
Db 24 RSSQSIVSNGFTYLE 39

RESULT 13
KV2E_MOUSE
ID KV2E_MOUSE STANDARD; PRT; 113 AA.
AC P03976;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-II region 17S29.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Hybridoma;
RX MEDLINE=85128968; PubMed=6441768;
RA Hebersold R., Herbet H., Grutter T., Chang J.Y., Braun D.G.;
RT "Murine V kappa 25 and V kappa 27 amino-acid sequences of C57B1/6
RT origin: monoclonal antibodies 17S29.1 and 22S25.1 specific for the
RT group A-streptococcal polysaccharide.";
RL Hoppe-Seyler's Z. Physiol. Chem. 365:1375-1383(1984).
CC -!- FUNCTION: Anti-streptococcal group A carbohydrate antibody.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR; A01912; KWSM17.
DR HSP; Q99M37; I191.
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DR SMR; P03976; 1-113.
DR Ensembl; ENSMUSG00000055315; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Hybridoma; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23
FT REGION 24 39
FT REGION 40 54
FT REGION 55 61
FT REGION 62 93
FT REGION 94 102
FT REGION 103 112
FT DISULFID 23 93
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12390 MW; 4E93797046F8DB33 CRC64;

Query Match 71.6%; Score 58; DB 1; Length 113;
Best Local Similarity 73.3%; Pred. No. 0.037;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGTYL 15
Db 24 RSSKSLHSHNGITYL 38

RESULT 14
Q9UL80_HUMAN
ID Q9UL80_HUMAN PRELIMINARY; PRT; 114 AA.
AC Q9UL80;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1322670;
RA Stuber F., Lee S.K., Bridges S.L. Jr, Koopman W.J., Schroeder H.W. Jr,
RA Gaskin F., Fu S.M.;
RT "A rheumatoid factor from a normal individual encoded by VH2 and V
RL Arthritis Rheum. 35:900-904(1992).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=8436174;
RA Wagner S.D., Luzzatto L.;
RT "v kappa gene segments rearranged in chronic lymphocytic leukemia are
RT distributed over a large portion of the v kappa locus and do not show
RT somatic mutation.";
RL Eur. J. Immunol. 23:391-397(1993).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1601042;
RA Huber C., Klobeck H.G., Zachau H.G.;
RT "Ongoing v kappa-J kappa recombination after formation of a productive
RT v kappa-J kappa coding joint.";
RL Eur. J. Immunol. 22:1561-1565(1992).
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DR EMBL; AF035034; AAD56270.1; -; mRNA.
DR PIR; B49002; B49002.
DR PIR; S23638; S23638.
DR PIR; S34094; S34094.
DR PIR; S34095; S34095.
DR HSP; P01625; ILVE.
DR SMR; Q9UL80; 1-114.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
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Best Local Similarity 80.0%; Pred. No. 0.037;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Db |||||:|:|||||
24 RSSQSPVSDGNTYL 38

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ID KV2E_HUMAN STANDARD; PRT; 117 AA.
AC P06309;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-II region GM607 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=84191506; PubMed=6325927;
RA Klobek H.G., Solomon A., Zachau H.G.;
RT "Contribution of human V kappa II germ-line genes to light-chain
diversity.";
RL Nature 309:73-76(1984).
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; Z00009; -; NOT_ANNOTATED_CDS; Genomic_DNA.
DR PIR; A01889; K2HUGM.
DR HSSP; Q99M37; 1I91.
DR SMR; P06309; 5-117.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL <1 4
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FT REGION 5 27 Framework-1.
FT REGION 28 43 Complementarity-determining-1.
FT REGION 44 58 Framework-2.
FT REGION 59 65 Complementarity-determining-2.
FT REGION 66 97 Framework-3.
FT REGION 98 106 Complementarity-determining-3.
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FT DISULFID 27 97 By similarity.

FT NON TER 1
FT NON TER 117
SQ SEQUENCE 117 AA; 12664 MW; 92C57DC719E558B1 CRC64;

Query Match 71.6%; Score 58; DB 1; Length 117;
Best Local Similarity 73.3%; Pred. No. 0.038;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Db |||||:|:|||||
28 RSSQSILHSGNTYL 42

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Title: US-10-735-916A-2

Perfect score: 81

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Maximum DB seq length: 16

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	78	96.3	16	1	US-08-129-930B-30
4	78	96.3	16	2	US-08-134-346A-17
5	78	96.3	16	2	US-08-976-288A-30
6	78	96.3	16	2	US-10-226-795-28
7	78	96.3	16	2	US-09-947-839B-30
8	76	93.8	16	2	US-08-563-222C-29
9	74	91.4	16	1	US-08-244-626-4
10	74	91.4	16	2	US-09-914-695-20
11	74	91.4	16	2	US-09-518-737-8
12	73	90.1	16	1	US-08-560-558E-29
13	70	86.4	16	2	US-09-724-409-3
14	70	86.4	16	2	US-09-724-530-3
15	70	86.4	16	2	US-09-328-296-3
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20	67	82.7	16	1	US-08-438-123-1
21	61	75.3	16	2	US-09-406-532-18
22	61	75.3	16	2	US-09-563-222C-8
23	51	63.0	16	1	US-08-672-345C-43
24	51	63.0	16	2	US-09-214-095D-43
25	51	63.0	16	2	US-09-940-727B-43
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Sequence 515, App

ALIGNMENTS

RESULT 1
US-08-053-171-27
; Sequence 27, Application US/08053171
; Patent No. 5562903
; GENERAL INFORMATION:
; APPLICANT: Co, Loibner
; TITLE OF INVENTION: Antibody Derivatives
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,171
; FILING DATE: 22-APR-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-54-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEetical: NO
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..16
; OTHER INFORMATION: /note= "First
; OTHER INFORMATION: complementarity-determining region (CDR1) of
; OTHER INFORMATION: BR55-1 antibody light chain"
US-08-053-171-27

Query Match 96.3%; Score 78; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 4e-06;
Matches 15; Conservative 1; Mismatches 0; Gaps 0;

QY 1 RSSQSIHNSNGNTYLQ 16
Db 1 RSSQSIHNSNGNTYLE 16

RESULT 2

US-07-977-696C-30
; Sequence 30, Application US/07977696C
; Patent No. 5792852
; GENERAL INFORMATION:
; APPLICANT: do Couto, Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides with Specificity
; TITLE OF INVENTION: for Carcinomas and Kit and Diagnostic Vaccination
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/977,696C
; FILING DATE: 11-16-92
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel Ph.D., Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P66 38227
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 748-6868
; TELEFAX: (510) 748-6688
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-977-696C-30

Query Match 96.3%; Score 78; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 4e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIHNSNGNTYLQ 16
Db 1 RSSQSIHNSNGNTYLE 16

RESULT 3

US-08-129-930B-30
; Sequence 30, Application US/08129930B
; Patent No. 5804187
; GENERAL INFORMATION:
; APPLICANT: do Couto Dr., Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides With Broad
; TITLE OF INVENTION: Carcinoma Specificity, and Kit and
; TITLE OF INVENTION: Diagnostic Vaccination and
; TITLE OF INVENTION: Therapeutic Methods
; NUMBER OF SEQUENCES: 96

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: V. AMZEL & ASSOC.
; STREET: 2055 No. 5804187th Broadway, Suite 201
; CITY: Walnut Creek
; STATE: California
; COUNTRY: USA
; ZIP: 94596
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/129,930B
; FILING DATE: September 30, 1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel Ph.D., Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: CRPCC-008A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 521-1333
; TELEFAX: (510) 521-3541
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-129-930B-30

Query Match 96.3%; Score 78; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 4e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIHNSNGNTYLQ 16
Db 1 RSSQSIHNSNGNTYLE 16

RESULT 4

US-08-134-346A-17
; Sequence 17, Application US/08134346A
; Patent No. 6281335
; GENERAL INFORMATION:
; APPLICANT: do Couto, F.J.R.
; APPLICANT: Ceriani, R.L.C.
; APPLICANT: Petersen, J.A.
; TITLE OF INVENTION: HYBRIDOMA AND ANTI-KC-4 HUMANIZED
; TITLE OF INVENTION: MONOCLONAL ANTIBODY AND DNA AND RNA
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ostrager, Chong & Flaherty
; STREET: 300 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10022-7499

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette-3.50 inch, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/134,346A
; FILING DATE: 08-OCT-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Onofrio, Dara L.
; REGISTRATION NUMBER: 34,889
; REFERENCE/DOCKET NUMBER: CLT 149,608

TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-826-6565
TELEFAX: 212-826-5909
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-134-346A-17

Query Match 96.3%; Score 78; DB 2; Length 16;
Best Local Similarity 93.8%; Pred. No. 4e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGNTYLQ 16
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Db 1 RSSQSIVHSGNGNTYLE 16

RESULT 5

US-08-976-288A-30
Sequence 30, Application US/08976288A
Patent No. 6315997

GENERAL INFORMATION:

APPLICANT: do Couto Dr., Fernando J.R.
APPLICANT: Ceriani Dr., Roberto L.
APPLICANT: Peterson Dr., Jerry A.
APPLICANT: Padlan Dr., Eduardo A.
TITLE OF INVENTION: Analogue Peptides with Broad
TITLE OF INVENTION: Carcinoma Specificity, and Kit and
TITLE OF INVENTION: Diagnostic Vaccination and
TITLE OF INVENTION: Therapeutic Methods
NUMBER OF SEQUENCES: 96

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pretty, Schroeder & Poplawski
STREET: 444 South Flower St., 19th Floor
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/976,288A
FILING DATE: No. 6315997ember 21, 1997

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/129,930
FILING DATE: September 30, 1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/977,696
FILING DATE: No. 6315997ember 16, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Viviana Amzel Ph.D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P6639938

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
TELEX: n.a.

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-976-288A-30

Query Match 96.3%; Score 78; DB 2; Length 16;
Best Local Similarity 93.8%; Pred. No. 4e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGNTYLQ 16
|||||
Db 1 RSSQSIVHSGNGNTYLE 16

RESULT 6

US-10-226-795-28
Sequence 28, Application US/10226795
Patent No. 6875433

GENERAL INFORMATION:

APPLICANT: HART, MARY KATE
APPLICANT: WILSON, JULIE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND COMPLEMENTARITY-DETERMINING
TITLE OF INVENTION: REGIONS BINDING TO EBOLA GLYCOPROTEIN
FILE REFERENCE: ARMY 166
CURRENT APPLICATION NUMBER: US/10/226,795
CURRENT FILING DATE: 2002-11-18
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 28
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION:

Description of Artificial Sequence: Synthetic light

OTHER INFORMATION: chain of Mab EGP6D8-1-2 amino acid sequence

US-10-226-795-28

Query Match 96.3%; Score 78; DB 2; Length 16;
Best Local Similarity 93.8%; Pred. No. 4e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGNTYLQ 16
|||||
Db 1 RSSQSIVHSGNGNTYLE 16

RESULT 7

US-09-947-839B-30

Sequence 30, Application US/09947839B
Patent No. 6936706

GENERAL INFORMATION:

APPLICANT: do Couto, Fernando J.R.
Ceriani Dr., Roberto L.
Peterson Dr., Jerry A.
Padlan Dr., Eduardo A.

TITLE OF INVENTION: Analogue Peptides with Specificity
for Carcinomas and Kit and Diagnostic Vaccination
and Therapeutic Methods.

NUMBER OF SEQUENCES: 81

CORRESPONDENCE ADDRESS:

ADDRESSEE: V. Amzel & Assoc.

STREET: P.O.Box 159

CITY: Gladwyne

STATE: Pennsylvania

COUNTRY: USA

ZIP: 19035

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS 5.0

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/947,839B

FILING DATE: 06-Sep-2001

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Amzel Viviana

REGISTRATION NUMBER: 30,930

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/ REFERENCE/DOCKET NUMBER: CRFC-083
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 610-649-0609
/ TELEFAX: 240-359-0299
/ TELEX: n.a.
/ INFORMATION FOR SEQ ID NO: 30:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 16 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-947-839B-30

Query Match          96.3%; Score 78; DB 2; Length 16;
Best Local Similarity 93.8%; Pred. No. 4e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGTYLQ 16
Db 1 RSSQSIVHSGNGTYLE 16

RESULT 8
US-09-563-222C-29
; Sequence 29, Application US/09563222C
; Patent No. 6696620
; GENERAL INFORMATION:
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICHAEL B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT APPLICATION NUMBER: US/09/563,222C
; CURRENT FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 29
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-563-222C-29

Query Match          93.8%; Score 76; DB 2; Length 16;
Best Local Similarity 87.5%; Pred. No. 8.4e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGTYLQ 16
Db 1 RSSQSIVHSGNGTYLE 16

RESULT 9
US-08-244-626-4
; Sequence 4, Application US/08244626
; Patent No. 5502167
; GENERAL INFORMATION:
; APPLICANT: Walldmann, Herman
; APPLICANT: Walsh, Louise
; APPLICANT: Crowe, James Scott
; APPLICANT: Lewis, Alan Peter
; TITLE OF INVENTION: CDR GRAFTED HUMANISED CHIMERIC T-CELL
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth Street, N. W.
; CITY: Washington
; STATE: D. C.
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/ COUNTRY: USA
/ ZIP: 20004
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/244,626
/ FILING DATE: July 15, 1994
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/GB92/02251
/ FILING DATE: December 4, 1992
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Ernst, Barbara G.
/ REGISTRATION NUMBER: 30,377
/ REFERENCE/DOCKET NUMBER: 1808-153A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 783-6040
/ TELEFAX: (202) 783-6031
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 16 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-244-626-4

Query Match          91.4%; Score 74; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 1.8e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGTYL 15
Db 1 RSSQSIVHSGNGTYL 15

RESULT 10
US-09-914-695-20
; Sequence 20, Application US/09914695
; Patent No. 6706487
; GENERAL INFORMATION:
; APPLICANT: Abdel-Meguid, Sherin
; APPLICANT: Ho, Yen Sen
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Taylor, Alexander H.
; TITLE OF INVENTION: Recombinant IL-18 Antagonists Useful in
; FILE REFERENCE: P50897
; CURRENT APPLICATION NUMBER: US/09/914,695
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: PCT/US00/07349
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/125,299
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 20
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-914-695-20

Query Match          91.4%; Score 74; DB 2; Length 16;
Best Local Similarity 93.3%; Pred. No. 1.8e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGTYL 15
Db 1 RSSQSIVHSGNGTYL 15
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Db 1 RSSQSLVHNGNTFL 15

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RESULT 15
US-09-328-296-3
; Sequence 3, Application US/09328296
; Patent No. 6946129
; GENERAL INFORMATION:
; APPLICANT: Siegal, Clay
; APPLICANT: Wahl, Alan
; APPLICANT: Francisco, Joseph
; APPLICANT: Fell, H. Perry
; TITLE OF INVENTION: RECOMBINANT ANTI-CD40 ANTIBODY AND USES THEREOF
; FILE REFERENCE: 9632-005
; CURRENT APPLICATION NUMBER: US/09/328,296
; CURRENT FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-328-296-3

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Query Match 86.4%; Score 70; DB 2; Length 16;
 Best Local Similarity 86.7%; Pred. No. 7.7e-05;
 Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSLVHNGNTYL 15
 Db 1 RSSQSLVHNGNTFL 15

Search completed: December 30, 2005, 14:26:44
 Job time : 32.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:14:26 ; Search time 35.871 Seconds
(without alignments)
36.877 Million cell updates/sec

Title: US-10-735-916A-2

Perfect score: 81

Sequence: 1 RSSQSVHNGNYLQ 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: /cgm2_6/ptodata/1/iaa/PTUS COMB.pap.*
5: /cgm2_6/ptodata/1/iaa/RE COMB.pap.*
6: /cgm2_6/ptodata/1/iaa/backfiles.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	78	96.3	16	1	US-07-977-696C-30
3	78	96.3	16	1	US-08-129-930B-30
4	78	96.3	16	2	US-08-134-346A-17
5	78	96.3	16	2	US-08-976-288A-30
6	78	96.3	16	2	US-10-226-795-28
7	78	96.3	16	2	US-09-947-839B-30
8	78	96.3	100	2	US-09-840-459-26
9	78	96.3	100	2	US-09-840-459-28
10	78	96.3	100	2	US-09-497-625A-26
11	78	96.3	100	2	US-09-497-625A-28
12	78	96.3	110	2	US-10-114-716A-42
13	78	96.3	111	2	US-09-823-746-12
14	78	96.3	112	1	US-08-053-171-15
15	78	96.3	112	1	US-08-752-844-15
16	78	96.3	112	1	US-08-888-366-16
17	78	96.3	112	1	US-08-591-196-15
18	78	96.3	112	2	US-08-815-190A-14
19	78	96.3	112	2	US-09-293-533-15
20	78	96.3	112	2	US-09-823-746-8
21	78	96.3	125	1	US-08-331-398A-67
22	78	96.3	125	1	US-08-331-397B-67
23	78	96.3	125	1	US-08-759-804A-66
24	78	96.3	131	1	US-08-053-171-5
25	78	96.3	131	1	US-08-053-171-9
26	78	96.3	131	1	US-08-129-930B-95
27	78	96.3	131	2	US-08-134-346A-50

28	78	96.3	131	2	US-08-976-288A-95	Sequence 95, Appl
29	78	96.3	149	1	US-08-752-844-2	Sequence 2, Appl
30	78	96.3	149	1	US-08-591-196-2	Sequence 2, Appl
31	78	96.3	149	2	US-09-192-838B-2	Sequence 2, Appl
32	78	96.3	149	2	US-09-293-533-2	Sequence 2, Appl
33	78	96.3	149	2	US-09-324-191-2	Sequence 2, Appl
34	78	96.3	149	2	US-10-226-795-27	Sequence 27, Appl
35	78	96.3	238	2	US-09-192-545-4	Sequence 4, Appl
36	78	96.3	249	2	US-09-726-219A-190	Sequence 190, App
37	78	96.3	249	2	US-09-196-522-190	Sequence 190, App
38	78	96.3	263	1	US-08-752-844-66	Sequence 66, Appl
39	78	96.3	263	2	US-09-293-533-66	Sequence 66, Appl
40	76	93.8	16	2	US-09-563-222C-29	Sequence 29, Appl
41	75	93.8	112	1	US-08-888-366-18	Sequence 18, Appl
42	75	92.6	238	1	US-08-224-591-12	Sequence 12, Appl
43	75	92.6	238	1	US-08-392-338A-21	Sequence 21, Appl
44	75	92.6	238	1	US-08-926-789-12	Sequence 12, Appl
45	75	92.6	238	2	US-09-166-750-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-08-053-171-27
Sequence 27, Application US/08053171
Patent No. 5562903
GENERAL INFORMATION:
APPLICANT: Co, Loibner
TITLE OF INVENTION: Antibody Derivatives
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,171
FILING DATE: 22-APR-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-54-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..16
OTHER INFORMATION: /note= "First
OTHER INFORMATION: Complementarity-determining region (CDR1) of
OTHER INFORMATION: BR55-1 antibody light chain"
US-08-053-171-27

Query Match 96.3%; Score 78; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 4e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 RSSQSIHNSNGNTYLQ 16
DB 1 RSSQSIHNSNGNTYLE 16

RESULT 2
US-07-977-696C-30
; Sequence 30, Application US/07977696C
; Patent No. 5792852
; GENERAL INFORMATION:
; APPLICANT: do Couto, Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides with Specificity
; TITLE OF INVENTION: for Carcinomas and Kit and Diagnostic Vaccination
; TITLE OF INVENTION: and Therapeutic Methods.
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 11-16-92
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel Ph.D., Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P66 38227
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 748-6868
; TELEFAX: (510) 748-6868
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-977-696C-30

Query Match 96.3%; Score 78; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 4e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIHNSNGNTYLQ 16
DB 1 RSSQSIHNSNGNTYLE 16

RESULT 3
US-08-129-930B-30
; Sequence 30, Application US/08129930B
; Patent No. 5804187
; GENERAL INFORMATION:
; APPLICANT: do Couto Dr., Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides With Broad
; TITLE OF INVENTION: Carcinoma Specificity, and Kit and
; TITLE OF INVENTION: Diagnostic Vaccination and
; TITLE OF INVENTION: Therapeutic Methods
; NUMBER OF SEQUENCES: 96
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: V. AMZEL & ASSOC.
; STREET: 2055 No. 5804187th Broadway, Suite 201
; CITY: Walnut Creek
; STATE: California
; COUNTRY: USA
; ZIP: 94596
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: September 30, 1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel Ph.D., Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: CRPCC-008A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 521-1333
; TELEFAX: (510) 521-3541
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-129-930B-30

Query Match 96.3%; Score 78; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 4e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIHNSNGNTYLQ 16
DB 1 RSSQSIHNSNGNTYLE 16

RESULT 4
US-08-134-346A-17
; Sequence 17, Application US/08134346A
; Patent No. 6281335
; GENERAL INFORMATION:
; APPLICANT: do Couto, F.J.R.
; APPLICANT: Ceriani, R.L.C.
; APPLICANT: Petersen, J.A.
; TITLE OF INVENTION: HYBRIDOMA AND ANTI-KC-4 HUMANIZED
; TITLE OF INVENTION: MONOCLONAL ANTIBODY AND DNA AND RNA
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ostrager, Chong & Flaherty
; STREET: 300 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10022-7499
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette-3.50 inch, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 08-OCT-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Onofrio, Dara L.
; REGISTRATION NUMBER: 34,889
; REFERENCE/DOCKET NUMBER: CLT 149,608
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TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-826-6565
TELEFAX: 212-826-5909
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-134-346A-17

Query Match 96.3%; Score 78; DB 2; Length 16;
Best Local Similarity 93.8%; Pred. No. 4e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSNGNTYLQ 16
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DB 1 RSSQSIVHSNGNTYLE 16

RESULT 5

US-08-976-288A-30
Sequence 30, Application US/08976288A
Patent No. 6315997

GENERAL INFORMATION:

APPLICANT: do Couto Dr., Fernando J.R.
APPLICANT: Ceriani Dr., Roberto L.
APPLICANT: Peterson Dr., Jerry A.
APPLICANT: Padlan Dr., Eduardo A.
TITLE OF INVENTION: Analogue Peptides With Broad
TITLE OF INVENTION: Carcinoma Specificity, and Kit and
TITLE OF INVENTION: Diagnostic Vaccination and
TITLE OF INVENTION: Therapeutic Methods
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder & Poplawski
STREET: 444 South Flower St., 19th Floor
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,288A
FILING DATE: No. 6315997ember 21, 1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/129,930
FILING DATE: September 30, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/977,696
FILING DATE: No. 6315997ember 16, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Anzel Ph.D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P6639938
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 499-4210
TELEX: n.a.

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-976-288A-30

Query Match 96.3%; Score 78; DB 2; Length 16;
Best Local Similarity 93.8%; Pred. No. 4e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSNGNTYLQ 16
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DB 1 RSSQSIVHSNGNTYLE 16

RESULT 6

US-10-226-795-28
Sequence 28, Application US/10226795
Patent No. 6875433

GENERAL INFORMATION:

APPLICANT: HART, MARY KATE
APPLICANT: WILSON, JULIE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND COMPLEMENTARITY-DETERMINING
TITLE OF INVENTION: REGIONS BINDING TO EBOLA GLYCOPROTEIN
FILE REFERENCE: ARMY 166
CURRENT APPLICATION NUMBER: US/10/226,795
CURRENT FILING DATE: 2002-11-18
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 28
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic light
OTHER INFORMATION: chain of Mab EGP6D8-1-2 amino acid sequence
US-10-226-795-28

Query Match 96.3%; Score 78; DB 2; Length 16;
Best Local Similarity 93.8%; Pred. No. 4e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSNGNTYLQ 16
|||||
DB 1 RSSQSIVHSNGNTYLE 16

RESULT 7

US-09-947-839B-30
Sequence 30, Application US/09947839B
Patent No. 6936706

GENERAL INFORMATION:

APPLICANT: do Couto, Fernando J.R.
Ceriani Dr., Roberto L.
Peterson Dr., Jerry A.
Padlan Dr., Eduardo A.

TITLE OF INVENTION: Analogue Peptides with Specificity
for Carcinomas and Kit and Diagnostic Vaccination
and Therapeutic Methods.

NUMBER OF SEQUENCES: 81

CORRESPONDENCE ADDRESS:

ADDRESSEE: V. Amzel & Assoc.
STREET: P.O.Box 159
CITY: Gladwyne
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19035

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/947,839B
FILING DATE: 06-Sep-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Anzel Viviana
REGISTRATION NUMBER: 30,930

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; REFERENCE/DOCKET NUMBER: CRFC-083
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-649-0609
; TELEFAX: 240-359-0299
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-947-839B-30

Query Match          96.3%; Score 78; DB 2; Length 16;
Best Local Similarity 93.8%; Pred. No. 4e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGTYLQ 16
Db 1 RSSQSIVHSGNGTYLE 16

RESULT 8
US-09-840-459-26
; Sequence 26, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-26

Query Match          96.3%; Score 78; DB 2; Length 100;
Best Local Similarity 93.8%; Pred. No. 2.9e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGTYLQ 16
Db 24 RSSQSIVHSGNGTYLE 39

RESULT 10
US-09-497-625A-26
; Sequence 26, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; CURRENT FILING DATE: 2000-02-03
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-497-625A-26

Query Match          96.3%; Score 78; DB 2; Length 100;
Best Local Similarity 93.8%; Pred. No. 2.9e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGTYLQ 16
Db 24 RSSQSIVHSGNGTYLE 39

RESULT 11
US-09-497-625A-28
; Sequence 28, Application US/09497625A
; Patent No. 6727349
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; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-497-625A-28

Query Match          96.3%; Score 78; DB 2; Length 100;
Best Local Similarity 93.8%; Pred. No. 2.9e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIHVSNGNTYLQ 16
Db 24 RSSQSIHVSNGNTYLE 39

RESULT 12
US-10-114-716A-42
; Sequence 42, Application US/10114716A
; Patent No. 6855804
; GENERAL INFORMATION:
; APPLICANT: Sudhir Paul
; APPLICANT: Yasuhiro Nishiyama
; TITLE OF INVENTION: Covalently Reactive Transition State
; TITLE OF INVENTION: Analogs and Methods of Use Thereof
; FILE REFERENCE: UTH001HB
; CURRENT APPLICATION NUMBER: US/10/114,716A
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 09/862,849
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: 09/046,373
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: 60/280,624
; PRIOR FILING DATE: 2001-03-31
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Mus musculus domesticus
; US-10-114-716A-42

Query Match          96.3%; Score 78; DB 2; Length 110;
Best Local Similarity 93.8%; Pred. No. 3.2e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIHVSNGNTYLQ 16
Db 24 RSSQSIHVSNGNTYLE 39

RESULT 13
US-09-823-746-12
; Sequence 12, Application US/09823746
; Patent No. 6962702
; GENERAL INFORMATION:
; APPLICANT: HANSEN, HANS J.
; APPLICANT: GRIFFITHS, GARY L.
; APPLICANT: MCBRIDE, WILLIAM J.
; APPLICANT: LEUNG, SHUI-ON
; APPLICANT: QU, ZHENGXING
; TITLE OF INVENTION: PRODUCTION AND USE OF NOVEL PEPTIDE-BASED AGENTS FOR
; TITLE OF INVENTION: USE WITH BI-SPECIFIC ANTIBODIES
; FILE REFERENCE: 40923-0074US4
; CURRENT APPLICATION NUMBER: US/09/823,746
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 09/337,756
; PRIOR FILING DATE: 1999-06-22
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 12
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic humanized
; OTHER INFORMATION: Mu-9 amino acid sequence
; US-09-823-746-12

Query Match          96.3%; Score 78; DB 2; Length 111;
Best Local Similarity 93.8%; Pred. No. 3.3e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIHVSNGNTYLQ 16
Db 24 RSSQSIHVSNGNTYLE 39

RESULT 14
US-08-053-171-15
; Sequence 15, Application US/08053171
; Patent No. 5562903
; GENERAL INFORMATION:
; APPLICANT: Co. Loibner
; TITLE OF INVENTION: Antibody Derivatives
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,171
; FILING DATE: 22-APR-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-54-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..112
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OTHER INFORMATION: /note= "Sequence of the Light Chain
Patent No. 5562903
OTHER INFORMATION: of Humanized BR55-2 Antibody"
FEATURE:
NAME/KEY: Region
LOCATION: 24..39
OTHER INFORMATION: /note= "Complementarity-determining
OTHER INFORMATION: region"
FEATURE:
NAME/KEY: Region
LOCATION: 55..61
OTHER INFORMATION: /note= "Complementarity-determining
OTHER INFORMATION: region"
FEATURE:
NAME/KEY: Region
LOCATION: 94..102
OTHER INFORMATION: /note= "Complementarity-determining
OTHER INFORMATION: region"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 54
OTHER INFORMATION: /note= "Residue that has been
OTHER INFORMATION: replaced with mouse amino acid in the humanized
OTHER INFORMATION: antibody."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 108
OTHER INFORMATION: /note= "Residue in the framework
OTHER INFORMATION: that is replaced with mouse amino acid in the
OTHER INFORMATION: humanized antibody."
US-08-053-171-15

Query Match 96.3%; Score 78; DB 1; Length 112;
Best Local Similarity 93.8%; Pred. No. 3.3e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGNTYLQ 16
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DB 24 RSSQSIVHSGNGNTYLE 39

RESULT 15
US-08-752-844-15
Sequence 15, Application US/08752844
Patent No. 5935821
GENERAL INFORMATION:
APPLICANT: Chatterjee, Malaya
APPLICANT: Foon, Kenneth A.
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,844
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Schiff, J. Michael
REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 30414-20002.21
TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-752-844-15
Query Match 96.3%; Score 78; DB 1; Length 112;
Best Local Similarity 93.8%; Pred. No. 3.3e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGNTYLQ 16
|||||
DB 24 RSSQSIVHSGNGNTYLE 39

Search completed: December 30, 2005, 13:37:16
Job time : 36.871 secs

GenCore version 5.1.6
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QM protein - protein search, using sw model

Run on: December 30, 2005, 13:33:42 ; Search time 118.968 Seconds
(without alignments)
56.194 Million cell updates/sec

Title: US-10-735-916A-2

Perfect score: 81

Sequence: 1 RSSQSIVHSGNTYLQ 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications AA Main.*
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2: /cgm2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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2	81	100.0	112	5	US-10-735-916A-54
3	81	100.0	112	5	US-10-735-916A-61
4	81	100.0	112	5	US-10-735-916A-65
5	81	100.0	122	5	US-10-735-916A-49
6	81	100.0	131	5	US-10-735-916A-63
7	81	100.0	131	5	US-10-735-916A-67
8	78	96.3	16	3	US-09-995-529-32
9	78	96.3	16	3	US-09-947-839-30
10	78	96.3	16	3	US-09-995-529-28
11	78	96.3	16	4	US-10-226-795-28
12	78	96.3	16	4	US-10-470-045-53
13	78	96.3	16	6	US-11-070-697-1
14	78	96.3	60	4	US-10-470-045-91
15	78	96.3	100	3	US-09-840-459-26
16	78	96.3	100	3	US-09-840-459-28
17	78	96.3	100	4	US-10-766-773-26
18	78	96.3	100	4	US-10-766-773-28
19	78	96.3	100	4	US-10-766-610-26
20	78	96.3	100	4	US-10-766-610-28
21	78	96.3	100	4	US-10-733-563-26
22	78	96.3	100	4	US-10-733-563-28
23	78	96.3	100	5	US-10-729-441-56
24	78	96.3	100	5	US-10-897-406-56
25	78	96.3	105	5	US-10-764-730-4
26	78	96.3	110	4	US-10-114-716A-42
27	78	96.3	110	5	US-10-930-548-42

28 78 96.3 112 3 US-09-995-529-10 Sequence 10, Appl
29 78 96.3 112 3 US-09-995-529-10 Sequence 10, Appl
30 78 96.3 112 4 US-10-153-401-15 Sequence 15, Appl
31 78 96.3 112 4 US-10-258-728-4 Sequence 4, Appl
32 78 96.3 112 4 US-10-258-728-25 Sequence 25, Appl
33 78 96.3 112 4 US-10-258-728-27 Sequence 27, Appl
34 78 96.3 112 4 US-10-258-728-28 Sequence 28, Appl
35 78 96.3 112 5 US-10-735-916A-55 Sequence 55, Appl
36 78 96.3 112 5 US-10-735-916A-56 Sequence 56, Appl
37 78 96.3 112 5 US-10-858-855-7 Sequence 7, Appl
38 78 96.3 112 6 US-11-070-697-32 Sequence 32, Appl
39 78 96.3 113 5 US-10-729-441-59 Sequence 59, Appl
40 78 96.3 113 5 US-10-729-441-61 Sequence 61, Appl
41 78 96.3 113 5 US-10-897-406-59 Sequence 59, Appl
42 78 96.3 113 5 US-10-897-406-61 Sequence 61, Appl
43 78 96.3 113 6 US-11-070-697-36 Sequence 36, Appl
44 78 96.3 113 6 US-11-070-697-40 Sequence 40, Appl
45 78 96.3 116 5 US-10-787-219A-49 Sequence 49, Appl

ALIGNMENTS

RESULT 1
US-10-735-916A-2
; Sequence 2, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFILOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUM, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10/735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-735-916A-2

Query Match 100.0%; Score 81; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSGNTYLQ 16
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Db 1 RSSQSIVHSGNTYLQ 16

RESULT 2
US-10-735-916A-54
; Sequence 54, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier

; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10/735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-735-916A-54

Query Match 100.0%; Score 81; DB 5; Length 112;
Best Local Similarity 100.0%; Pred. No. 8.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSNGNTYIQ 16
|||||

DB 24 RSSQSIVHSNGNTYIQ 39
|||||

RESULT 3
US-10-735-916A-61
; Sequence 61, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10/735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 61
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-735-916A-61

Query Match 100.0%; Score 81; DB 5; Length 112;
Best Local Similarity 100.0%; Pred. No. 8.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSNGNTYIQ 16
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DB 24 RSSQSIVHSNGNTYIQ 39
RESULT 4
US-10-735-916A-65
; Sequence 65, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10/735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-735-916A-65

Query Match 100.0%; Score 81; DB 5; Length 112;
Best Local Similarity 100.0%; Pred. No. 8.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSNGNTYIQ 16
|||||

DB 24 RSSQSIVHSNGNTYIQ 39
|||||

RESULT 5
US-10-735-916A-49
; Sequence 49, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10/735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49

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; LENGTH: 122
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-735-916A-49

Query Match      100.0%; Score 81; DB 5; Length 122;
Best Local Similarity 100.0%; Pred. No. 9e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSNGNTYLQ 16
Db 34 RSSQSIVHSNGNTYLQ 49

RESULT 6
US-10-735-916A-63
; Sequence 63, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10/735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-735-916A-63

Query Match      100.0%; Score 81; DB 5; Length 131;
Best Local Similarity 100.0%; Pred. No. 9.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSNGNTYLQ 16
Db 43 RSSQSIVHSNGNTYLQ 58

RESULT 7
US-10-735-916A-67
; Sequence 67, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10/735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
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; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-735-916A-67

Query Match      100.0%; Score 81; DB 5; Length 131;
Best Local Similarity 100.0%; Pred. No. 9.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSNGNTYLQ 16
Db 43 RSSQSIVHSNGNTYLQ 58

RESULT 8
US-09-995-529-32
; Sequence 32, Application US/09995529
; Publication No. US2003009655A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-995-529-32

Query Match      96.3%; Score 78; DB 3; Length 16;
Best Local Similarity 93.8%; Pred. No. 3e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSNGNTYLQ 16
Db 1 RSSQSIVHSNGNTYLQ 16

RESULT 9
US-09-947-839-30
; Sequence 30, Application US/09947839
; Publication No. US20030138428A1
; GENERAL INFORMATION:
; APPLICANT: do Couto Dr., Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides With Broad
; Carcinoma Specificity, and Kit and
; Diagnostic Vaccination and
; Therapeutic Methods
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder & Poplawski
; STREET: 444 South Flower St., 19th Floor
; CITY: Los Angeles
```

STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/947,839
FILING DATE: 06-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/976,288
FILING DATE: <Unknown>
APPLICATION NUMBER: 07/977,696
FILING DATE: No. US20030138428Aember 16, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Anzel Ph.D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P6639938
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
TELEX: n.a.
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-947-839-30

Query Match 96.3%; Score 78; DB 3; Length 16;
Best Local Similarity 93.8%; Pred. No. 3e-06; Indels 0; Gaps 0;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGTYLQ 16
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Db 1 RSSQSIVHSGNGTYLQ 16

RESULT 10
US-09-995-529-32
Sequence 32, Application US/09995529
Publication No. US20040091482A9
GENERAL INFORMATION:
APPLICANT: Watkins, Jeffrey D.
APPLICANT: Huse, William D.
APPLICANT: Tang, Ying
TITLE OF INVENTION: Humanized Collagen Antibodies and
TITLE OF INVENTION: Related Methods
FILE REFERENCE: P-IX 4976
CURRENT APPLICATION NUMBER: US/09/995,529
CURRENT FILING DATE: 2001-11-26
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 32
LENGTH: 16
TYPE: PRT
ORGANISM: Mus musculus
US-09-995-529-32

Query Match 96.3%; Score 78; DB 3; Length 16;
Best Local Similarity 93.8%; Pred. No. 3e-06; Indels 0; Gaps 0;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGTYLQ 16
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Db 1 RSSQSIVHSGNGTYLQ 16

RESULT 11
US-10-226-795-28
Sequence 28, Application US/10226795
Publication No. US20040053865A1
GENERAL INFORMATION:
APPLICANT: HART, MARY KATE
APPLICANT: WILSON, JULIE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND COMPLEMENTARITY-DETERMINING
TITLE OF INVENTION: REGIONS BINDING TO EBOLA GLYCOPROTEIN
FILE REFERENCE: ARMY 166
CURRENT APPLICATION NUMBER: US/10/226,795
CURRENT FILING DATE: 2002-11-18
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 28
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic light
OTHER INFORMATION: chain of Mab EGP6D8-1-2 amino acid sequence
US-10-226-795-28

Query Match 96.3%; Score 78; DB 4; Length 16;
Best Local Similarity 93.8%; Pred. No. 3e-06; Indels 0; Gaps 0;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGTYLQ 16
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Db 1 RSSQSIVHSGNGTYLQ 16

RESULT 12
US-10-470-045-53
Sequence 53, Application US/10470045
Publication No. US20040146505A1
GENERAL INFORMATION:
APPLICANT: Scancell Limited
APPLICANT: Durrant, Linda Gillian
APPLICANT: Parsons, Tina
TITLE OF INVENTION: Substances
FILE REFERENCE: P32181WO/NJL
CURRENT APPLICATION NUMBER: US/10/470,045
CURRENT FILING DATE: 2003-07-24
PRIOR APPLICATION NUMBER: GB 0102145.0
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 101
SOFTWARE: Patentin version 3.1
SEQ ID NO 53
LENGTH: 16
TYPE: PRT
ORGANISM: Homo sapiens
US-10-470-045-53

Query Match 96.3%; Score 78; DB 4; Length 16;
Best Local Similarity 93.8%; Pred. No. 3e-06; Indels 0; Gaps 0;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGTYLQ 16
|||||
Db 1 RSSQSIVHSGNGTYLQ 16

RESULT 13
US-11-070-697-1
Sequence 1, Application US/11070697
Publication No. US2005016926A1
GENERAL INFORMATION:
APPLICANT: OU, ZHENGXING
APPLICANT: HANSEN, HANS
APPLICANT: GOLDENBERG, DAVID M.
TITLE OF INVENTION: CHIMERIC, HUMAN AND HUMANIZED ANTI-CSAP MONOCLONAL
TITLE OF INVENTION: ANTIBODIES

; FILE REFERENCE: 018733/1064
; CURRENT APPLICATION NUMBER: US/11/070,697
; CURRENT FILING DATE: 2005-03-03
; PRIOR APPLICATION NUMBER: US/10/116,116
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 09/823,746
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 09/337,756
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/104,156
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/090,142
; PRIOR FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-11-070-697-1

Query Match 96.3%; Score 78; DB 6; Length 16;
Best Local Similarity 93.8%; Pred. No. 3e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSGNGTYLQ 16
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Db 1 RSSQSIVHSGNGTYLE 16

RESULT 14

US-10-470-045-91
; Sequence 91, Application US/10470045
; Publication No. US20040146505A1
; GENERAL INFORMATION:
; APPLICANT: Scancell Limited
; APPLICANT: Durrant, Linda Gillian
; APPLICANT: Parsons, Tina
; TITLE OF INVENTION: Substances
; FILE REFERENCE: P32181WO/NJL
; CURRENT APPLICATION NUMBER: US/10/470,045
; CURRENT FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: GB 0102145.0
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 91
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-470-045-91

Query Match 96.3%; Score 78; DB 4; Length 60;
Best Local Similarity 93.8%; Pred. No. 1.3e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSGNGTYLQ 16
| | | | | | | | | | | | | | | |
Db 24 RSSQSIVHSGNGTYLE 39

RESULT 15

US-09-840-459-26
; Sequence 26, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran

; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-26

Query Match 96.3%; Score 78; DB 3; Length 100;
Best Local Similarity 93.8%; Pred. No. 2.3e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSGNGTYLQ 16
| | | | | | | | | | | | | | | |
Db 24 RSSQSIVHSGNGTYLE 39

Search completed: December 30, 2005, 14:14:50
Job time : 118.968 secs

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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:35:07 ; Search time 5.93548 Seconds
(without alignments)
20.187 Million cell updates/sec

Title: US-10-735-916a-2

Perfect score: 81
Sequence: 1 RSSQSIVHSNGNTYLQ 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 57103

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
1: /cgn2_6/ptodata/1/pubaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubaa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubaa/US07_NEW_PUB.pep.*
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5: /cgn2_6/ptodata/1/pubaa/US09_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubaa/US10_NEW_PUB.pep.*
7: /cgn2_6/ptodata/1/pubaa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	81	100.0	112	7	US-11-012-353-54
3	81	100.0	112	7	US-11-012-353-61
4	81	100.0	112	7	US-11-012-353-65
5	81	100.0	122	7	US-11-012-353-49
6	81	100.0	131	7	US-11-012-353-63
7	81	100.0	131	7	US-11-012-353-67
8	78	96.3	100	6	US-10-932-334-56
9	78	96.3	112	7	US-11-012-353-55
10	78	96.3	112	7	US-11-012-353-56
11	78	96.3	113	6	US-10-932-334-59
12	78	96.3	113	6	US-10-932-334-61
13	78	96.3	116	7	US-11-065-943-49
14	78	96.3	251	6	US-10-512-184-30
15	78	96.3	320	6	US-10-512-184-67
16	78	96.3	569	6	US-10-512-184-66
17	78	96.3	618	6	US-10-512-184-48
18	76	93.8	112	7	US-11-012-353-57
19	75	92.6	113	6	US-10-932-334-60
20	74	91.4	112	6	US-10-502-145-19
21	74	91.4	113	6	US-10-932-334-69
22	74	91.4	131	6	US-10-789-273-14
23	74	91.4	144	7	US-11-055-163-15
24	73	90.1	112	6	US-10-502-145-15
25	72	88.9	113	6	US-10-932-334-62

26	72	88.9	113	6	US-10-932-334-67	Sequence 67, Appl
27	71	87.7	16	7	US-11-125-837-13	Sequence 13, Appl
28	71	87.7	131	7	US-11-125-837-23	Sequence 23, Appl
29	70	86.4	16	7	US-11-102-743-3	Sequence 3, Appl
30	70	86.4	112	7	US-11-102-743-2	Sequence 2, Appl
31	69	85.2	16	6	US-10-932-334-4	Sequence 4, Appl
32	69	85.2	100	7	US-11-054-669-81	Sequence 81, Appl
33	69	85.2	100	7	US-11-084-554-112	Sequence 112, App
34	69	85.2	100	7	US-11-084-554-118	Sequence 118, App
35	69	85.2	112	6	US-10-502-145-23	Sequence 23, Appl
36	69	85.2	113	6	US-10-932-334-8	Sequence 8, Appl
37	69	85.2	113	6	US-10-932-334-9	Sequence 9, Appl
38	69	85.2	113	6	US-10-932-334-10	Sequence 10, Appl
39	69	85.2	113	6	US-10-932-334-11	Sequence 11, Appl
40	69	85.2	113	6	US-10-932-334-12	Sequence 12, Appl
41	69	85.2	113	6	US-10-932-334-58	Sequence 58, Appl
42	69	85.2	113	6	US-10-932-334-66	Sequence 66, Appl
43	69	85.2	113	6	US-10-932-334-68	Sequence 68, Appl
44	69	85.2	113	6	US-10-932-334-82	Sequence 82, Appl
45	69	85.2	113	6	US-10-932-334-83	Sequence 83, Appl

ALIGNMENTS

RESULT 1
US-11-012-353-2
; Sequence 2, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-1 HYBRID
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: Patent in Ver. 3.3
; SEQ ID NO 2
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mus musculus
; US-11-012-353-2

Query Match 100.0%; Score 81; DB 7; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSNGNTYLQ 16
| | | | | | | | | | | | | | | |
Db 1 RSSQSIVHSNGNTYLQ 16

RESULT 2
US-11-012-353-54
; Sequence 54, Application US/11012353

```
/ Publication No. US20050249730A1
/ GENERAL INFORMATION:
/ APPLICANT: GOETSCH, LILIANE
/ APPLICANT: CORVAIA, NATHALIE
/ APPLICANT: DUFLOS, ALAIN
/ APPLICANT: HAEUW, JEAN-FRANCOIS
/ APPLICANT: LEGER, OLIVIER
/ APPLICANT: BECK, ALAIN
/ TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
/ TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
/ FILE REFERENCE: 017753-198
/ CURRENT APPLICATION NUMBER: US/11/012,353
/ CURRENT FILING DATE: 2004-12-16
/ PRIOR APPLICATION NUMBER: 10/735,916
/ PRIOR FILING DATE: 2003-12-16
/ PRIOR APPLICATION NUMBER: FR 0308538
/ PRIOR FILING DATE: 2003-07-11
/ PRIOR APPLICATION NUMBER: PCT/FR03/00178
/ PRIOR FILING DATE: 2003-01-20
/ PRIOR APPLICATION NUMBER: FR 0205753
/ PRIOR FILING DATE: 2002-05-07
/ PRIOR APPLICATION NUMBER: FR 0200653
/ PRIOR FILING DATE: 2002-01-18
/ PRIOR APPLICATION NUMBER: FR 0200654
/ PRIOR FILING DATE: 2002-01-18
/ NUMBER OF SEQ ID NOS: 162
/ SOFTWARE: PatentIn Ver. 3.3
/ SEQ ID NO 54
/ LENGTH: 112
/ TYPE: PRT
/ ORGANISM: Mus musculus
/ US-11-012-353-54

Query Match      100.0%; Score 81; DB 7; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSNGNTYLQ 16
Db 24 RSSQSIVHSNGNTYLQ 39

RESULT 3
US-11-012-353-61
/ Sequence 61, Application US/11012353
/ Publication No. US20050249730A1
/ GENERAL INFORMATION:
/ APPLICANT: GOETSCH, LILIANE
/ APPLICANT: DUFLOS, ALAIN
/ APPLICANT: HAEUW, JEAN-FRANCOIS
/ APPLICANT: LEGER, OLIVIER
/ APPLICANT: BECK, ALAIN
/ TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
/ TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
/ FILE REFERENCE: 017753-198
/ CURRENT APPLICATION NUMBER: US/11/012,353
/ CURRENT FILING DATE: 2004-12-16
/ PRIOR APPLICATION NUMBER: 10/735,916
/ PRIOR FILING DATE: 2003-12-16
/ PRIOR APPLICATION NUMBER: FR 0308538
/ PRIOR FILING DATE: 2003-07-11
/ PRIOR APPLICATION NUMBER: PCT/FR03/00178
/ PRIOR FILING DATE: 2003-01-20
/ PRIOR APPLICATION NUMBER: FR 0205753
/ PRIOR FILING DATE: 2002-05-07
/ PRIOR APPLICATION NUMBER: FR 0200653
/ PRIOR FILING DATE: 2002-01-18
/ PRIOR APPLICATION NUMBER: FR 0200654
/ NUMBER OF SEQ ID NOS: 162
/ SOFTWARE: PatentIn Ver. 3.3
/ SEQ ID NO 61
/ LENGTH: 112
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-11-012-353-65

Query Match      100.0%; Score 81; DB 7; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSNGNTYLQ 16
Db 24 RSSQSIVHSNGNTYLQ 39

RESULT 4
US-11-012-353-65
/ Sequence 65, Application US/11012353
/ Publication No. US20050249730A1
/ GENERAL INFORMATION:
/ APPLICANT: GOETSCH, LILIANE
/ APPLICANT: CORVAIA, NATHALIE
/ APPLICANT: DUFLOS, ALAIN
/ APPLICANT: HAEUW, JEAN-FRANCOIS
/ APPLICANT: LEGER, OLIVIER
/ APPLICANT: BECK, ALAIN
/ TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
/ TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
/ FILE REFERENCE: 017753-198
/ CURRENT APPLICATION NUMBER: US/11/012,353
/ CURRENT FILING DATE: 2004-12-16
/ PRIOR APPLICATION NUMBER: 10/735,916
/ PRIOR FILING DATE: 2003-12-16
/ PRIOR APPLICATION NUMBER: FR 0308538
/ PRIOR FILING DATE: 2003-07-11
/ PRIOR APPLICATION NUMBER: PCT/FR03/00178
/ PRIOR FILING DATE: 2003-01-20
/ PRIOR APPLICATION NUMBER: FR 0205753
/ PRIOR FILING DATE: 2002-05-07
/ PRIOR APPLICATION NUMBER: FR 0200653
/ PRIOR FILING DATE: 2002-01-18
/ PRIOR APPLICATION NUMBER: FR 0200654
/ NUMBER OF SEQ ID NOS: 162
/ SOFTWARE: PatentIn Ver. 3.3
/ SEQ ID NO 65
/ LENGTH: 112
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-11-012-353-65

Query Match      100.0%; Score 81; DB 7; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSNGNTYLQ 16
Db 24 RSSQSIVHSNGNTYLQ 39

RESULT 5
US-11-012-353-49
/ Sequence 49, Application US/11012353
/ Publication No. US20050249730A1
/ GENERAL INFORMATION:
/ APPLICANT: GOETSCH, LILIANE
/ APPLICANT: CORVAIA, NATHALIE
/ APPLICANT: DUFLOS, ALAIN
/ APPLICANT: HAEUW, JEAN-FRANCOIS
/ APPLICANT: LEGER, OLIVIER
/ APPLICANT: BECK, ALAIN
/ TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
/ TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
/ FILE REFERENCE: 017753-198
```



```
QY 1 RSSQSIVHSGNGTYLQ 16
Db 24 RSSQSIVHSGNGTYLQ 39

RESULT 9
US-11-012-353-55
; Sequence 55, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GORTSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 55
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-012-353-55

Query Match 96.3%; Score 78; DB 7; Length 112;
Best Local Similarity 93.8%; Pred. No. 3.6e-07;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGTYLQ 16
Db 24 RSSQSIVHSGNGTYLQ 39

RESULT 11
US-10-932-334-59
; Sequence 59, Application US/10932334
; Publication No. US20050249728A1
; GENERAL INFORMATION:
; APPLICANT: ImmunoGen, Inc.
; TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
; FILE REFERENCE: A8689
; CURRENT APPLICATION NUMBER: US/10/932,334
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US/10/729,441
; PRIOR FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: 10/170,390
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 59
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody structure
US-10-932-334-59

Query Match 96.3%; Score 78; DB 6; Length 113;
Best Local Similarity 93.8%; Pred. No. 3.7e-07;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGTYLQ 16
Db 24 RSSQSIVHSGNGTYLQ 39

RESULT 12
US-10-932-334-61
; Sequence 61, Application US/10932334
; Publication No. US20050249728A1
; GENERAL INFORMATION:
; APPLICANT: ImmunoGen, Inc.
; TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
; FILE REFERENCE: A8689
; CURRENT APPLICATION NUMBER: US/10/932,334
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US/10/729,441
; PRIOR FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: 10/170,390
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
```

```
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody structure
US-10-932-334-61

Query Match          96.3%; Score 78; DB 6; Length 113;
Best Local Similarity 93.8%; Pred. No. 3.7e-07;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSGNGTYLQ 16
Db 24 RSSQSIVHSGNGTYLQ 39

RESULT 13
US-11-065-943-49
; Sequence 49, Application US/11065943
; Publication No. US20050250131A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, JEAN-JUC
; APPLICANT: VICHIER-GUERRE, SOPHIE
; APPLICANT: FERRIS, STEPHANE
; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
; FILE REFERENCE: 266426USOXCP
; CURRENT APPLICATION NUMBER: US/11/065,943
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: US 10/787,219
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 49
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-11-065-943-49

Query Match          96.3%; Score 78; DB 7; Length 116;
Best-Local Similarity 93.8%; Pred. No. 3.8e-07;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSGNGTYLQ 16
Db 27 RSSQSIVHSGNGTYLQ 42

RESULT 14
US-10-512-184-30
; Sequence 30, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv VD2 with
; OTHER INFORMATION: specificity against Verticillium dahliae;
; OTHER INFORMATION: originates from Mus musculus.
```

US-10-512-184-30

```
Query Match          96.3%; Score 78; DB 6; Length 251;
Best Local Similarity 93.8%; Pred. No. 9.1e-07;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 RSSQSIVHSGNGTYLQ 16
Db 161 RSSQNIHVHSGNGTYLQ 176
```

```
RESULT 15
US-10-512-184-67
; Sequence 67, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: precursor
; OTHER INFORMATION: fusion protein comprising AG - linker - scFv VD2.
US-10-512-184-67
```

```
Query Match          96.3%; Score 78; DB 6; Length 320;
Best Local Similarity 93.8%; Pred. No. 1.2e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 RSSQSIVHSGNGTYLQ 16
Db 230 RSSQNIHVHSGNGTYLQ 245
```

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Search completed: December 30, 2005, 14:15:20
Job time : 6.93548 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:37:27 ; Search time 132.5 Seconds
(without alignments)
53.057 Million cell updates/sec

Title: US-10-735-916A-2

Perfect score: 81

Sequence: 1 RSSQSVHSNGNTYLQ 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 19975

Minimum DB seq length: 16

Maximum DB seq length: 16

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq 21:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	16	7	ADJ76836 CDR seque
2	81	100.0	16	9	ADZ67006 Murine in
3	78	96.3	16	2	AAR70451 VL sequen
4	78	96.3	16	5	ABP52343 Fv region
5	78	96.3	16	7	ADC03151 Colon spe
6	78	96.3	16	7	ADG94147 Mouse HUI
7	78	96.3	16	7	ADH61992 Mouse ant
8	78	96.3	16	8	ADL27487 CDR from
9	78	96.3	16	8	ADM78123 Human SJB
10	78	96.3	16	8	ADM78129 Human SJB
11	78	96.3	16	8	ADM78081 Human SJB
12	78	96.3	16	8	ADP84865 Complemen
13	78	96.3	16	8	ADR19270 Glycosyla
14	78	96.3	16	8	ADS87339 Humanise
15	76	93.8	16	5	AAU70349 Mouse Kap
16	76	93.8	16	8	ADP84887 Complemen
17	76	93.8	16	9	ADZ08831 Mammalian
18	75	92.6	16	7	ADZ94234 Mouse HUI
19	74	91.4	16	2	AAR75487 Mouse ant
20	74	91.4	16	3	AAZ21364 Mouse ant
21	74	91.4	16	4	AAZ97198 Murine an
22	74	91.4	16	6	ABP58276 Murine mo
23	74	91.4	16	7	ADD94233 Mouse HUI
24	74	91.4	16	8	ADP84888 Complemen

25	74	91.4	16	8	ADRI9288 Glycosyla
26	74	91.4	16	8	ADS94307 Antibody
27	74	91.4	16	9	ADY80101 Anti-ghre
28	74	91.4	16	9	ADY80084 Anti-ghre
29	74	91.4	16	9	ABZ21685 Anti-Nogo
30	74	91.4	16	9	ABZ08720 antibody
31	74	91.4	16	8	ADP84893 Complemen
32	73	90.1	16	8	ADP84886 Complemen
33	73	90.1	16	8	ADRI9287 Glycosyla
34	72	88.9	16	2	AAR40216 Humanised
35	72	88.9	16	7	ADD94261 Mouse HUI
36	72	88.9	16	7	ADD94225 Mouse HUI
37	72	88.9	16	8	ADP84891 Complemen
38	71	87.7	16	2	AAW58534 CDR-1 of
39	71	87.7	16	3	AAV51154 Murine CD
40	71	87.7	16	7	ADD94229 Mouse HUI
41	71	87.7	16	7	ADD94226 Mouse HUI
42	71	87.7	16	8	ADP84866 Complemen
43	71	87.7	16	8	ADP84889 Complemen
44	71	87.7	16	9	AEA45027 Apolipop
45	70	86.4	16	2	AAW31747 CDRL1 reg

ALIGNMENTS

RESULT 1

ADJ76836

ID ADJ76836 standard; peptide; 16 AA.

XX AC ADJ76836;

DT 06-MAY-2004 (first entry)

DE CDR sequence for anti-IGF-1R antibody.

XX KW

XX KW cytosolic; antipsoriatic; antibody;

XX KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;

XX KW or epidermal growth factor receptor; EGFR; signal transduction pathway;

XX KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;

XX KW CDR.

XX OS Mus musculus.

XX PN W02003059551-A2.

XX PD 24-JUL-2003.

XX PF 20-JAN-2003; 2003WO-FR000178.

XX PR 18-JAN-2002; 2002FR-00000653.

XX PR 18-JAN-2002; 2002FR-00000654.

XX PR 07-MAY-2002; 2002FR-00005753.

XX PA (FABR) FABRE MEDICAMENT SA PIERRE.

XX PI Goetsch L, Corvaia N, Leger O;

XX DR WPI; 2003-569653/53.

XX DR N-PSDB; ADJ76835.

XX PT New antibodies that bind to human insulin-like growth factor receptor,

XX PT useful for treatment, prevention and diagnosis of cancers.

XX PS Claim 1; SEQ ID NO 2; 164pp; French.

XX CC The invention relates to an isolated antibody (Ab), and its functional

XX CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-

XX CC IR) and optionally: (i) inhibit natural binding of insulin-like growth

XX CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine

XX CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or

XX CC treat diseases associated with overexpression and/or abnormal activity of

XX CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with

CC hyperactivity of signal transduction pathways mediated by interaction of
 CC these receptors with their ligands. Especially they inhibit
 CC transformation of normal cells to tumor cells, inhibit growth and/or
 CC proliferation of tumor cells, so are useful against cancers of the
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused
 CC by abnormal expression of IGF-IR and/or EGFR. This sequence represents an
 CC CDR sequence used to generate the Ab of the invention.
 XX
 SQ Sequence 16 AA;

Query Match 100.0%; Score 81; DB 7; Length 16;
 Best Local Similarity 100.0%; Pred. No. 4.8e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGNTYLQ 16
 |||||
 Db 1 RSSQSIVHSGNGNTYLQ 16

RESULT 2
 ADZ67006
 ID ADZ67006 standard; peptide; 16 AA.

XX ADZ67006;

XX 30-JUN-2005 (first entry)

DE Murine insulin-like growth factor T receptor IGF-IR CDR SEQ ID NO:2.

XX Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
 KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;
 KW musculoskeletal disease; respiratory disease; lung tumor;
 KW endocrine disease; gynecology and obstetrics; breast tumor;
 KW endometrial carcinoma; gastrointestinal disease; colon tumor;
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder.

XX Mus musculus.

XX US2005084906-A1.

XX 21-APR-2005.

XX 16-DEC-2003; 2003US-00735916.

XX 18-JAN-2002; 2002FR-00000653.

PR 18-JAN-2002; 2002FR-00000654.

PR 07-MAY-2002; 2002FR-00005753.

PR 20-JAN-2003; 2003WO-FR000178.

PR 11-JUL-2003; 2003FR-00008538.

XX (GOET/) GOETSCH L.

PA (CORV/) CORVAIA N.

PA (LEGE/) LEGER O.

PA (DUFL/) DUFLOS A.

PA (HAEU/) HAEUW J.

PA (BECK/) BECK A.

XX Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;

XX WPI; 2005-321968/33.

DR N-PSDB; ADZ67005.

XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)

PT antibody or its functional fragment, being capable of binding human IGF-

PT IR and specifically inhibiting tyrosine kinase activity of receptor,

PT useful for treating cancer.

XX Claim 1; SEQ ID NO 2; 125pp; English.

PS The invention relates to a novel isolated anti-insulin-like growth factor

CC I receptor (IGF-IR) antibody (I) or its functional fragment, being

CC capable of binding to human IGF-IR and, if necessary, capable of

CC specifically inhibiting tyrosine kinase activity of the receptor,
 CC comprising a light or heavy chain having at least one complementary
 CC determining region (CDR) consisting of one of two fully defined 16 amino
 CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in
 CC the preparation of a medicament intended for the prevention or treatment
 CC of an illness connected with an overexpression and/or an abnormal
 CC activation of the IGF-IR and/or EGFR, and/or connected with a
 CC hyperactivation of the transduction pathway of the signal mediated by the
 CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where
 CC the administration of the medicament does not induce or only slightly
 CC induces secondary effects connected with inhibition of the insulin
 CC receptor. The antibody is useful for preparation of a medicament intended
 CC to inhibit the transformation of normal cells into cells with tumoral
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is
 CC useful for preparation of a medicament intended to inhibit the growth
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a
 CC medicament intended for prevention or for the treatment of cancer, where
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the
 CC preparation of a medicament intended for the prevention or for the
 CC treatment of psoriasis. (I) is useful in preparation of a medicament
 CC intended for the specific targeting of a biologically active compound to
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)
 CC is useful for in vitro diagnosis of illnesses induced by an
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor
 CC starting from a biological sample in which the abnormal presence, of IGF-
 CC IR and/or EGFR receptor is suspected, which involves contacting the
 CC biological sample with (I), which is optionally labeled. The present
 CC sequence is used in the exemplification of the invention.

XX Sequence 16 AA;

Query Match 100.0%; Score 81; DB 9; Length 16;
 Best Local Similarity 100.0%; Pred. No. 4.8e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGNTYLQ 16
 |||||
 Db 1 RSSQSIVHSGNGNTYLQ 16

RESULT 3

AAR70451

ID AAR70451 standard; peptide; 16 AA.

XX AAR70451;

XX 25-MAR-2003 (revised)

DT 27-OCT-1995 (first entry)

DE VL sequence of anti-KC-4 monoclonal antibody (kII-Jk2) corresp. to.

DE complementarity determining region 1 (CDR1).

XX Anti-KC-4 antibody; monoclonal antibody; cancer; VL chain.

XX Synthetic.

XX WO9510776-A1.

XX 20-APR-1995.

XX 16-NOV-1993; 93WO-US011444.

XX 08-OCT-1993; 93US-00134346.

XX (CANC-) CANCER RES FUND CONTRA COSTA.

XX Do Couto JJR, Ceriani RL, Peterson JA;

XX WPI; 1995-161912/21.

DR N-PSDB; AAQ87531.
XX New humanised anti-KC-4 monoclonal antibody - used for detection of
PT cancer cells, in vivo imaging, ex-vivo purging and treatment of cancers.
XX Example; Table 14, Page 31; 61pp; English.
XX
CC The cDNAs that encode the anti-KC-4 murine immunoglobulin VH and VL were
CC prepared by PCR from polyadenylated RNA isolated from 100 million KC-4
CC hybridoma cells. All clones were obtd. from independent PCRs. The
CC sequences of the primers are given in AAQ87519-Q87526. The PCR products
CC were cloned, without prior purificn., into pCR1000 (Invitrogen) and
CC sequenced in both directions. The VL DNA sequence and its derived protein
CC sequences are shown in AAQ87531 and AAR70449-R70457. The mature VL chain
CC begins at AA D of framework 1 (FR1). VL is a group II kappa chain. Part
CC of the CDR3 and all of the FR4 are encoded by Jk2. There is a an
CC asparagine glycosylation site in the light chain in FR3. The site reads
CC NIS. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-
CC 2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 16 AA;
Query Match 96.3%; Score 78; DB 2; Length 16;
Best Local Similarity 93.8%; Pred. No. 1.6e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RSSQSIVHSGNGTYLQ 16
Db 1 RSSQSIVHSGNGTYLQ 16
RESULT 4
ABP52343
ID ABP52343 standard; peptide; 16 AA.
XX
AC ABP52343;
XX
DT 17-OCT-2002 (first entry)
XX
DE Fv region SC100 antibody CDR-L1 amino acid sequence.
XX
KW Cytotoxic T lymphocyte; CTL; T helper; MAGE3; cytotoxic T cell response;
KW tumour; immune response; cancer; vaccine; antibody.
XX
OS Mus musculus.
OS Synthetic.
XX
FN WO200258728-A2.
XX
PD 01-AUG-2002.
XX
PF 28-JAN-2002; 2002WO-GB000354.
XX
PR 26-JAN-2001; 2001GB-00002145.
XX
PA (SCAN-) SCANCEL LTD.
PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
PI Durrant LG, Parsons T, Robins A;
XX WPI; 2002-608418/65.
XX
PT Use of polypeptides and nucleic acids encoding the polypeptides, in
PT manufacturing medicament for stimulating a cytotoxic T cell response and
PT for preventing or treating cancer, e.g. colorectal, lung, breast or
PT ovarian cancer.
XX
PS Example 11; Page 45; 87pp; English.
XX
CC The present invention describes the use of a polypeptide (I) in the
CC manufacture of a medicament for stimulating a cytotoxic T cell response,
CC where (I) comprises a first portion comprising the part of human PC that
CC binds to CD64 and a second portion comprising one or more heterologous T.

CC cell epitopes. Also described is a method of stimulating a cytotoxic T
CC cell response in a patient such as a mammal, preferably human, by
CC administering (I) to the patient. (I) has cytostatic activity and can be
CC used in vaccine production. (I) and the nucleic acid encoding (I) are
CC useful in the manufacture of a medicament for stimulating cytotoxic T
CC cell response. The medicament is useful for preventing and/or treating
CC cancer, e.g. colorectal, lung, breast, gastric or ovarian cancer. The
CC medicament stimulates cytotoxic and helper T cell responses. The
CC antibodies are useful as vaccines to stimulate helper and cytotoxic T
CC cell responses. The polypeptides and nucleic acids are useful in
CC optimising immunisation schedules for enhancing a protective immune
CC response against cancer. The present sequence represents an Fv region
CC SC100 antibody CDR-L1 amino acid sequence which is used in an example
CC from the present invention
XX
SQ Sequence 16 AA;
Query Match 96.3%; Score 78; DB 5; Length 16;
Best Local Similarity 93.8%; Pred. No. 1.6e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RSSQSIVHSGNGTYLQ 16
Db 1 RSSQSIVHSGNGTYLQ 16
RESULT 5
ADC03151
ID ADC03151 standard; peptide; 16 AA.
XX
AC ADC03151;
XX
DT 18-DEC-2003 (first entry)
XX
DE Colon specific antigen-p mucin murine antibody light chain CDRI.
XX
KW cytostatic; antitumour; antibody; colon specific antigen-p mucin;
KW hapten binding site; immunoconjugate; close-range lesion; tumour; ovary;
KW thymus; parathyroid; spleen; carcinoma; gastrointestinal cancer;
KW colorectal cancer; pancreatic cancer; ovarian cancer;
KW complementarity determining region.
XX
OS Mus sp.
XX
FN WO200282041-A2.
XX
PD 17-OCT-2002.
XX
PF 03-APR-2002; 2002WO-US010235.
XX
PR 03-APR-2001; 2001US-00823746.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Hansen HJ, Griffiths GL, Leung S, McBride WJ, Qu Z;
PI Goldenberg DM;
XX
DR WPI; 2003-167089/16.
XX
PT Novel multivalent, multispecific antibody for detecting/treating tumors
PT expressing colon specific antigen-p mucin in mammal, comprises antigen
PT and hapten binding sites.
XX
PS Claim 9; Page 132; 202pp; English.
XX
CC The invention relates to a multivalent, multispecific antibody or its
CC fragment comprising one more antigen binding sites having affinity
CC towards colon specific antigen-p mucin (CSAp) target antigen and one
CC more hapten binding sites having affinity towards hapten molecules. The
CC antibody is useful for screening a targetable conjugate. A therapeutic
CC immunoconjugate comprising the antibody is useful for detecting close-
CC range lesion. The antibody or immunoconjugate are also useful for
CC delivering a diagnostic/detection or therapeutic agent, or their

CC combination, to a target. The antibody or a targetable conjugate are
 CC useful for detecting or treating tumours expressing CSAP in a mammal, for
 CC imaging malignant tissue or normal tissue or cells in a mammal expressing
 CC CSAP, where the normal tissue is from ovary, thymus, parathyroid or
 CC spleen, for intraoperatively identifying/disclosing the diseased tissues
 CC expressing CSAP in a subject, and for endoscopic identification of
 CC diseased tissues expressing CSAP. They are also useful for intravascular
 CC identification of diseased tissues expressing CSAP, for detecting lesions
 CC during an endoscopic, laparoscopic, intravascular catheter or surgical
 CC procedure, and for detecting and treating target cells, tissues or
 CC pathogens in a mammal. A method using the antibody is useful for
 CC diagnosing or detecting a malignancy in a subject, where the malignancy
 CC is carcinoma, gastrointestinal cancer, colorectal or pancreatic cancer or
 CC ovarian cancer, the subject is human or a domestic pet. This sequence
 CC represents the light chain complementarity determining region 1 (CDR1)
 CC from the antibodies of the invention.

XX
 SQ Sequence 16 AA;

Query Match 96.3%; Score 78; DB 7; Length 16;
 Best Local Similarity 93.8%; Pred. No. 1.6e-06;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RSSQSIVHSGNTYLQ 16
 DB 1 RSSQSIVHSGNTYLE 16

RESULT 6
 ADD94147
 ID ADD94147 standard; peptide; 16 AA.
 AC ADD94147;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Mouse HUI77 light chain CDR1 partial amino acid sequence SeqID32.
 XX
 KW grafted antibody; complementarity determining region; CDR; light CDR;
 KW heavy CDR; cryptic collagen epitope; solid tumour;
 KW new blood vessel growth; angiogenesis; tumour growth; cytostatic;
 KW collagen agonist; collagen antagonist; cancer metastasis;
 KW anti-cryptic collagen; antibody; HUI77; variable region light chain;
 KW mouse; murine.
 XX
 OS Mus musculus.
 XX
 PN WO2003046204-A2.
 XX
 PD 05-JUN-2003.
 XX
 PF 26-NOV-2002; 2002WO-US038147.
 XX
 PR 26-NOV-2001; 2001US-00995529.
 PR 06-DEC-2001; 2001US-00011250.
 XX
 PA (CELL-) CELL MATRIX INC.
 XX
 PI Watking JD, Huse WD, Tang Y, Broek D, Brooks PC;
 XX
 DR WPI; 2003-513649/48.
 DR N-PSDB; ADD94146.
 XX
 XX New cryptic collagen antibody with one or more complementarity
 PT determining regions, useful for diagnosing and treating disorders
 PT associated with angiogenesis, tumor growth and/or cancer metastasis.
 XX
 PS Claim 25; SEQ ID NO 32; 232pp; English.
 XX
 XX This invention relates to a novel grafted antibody or its functional
 CC fragment comprising one or more complementarity determining regions
 CC (CDRs) of a defined light CDR and a heavy CDR with at least one amino
 CC acid (aa) substitution where the antibody has specific binding activity

CC for a cryptic collagen epitope. The growth of all solid tumours requires
 CC new blood vessel growth, angiogenesis, inhibition of which is an approach
 CC to limiting tumour growth. The invention may allow development of
 CC therapeutics with a cytostatic activity as a collagen agonist or
 CC antagonist. The invention is useful for diagnosing and treating disorders
 CC associated with angiogenesis, tumour growth and/or cancer metastasis. The
 CC present sequence is the partial amino acid sequence of a mouse anti-
 CC cryptic collagen site antibody HUI77 variable region light chain CDR
 CC which is related to the invention.

XX
 SQ Sequence 16 AA;

Query Match 96.3%; Score 78; DB 7; Length 16;
 Best Local Similarity 93.8%; Pred. No. 1.6e-06;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RSSQSIVHSGNTYLQ 16
 DB 1 RSSQSIVHSGNTYLE 16

RESULT 7
 ADH61992
 ID ADH61992 standard; peptide; 16 AA.
 XX
 AC ADH61992;
 XX
 DT 25-MAR-2004 (first entry)
 XX
 DE Mouse antibody 2K1 VL region CDR1 SEQ ID NO:24.
 XX
 KW osteopontin; antibody; integrin; OPN; immunosuppressive; anti-arthritis;
 KW anti-rheumatic; osteopathic; autoimmune disease; rheumatism;
 KW rheumatoid arthritis; arthritis deformans; mouse; 2K1; CDR1.
 XX
 OS Mus sp.

XX
 PN WO2003027151-A1.
 XX
 PD 03-APR-2003.
 XX
 PF 25-SEP-2002; 2002WO-JP009868.
 XX
 PR 25-SEP-2001; 2001JP-00290700.
 XX
 PR (IMMU-) IMMUNO BIOLOGICAL LAB CO LTD.
 PA (FUJI) FUJISAWA PHARM CO LTD.
 XX
 PI Ueda T, Kon S, Yamamoto N, Higuchi H, Torikai M, Tokieda Y;
 PI Nakashima T, Maeda H;
 XX
 DR WPI; 2003-393331/37.
 XX
 PT Recombinant anti-osteopontin antibodies with human-origin heavy and light
 PT chain constant regions, useful in diagnostics and developing drugs for
 PT autoimmune diseases, rheumatism and rheumatoid arthritis.
 XX
 PS Claim 14; SEQ ID NO 24; 111pp; Japanese.

XX
 CC The invention relates to a novel anti-osteopontin antibody or antibody
 CC fragment which inhibits the binding of and integrin recognising the RGD
 CC sequence to osteopontin (OPN) or its fragment and inhibits the binding of
 CC an integrin recognising the SVYIGR sequence to osteopontin or its
 CC fragment. An antibody of the invention has immunosuppressive, anti-
 CC arthritic, anti-rheumatic, and osteopathic activity. The antibodies are
 CC useful in diagnostics and developing drugs for autoimmune diseases,
 CC rheumatism, rheumatoid arthritis and arthritis deformans. With these
 CC antibodies, it is possible to distinguish rheumatoid arthritis from
 CC arthritis deformans. The present sequence is used in the exemplification
 CC of the invention.

XX Sequence 16 AA;

Query Match 96.3%; Score 78; DB 7; Length 16;
 Best Local Similarity 93.8%; Pred. No. 1.6e-06;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSGNGTYLQ 16
 |||||
 Db 1 RSSQSIVHSGNGTYLQ 16

RESULT 8
 ADL27487
 ID ADL27487 standard; peptide; 16 AA.
 XX
 AC ADL27487;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE CDR from the light chain of antibody EGP6D8-1-2.
 XX
 KW glycoprotein; EGP6D8-1-1; EGP13F6-1-2; EGP13C6-1-1;
 KW Ebola virus infection; antibody; light chain;
 KW Complementarity determining region; CDR.
 XX
 OS Mus sp.
 XX
 XX WO2004018649-A2.
 PN
 XX
 PD 04-MAR-2004.
 XX
 XX 21-AUG-2003; 2003WO-US027450.
 PF
 XX
 XX 23-AUG-2002; 2002US-00226795.
 PR
 XX (USSA) US ARMY MEDICAL RES INST INFECTIOUS DISE.
 PA
 XX Hart MK, Wilson JA;
 PI WPT; 2004-226835/21.
 XX
 DR New isolated monoclonal antibody that binds Ebola virus GP, which
 PT monoclonal antibody comprises a heavy chain variable region, useful for
 PT treating or ameliorating Ebola virus infection.
 XX
 PS Claim 33; Page 65; 68pp; English.
 XX

The specification describes monoclonal antibodies that bind Ebola virus glycoprotein. The antibodies are EGP6D8-1-1, EGP13F6-1-2, and EGP13C6-1-1. The monoclonal antibodies of the invention are useful for treating or ameliorating an Ebola virus infection. The antibodies were found to be effective when administered 2 days after challenge, after significant viral replication had occurred. ADL27487-ADL27489 represent complementarity determining regions (CDRs) from the light chain of a monoclonal antibody of the invention.

SQ Sequence 16 AA;

Query Match 96.3%; Score 78; DB 8; Length 16;
 Best Local Similarity 93.8%; Pred. No. 1.6e-06;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSGNGTYLQ 16
 |||||
 Db 1 RSSQSIVHSGNGTYLQ 16

RESULT 9
 ADM78123
 ID ADM78123 standard; peptide; 16 AA.
 XX
 AC ADM78123;
 XX
 DT 01-JUL-2004 (first entry)
 XX

DE Human SUB3-38 antibody variable light chain CDR1 peptide region.
 XX monoclonal antibody; adenylate kinase isozyme 3;
 KW complementarity determining region; CDR; heart disease; marker AK3;
 KW biochemical; human; variable; light chain.
 XX
 OS Homo sapiens.
 XX
 PN WO2004029094-A1.
 XX
 PD 08-APR-2004.
 XX
 XX 27-SEP-2003; 2003WO-KR001979.
 PF
 XX
 PR 28-SEP-2002; 2002KR-00059211.
 XX
 XX (KIMH/) KIM H.
 PA
 XX Kim H;
 PI WPI; 2004-316088/29.
 DR
 XX New monoclonal antibody specific to human mitochondrial adenylate kinase
 PT isozyme 3, useful for preparing a composition for detecting a heart
 PT disease marker AK3.
 XX
 PS Claim 1; SEQ ID NO 86; 126pp; English.
 XX

The invention relates to a novel monoclonal antibody specific to adenylate kinase isozyme 3, comprising 4 or more of 6 complementarity determining regions (CDRs) of a sequence having 6-18 amino acids. The invention further relates to: a composition comprising the monoclonal antibody for detecting a heart disease marker AK3; a kit comprising the monoclonal antibody for the diagnosis of heart disease; and a method of detecting a heart disease marker AK3. The monoclonal antibody is useful for preparing a composition for detecting a heart disease marker AK3. The monoclonal antibody reduces false positive results of the conventional biochemical markers. This sequence represents a human antibody variable light chain CDR peptide region of the invention.

SQ Sequence 16 AA;

Query Match 96.3%; Score 78; DB 8; Length 16;
 Best Local Similarity 93.8%; Pred. No. 1.6e-06;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSGNGTYLQ 16
 |||||
 Db 1 RSSQSIVHSGNGTYLQ 16

RESULT 10
 ADM78129
 ID ADM78129 standard; peptide; 16 AA.
 XX
 AC ADM78129;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Human SUB3-39 antibody variable light chain CDR1 peptide region.
 XX
 KW monoclonal antibody; adenylate kinase isozyme 3;
 KW complementarity determining region; CDR; heart disease; marker AK3;
 KW biochemical; human; variable; light chain.
 XX
 OS Homo sapiens.
 XX
 PN WO2004029094-A1.
 XX
 PD 08-APR-2004.
 XX
 XX 27-SEP-2003; 2003WO-KR001979.
 PF
 XX

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PR 28-SEP-2002; 2002KR-00059211.
XX (KIMH/) KIM H.
XX Kim H;
XX WPI; 2004-316088/29.
XX New monoclonal antibody specific to human mitochondrial adenylate kinase
PT isozyme 3, useful for preparing a composition for detecting a heart
PT disease marker AK3.
XX Claim 1; SEQ ID NO 92; 126pp; English.
XX The invention relates to a novel monoclonal antibody specific to
CC adenylate kinase isozyme 3, comprising 4 or more of 6 complementarity
CC determining regions (CDRs) of a sequence having 6-18 amino acids. The
CC invention further relates to: a composition comprising the monoclonal
CC antibody for detecting a heart disease marker AK3; a kit comprising the
CC monoclonal antibody for the diagnosis of heart disease; and a method of
CC detecting a heart disease marker AK3. The monoclonal antibody is useful
CC for preparing a composition for detecting a heart disease marker AK3. The
CC monoclonal antibody reduces false positive results of the conventional
CC biochemical markers. This sequence represents a human antibody variable
CC light chain CDR peptide region of the invention.
XX Sequence 16 AA;
XX Query Match 96.3%; Score 78; DB 8; Length 16;
XX Best Local Similarity 93.8%; Pred. No. 1.6e-06;
XX Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RSSQSIVHSGNGNTYLQ 16
DB |||||:
1 RSSQSIVHSGNGNTYLE 16

RESULT 12
ADP84865
ID ADP84865 standard; peptide; 16 AA.
XX AC ADP84865;
XX DT 09-SEP-2004 (first entry)
XX DE Complementarity determining region SEQ ID NO 7.
XX antibody; Core-1 antigen; framework region; immunoglobulin superfamily;
KW protease inhibitor; lectin; helix-bundle protein; lipocalin;
KW variable heavy chain; VH; variable light chain; VL; vaccine; diagnosis;
KW alleviation; treatment; tumour; breast; colon; stomach; pancreas;
KW large/small intestine; ovary; cervix; lung; prostate; kidney; liver;
KW metastasis.
XX OS Unidentified.
XX PN WO2004050707-A2.
XX PD 17-JUN-2004.
XX PF 01-DEC-2003; 2003WO-DE003994.
XX PR 29-NOV-2002; 2002DE-01056900.
XX PA (NEMO-) NEMOD BIOTHERAPEUTICS GMBH & CO KG.
XX PI Goletz S, Danielczyk A, Karsten U, Ravn P, Stahn R;
XX Christensen PA;
XX WPI; 2004-461095/43.
XX New recognition molecules, e.g. antibodies (and nucleic acids) that bind
PT specifically to Core-1 antigens, useful for diagnosis, treatment and
PT prevention of tumors and metastases.
XX Claim 2; SEQ ID NO 7; 136pp; German.
XX This invention describes novel recognition molecules, especially
CC antibodies that bind specifically to the Core-1 antigen. The recognition
CC molecules are used to make constructs containing the framework regions
CC that separate, include and/or flank the specified sequences, especially
CC where the framework regions are from the immunoglobulin (Ig) superfamily,
CC protease inhibitors, lectins, helix-bundle proteins and/or lipocalins.
CC Most especially the framework regions are from antibodies, particularly
CC the variable heavy chain (VH) and the variable light chain (VL) of human
CC and/or murine origin. The constructs may also include a His or myc tag, a
CC lysine-rich region and/or a multimerisation domain, most particularly it

```

CC is a single-chain antibody fragment, multibody, Fab fragment, fusion
 CC protein of an antibody fragment with peptide or protein, and/or an Ig of
 CC types G, M, A, E or D and/or their subclasses. It may be human,
 CC humanised, murine or chimeric, e.g. IgM without the J chain. The
 CC additional sequences/structures in the constructs are Ig domains of
 CC various species, interacting or stabilising domains, signal sequences,
 CC fluorescent dyes, toxins, antibodies with catalytic activity or other
 CC specificities, cytolytic agents, enzymes, immuno-modulators or
 CC effectors, MHC molecules, antigens, chelators for radioactive labels,
 CC liposomes, transmembrane domains, viruses and/or cells, specifically
 CC macrophages. The antibodies, also constructs containing them, nucleic
 CC acid encoding them, and related vectors and host cells, are useful for
 CC prevention (e.g. as vaccine), diagnosis, alleviation, treatment,
 CC monitoring and/or secondary treatment of tumours (specifically of breast,
 CC colon, stomach, pancreas, large/small intestine, ovary, cervix, lung,
 CC prostate, kidney and/or liver) and/or metastases (particularly to liver),
 CC specifically where these are positive for the C1 antigen. The products of
 CC the invention provide simple, reliable and efficient detection of
 CC tumours. They are specific for carcinoma and show almost no binding to
 CC healthy tissue.

XX Sequence 16 AA;

Query Match 96.3%; Score 78; DB 8; Length 16;
 Best Local Similarity 93.8%; Pred. No. 1.6e-06;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSNGNTYLQ 16
 |||||
 Db 1 RSSQSIVHSNGNTYLE 16

RESULT 13

ADRI9270
 ID ADRI9270 standard; peptide; 16 AA.

XX AC ADRI9270;

XX DT 21-OCT-2004 (first entry)

XX DE Glycosylated MUC1 tumour epitope recognition peptide, SEQ ID 7.

XX KW Recognition molecule; bind; glycosylated MUC1 tumour epitope; mucin 1;
 XX KW tumour; metastatic; carcinoma; breast; colon; stomach; pancreas; ovary;
 XX KW liver; kidney cell; intestinal; lung cancer; multiple myeloma.

XX OS Unidentified.

XX PN WO2004065423-A2.

XX PD 05-AUG-2004.

XX PF 23-JAN-2004; 2004WO-DE000132.

XX PR 23-JAN-2003; 2003DE-01003664.

XX PA (NEMO-) NEMOD BIOTHERAPEUTICS GMBH & CO KG.

XX PI Goletz S, Danielczyk A, Stahn R, Karsten U;

XX DR WPI; 2004-593433/57.

XX PT New recognition molecules that bind the glycosylated MUC1 tumour epitope,
 XX PT useful for prevention, diagnosis, treatment and monitoring of tumors.

XX PS Claim 4; SEQ ID NO 7; 158pp; German.

XX CC The invention relates to novel recognition molecules comprising sequences
 XX CC that bind specifically to a glycosylated MUC1 tumour epitope. The novel
 XX CC recognition molecules comprise: sequences ADRI9264 or ADRI9265; sequences
 XX CC ADRI9266 or ADRI9267 and sequences ADRI9268 and ADRI9269, and bind
 XX CC specifically to the glycosylated mucin 1 (MUC1) tumour epitope. The
 XX CC invention further comprises: a construct comprising the recognition

CC molecule fused, chemically coupled or non-covalently associated with
 CC additional sequences and/or structures; an isolated nucleic acid that
 CC encodes the recognition molecule or construct; expression cassette or
 CC vector that contains the isolated nucleic acid, operatively linked to a
 CC promoter; virus or host cell comprising at least one cassette or vector
 CC of ADRI9266; an organism containing at least one host cell of ADRI9267; a
 CC method for preparing the recognition molecule and construct; and a kit
 CC containing the recognition molecule and/or construct. The recognition
 CC molecules have cytostatic activity. The recognition molecules, constructs
 CC containing them, the nucleic acid encoding them, and derived viruses,
 CC cells and organisms, are used for prevention, diagnosis, treatment and
 CC monitoring of tumours and/or metastases, specifically where MUC1
 CC positive, particularly carcinoma of breast, colon, stomach, pancreas,
 CC ovary, liver or kidney cells; (gastro)intestinal or lung cancers and
 CC multiple myeloma. The recognition molecules show little or no binding to
 CC MUC1 in either the serum or normal tissue, so provides simple, safe and
 CC efficient detection of tumours, even at an early stage (carcinoma in
 CC situ), and can differentiate between tumours and benign diseases. This
 CC sequence represents one of the novel glycosylated MUC1 tumour epitope
 CC recognition molecules of the invention.

XX Sequence 16 AA;

Query Match 96.3%; Score 78; DB 8; Length 16;
 Best Local Similarity 93.8%; Pred. No. 1.6e-06;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSNGNTYLQ 16
 |||||
 Db 1 RSSQSIVHSNGNTYLE 16

RESULT 14

ADS87339
 ID ADS87339 standard; peptide; 16 AA.

XX AC ADS87339;

XX DT 18-NOV-2004 (first entry)

XX DE Humanised antibody MN3 light chain variable region CDR1.

XX KW cytostatic; vasotropic; antimicrobial; antinflammatory; antipyretic;
 XX KW antiatherosclerotic; cardiac; monoclonal antibody; NCA90; NCA95;
 XX KW chimeric antibody; humanized antibody; inflammation; appendicitis;
 XX KW inflammatory bowel disease; pelvic inflammatory disease; fever;
 XX KW cystic fibrosis; granulocyte related disorder; atherosclerosis;
 XX KW infarction; cancer; ischemic lesion; complementarity determining region.

XX OS Homo sapiens.

XX OS Mus sp.

XX OS Chimeric.

XX PN WO2004029093-A2.

XX PD 08-APR-2004.

XX PF 30-SEP-2003; 2003WO-GB004229.

XX PR 30-SEP-2002; 2002US-0414341P.

XX PA (IMMU-) IMMUNOMEDICS INC.

XX PA (MCCA/) MCCALL J D.

XX PI Goldenberg DM, Hansen H, Leung S;

XX DR WPI; 2004-329873/30.

XX PT Monoclonal anti-granulocyte antibody that binds NCA90 and NCA95 antigens,
 XX PT useful for treating malignancy, inflammation, atherosclerosis,
 XX PT infarction, or other granulocyte related disorders.

XX PS Claim 4; Page 105; 134pp; English.

XX CC The invention relates to a monoclonal antibody (Mab) (I) or its fragment
CC that binds NCA90 or NCA95, where when the Mab or its fragment binds NCA90
CC the Mab or its fragment is chimeric, partially humanized or fully
CC humanized and where when the Mab or its fragment binds NCA95 the Mab or
CC its fragment is either fully humanized or chimeric, partially humanized
CC or fully humanized BW 250/183. (I) is useful for treating, detecting or
CC imaging sites of inflammation resulting from appendicitis, inflammatory
CC bowel disease, pelvic inflammatory disease, fever and cystic fibrosis and
CC treating granulocyte related disorders, atherosclerosis and infarction.
CC (I) is useful for detecting or treating cancer or ischemic lesion. This
CC sequence corresponds to the complementarity determining region 1 (CDR1)
CC of the light chain of the antibody of the invention.

XX SQ Sequence 16 AA;
SQ Query Match 96.3%; Score 78; DB 8; Length 16;
Best Local Similarity 93.8%; Pred. No. 1.6e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSNGNTYLQ 16
| | | | | | | | | | | | | | | |
Db 1 RSSQSIVHSNGNTYLE 16

RESULT 15
AAU70349
ID AAU70349 standard; peptide; 16 AA.
AC AAU70349;
XX 14-FEB-2002 (first entry)
XX Mouse Kappa II light chain CDR1.
DE Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
KW complementarity determining region; framework region; IgBP;
KW transgenic plant; immunoglobulin binding protein array; IgW; IgG; IgA;
KW IgD; IgE; IgY; IgM; kappa; lambda; CHBP.
XX Mus musculus.
OS
XX WO200183806-A1.
FN
XX 08-NOV-2001.
PD
XX 02-MAY-2001; 2001WO-US014349.
PF
XX 02-MAY-2000; 2000US-00563222.
PR
XX (EPIC-) EPICYTE PHARM INC.
PA
XX Hiatt AC, Hein MB;
PI
XX WPI; 2002-055482/07.
DR
XX
XX Preparing immunoglobulin binding protein array in plant cells by
PT transforming the cells with different polynucleotides encoding binding
PT protein polypeptides specific to ligand, selecting plant cells for
PT preparing array.
XX
PS Disclosure; Page 14; 129pp; English.
XX
XX The invention relates to transforming a population of cells (e.g. plant
CC cells), comprising using a library of two different polynucleotides
CC encoding different immunoglobulin binding protein (IgBP) polypeptides
CC that specifically bind to a ligand or form one or more disulphide bonds
CC with polypeptides in transfected cells, to generate an IgBP that binds to
CC a ligand, and transformed plant cells are selected, and preparing an IgBP
CC array in plant cells. At least one peptide sequence has at least 75%
CC sequence identity to a framework region (FR) of a native IgM, IgG, IgA,
CC IgD, IgE, IgY, kappa or lambda immunoglobulin molecule. The method is
CC useful for preparing an immunoglobulin binding protein array, preferably

CC heavy chain binding protein (CHBP) array in eukaryotic cells especially
CC plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic
CC cells (e.g. insect cells or mammalian cells). The CHBP is useful for
CC discovery of e.g. screening assays of IgBPs having desired
CC characteristics. The present sequence is a mammalian immunoglobulin
CC derived peptide that may be incorporated into an IgBP of the invention

XX SQ Sequence 16 AA;
SQ Query Match 93.8%; Score 76; DB 5; Length 16;
Best Local Similarity 87.5%; Pred. No. 3.6e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSNGNTYLQ 16
| | | | | | | | | | | | | | | |
Db 1 RSSQSIVHSNGNTYLE 16

Search completed: December 30, 2005, 14:19:57
Job time : 139.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: December 30, 2005, 14:07:14 ; Search time 22.5 seconds
(without alignments)
68.421 Million cell updates/sec

Title: US-10-735-916A-2
Perfect score: 81
Sequence: 1 RSSQSIVHNGNTYLQ 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 250

Minimum DB seq length: 16
Maximum DB seq length: 16

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: Pirl:*
2: Pirl:*
3: Pirl:*
4: Pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	34.6	16	2 A36285	site-specific meth
2	21	25.9	16	2 B45895	T-cell surface gly
3	18	22.2	16	2 A59046	alpha-conotoxin MI
4	18	22.2	16	2 G24304	ribosomal protein
5	18	22.2	16	2 A44352	candidapepsin (EC
6	18	22.2	16	2 H49039	T-cell receptor be
7	18	22.2	16	2 S42237	hypothetical prote
8	18	22.2	16	2 D89854	conserved hypotet
9	18	22.2	16	2 PD0002	inulin fructotrans
10	17	21.0	16	2 S51610	hypothetical prote
11	16.5	20.4	16	2 E28027	protein P8 - curle
12	16	19.8	16	2 C39509	mannose-specific l
13	16	19.8	16	2 A45681	orf 61.1 - phage r
14	16	19.8	16	2 S23184	redoxendonuclease
15	16	19.8	16	2 A49226	major outer membra
16	16	19.8	16	2 S09732	photosystem I prot
17	16	19.8	16	2 A36889	leu operon leader
18	15	18.5	16	2 S01689	rRNA N-glycosidase
19	15	18.5	16	2 PH1778	T cell receptor al
20	15	18.5	16	2 G49039	T-cell receptor be
21	15	18.5	16	2 PH0777	25K kidney and gal
22	15	18.5	16	2 E58501	melanotropin beta
23	14	17.3	16	1 MTDFPS	casein kinase II (
24	14	17.3	16	2 C45133	protein-tyrosine-p
25	14	17.3	16	2 C45143	chitinase (EC 3.2.
26	14	17.3	16	2 F4908	hypothetical prote
27	14	17.3	16	2 A39109	T-cell-receptor be
28	14	17.3	16	2 C49655	T-cell receptor be
29	14	17.3	16	2 G53284	T-cell receptor be

30	14	17.3	16	2 PH1622	Ig H chain V-D-J r
31	14	17.3	16	2 S33589	beta-crystallin A4
32	14	17.3	16	2 S69361	carbamoyl-phosphat
33	14	17.3	16	2 B44820	7K protein - Eache
34	13	16.0	16	2 S00123	dihydrolipoamide S
35	13	16.0	16	2 S10807	protein kinase c 1
36	13	16.0	16	2 A36300	T-cell receptor ga
37	13	16.0	16	2 A45133	casein kinase II (
38	13	16.0	16	2 C58503	proteoglycan assoc
39	13	16.0	16	2 B24099	crystal protein, 7
40	13	16.0	16	2 PH1770	T cell receptor al
41	13	16.0	16	2 H41299	T-cell receptor be
42	13	16.0	16	2 PH0137	T-cell receptor be
43	13	16.0	16	2 E49255	T-cell receptor be
44	13	16.0	16	2 E53284	T-cell receptor be
45	13	16.0	16	2 PH1588	Ig H chain V-D-J r

ALIGNMENTS

RESULT 1

A36285 site-specific methyltransferase (EC 2.1.1.-) - Escherichia coli (fragment)
C;Species: Escherichia coli
C;Date: 18-Jan-1991 #sequence_revision 18-Jan-1991 #text_change 21-Mar-1996
C;Accession: A36285
R;Reich, N.O.; Everett, E.A.
J. Biol. Chem. 265, 8929-8934, 1990
A;Title: Identification of peptides involved in S-adenosylmethionine binding in the Eco
A;Reference number: A36285; MUID:90256827; PMID:2341412
A;Accession: A36285
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-16 <REI>
A;Cross-references: UNIPARC:UPI000017AA66
C;Keywords: methyltransferase

Query Match 34.6%; Score 28; DB 2; Length 16;
Best Local Similarity 30.8%; Pred. No. 1.8e+02;
Matches 4; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 3 SQSIVHNGNTYL 15
::: : |||| :
DB 2 TEAXIDSGNXXII 14

RESULT 2

B45895 T-cell surface glycoprotein CD28 short form - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Feb-1994
C;Accession: B45895
R;Lee, K.P.; Taylor, C.; Petryniak, B.; Turka, L.A.; June, C.H.; Thompson, C.B.
J. Immunol. 145, 344-352, 1990
A;Title: The genomic organization of the CD28 gene. Implications for the regulation of
A;Reference number: A45895; MUID:90293482; PMID:2162892
A;Accession: B45895
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-16 <LEE>
A;Cross-references: UNIPARC:UPI000017C3C5; GB:M37813
C;Keywords: glycoprotein

Query Match 25.9%; Score 21; DB 2; Length 16;
Best Local Similarity 37.5%; Pred. No. 2.7e+03;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSSQSIVH 8
::: : ||: ||
DB 9 KSNGTIIH 16

```
RESULT 3
A59046
alpha-conotoxin MII - cone shell (Conus magus)
C:Species: Conus magus (magus cone)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: A59046
R:Cartier, G.E.; Yoshikami, D.; Gray, W.R.; Luo, S.; Olivera, B.M.; McIntosh, J.M.
J. Biol. Chem. 271, 7522-7528, 1996
A:Title: A new alpha-conotoxin which targets alpha3beta2 nicotinic acetylcholine recepto
A:Reference number: A59046; MUID:96205934; PMID:8631783
A:Accession: A59046
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-16 <CAR>
A:Cross-references: UNIPROT:P56636; UNIPARC:UPI00001287CA
C:Superfamily: alpha-conotoxin
C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuro
F:1-16/Product: alpha-conotoxin MII #status experimental <NAR>
F:2-8,3-16/Disulfide bonds: #status experimental
F:16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 22.2%; Score 18; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 HSN 10
Db 12 HSN 14

RESULT 4
G24304
ribosomal protein H [validated] - Haloarcula marismortui (fragment)
C:Species: Haloarcula marismortui
C:Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 21-Jul-2000
C:Accession: G24304
R:Shoham, M.; Dijk, J.; Reinhardt, R.; Wittmann-Liebold, B.
FEBS Lett. 204, 323-330, 1986
A:Title: Purification and characterization of ribosomal proteins from the 30 S subunit o
A:Reference number: A24304
A:Accession: G24304
A:Molecule type: protein
A:Residues: 1-16 <SHO>
A:Cross-references: UNIPARC:UPI000017ABA2
C:Keywords: protein biosynthesis; ribosome

Query Match 22.2%; Score 18; DB 2; Length 16;
Best Local Similarity 75.0%; Pred. No. 8.7e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 GNTY 14
Db 2 GNKY 5

RESULT 5
A44352
candidapepsin (EC 3.4.23.24), white-opaque switching regulated - yeast (Candida albicans
C:Species: Candida albicans
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 22-Nov-1996
C:Accession: A44352
R:Morrow, B.; Srikantha, T.; Soll, D.R.
Mol. Cell. Biol. 12, 2997-3005, 1992
A:Title: Transcription of the gene for a pepsinogen, PEP1, is regulated by white-opaque
A:Reference number: A44352; MUID:92318916; PMID:1620110
A:Accession: A44352
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-16 <MOR>
A:Cross-references: UNIPARC:UPI000017B22C
C:Keywords: aspartic proteinase; hydrolase

Query Match 22.2%; Score 18; DB 2; Length 16;
```

```
Best Local Similarity 25.0%; Pred. No. 8.7e+03;
Matches 3; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 2 SSQSIHVSNGNT 13
Db 5 TGSVLDLSGTT 16

RESULT 6
H49039
T-cell receptor beta chain V-D-J-C region (V beta 5, J beta 1.4) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
C:Accession: H49039
R:Rosenberg, W.M.; Moss, P.A.; Bell, J.I.
Eur. J. Immunol. 22, 541-549, 1992
A:Title: Variation in human T cell receptor V beta and J beta repertoire: analysis using
A:Reference number: A49039; MUID:92164737; PMID:1311263
A:Accession: H49039
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-16 <ROS>
A:Cross-references: UNIPARC:UPI000017C3B7
A:Note: sequence extracted from NCEI backbone (NCBIP:90720)
C:Keywords: T-cell receptor

Query Match 22.2%; Score 18; DB 2; Length 16;
Best Local Similarity 60.0%; Pred. No. 8.7e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 9 SNGNT 13
Db 5 ANGQT 9

RESULT 7
S42237
hypothetical protein 2 - Staphylococcus aureus plasmid pNS1
C:Species: Staphylococcus aureus
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S42237
R:Inoguchi, N.; Aoki, T.; Sasatsu, M.; Kono, M.; Shishido, K.; Ando, T.
FEMS Microbiol. Lett. 37, 283-288, 1986
A:Title: Determination of the complete nucleotide sequence of pNS1, a staphylococcal tet
A:Reference number: S42236
A:Accession: S42237
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-16 <NOG>
A:Cross-references: UNIPROT:Q51950; UNIPARC:UPI0000081F13; EMBL:M16217; NID:g150832; PII
C:Genetics:
A:Genome: plasmid pNS1

Query Match 22.2%; Score 18; DB 2; Length 16;
Best Local Similarity 75.0%; Pred. No. 8.7e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 GNTY 14
Db 9 GNLY 12

RESULT 8
DB9854
conserved hypothetical protein SAS021 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: DB9854
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
```

A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: D89854
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-16 <KUR>
A;Cross-references: UNIPROT:Q99VH9; UNIPARC:UPI00000CA988; GB:BA000018; FID:g13700694; R
A;Experimental source: strain N315
C;Genetics:
A;Gene: SAS021

Query Match 22.2%; Score 18; DB 2; Length 16;
Best Local Similarity 42.9%; Pred. No. 8.7e+03;
Matches 6; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

QY 1 RSSQSIVHNGNTY 14
||| ||| :|
DB 3 RSQASI--GTGHTY 14

RESULT 9

PD0002
inulin fructotransferase (depolymerizing, difructofuranose-1,2':2,3'-dianhydride-forming
C;Species: Bacillus sp.
C;Date: 10-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 09-Jul-2004
C;Accession: PD0002
R;Kang, S.I.; Kim, W.P.; Chang, Y.J.; Kim, S.I.
Biocell. Biotechnol. Biochem. 82, 628-631, 1998
A;Title: Purification and properties of inulin fructotransferase (DFA III-producing) frd
A;Reference number: PD0002
A;Accession: PD0002
A;Molecule type: protein
A;Residues: 1-16 <KAN>
A;Cross-references: UNIPROT:Q7M025; UNIPARC:UPI000017CD57
C;Keywords: glycosyltransferase; hexosyltransferase

Query Match 22.2%; Score 18; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 NTY 14
|||
DB 13 NTY 15

RESULT 10

S51610
hypothetical protein - tomato
C;Species: Lycopersicon esculentum (tomato)
C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 07-May-1999
C;Accession: S51610
R;Krolkiewicz, S.; Saenger, H.L.; Niesbach-Kloesgen, U.
Mol. Gen. Genet. 245, 565-576, 1994
A;Title: Structural and functional characterisation of the signal recognition particle-s
A;Reference number: S51597; MUID:95107255; PMID:7808407
A;Accession: S51610
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-16 <KRO>
A;Cross-references: UNIPARC:UPI000017B08B; EMBL:Z34527

Query Match 21.0%; Score 17; DB 2; Length 16;
Best Local Similarity 80.0%; Pred. No. 1.3e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSSQS 5
|||
DB 10 RSSSS 14

RESULT 11

E28027
protein P8 - curled-leaved tobacco (fragment)
C;Species: Nicotiana plumbaginifolia (curled-leaved tobacco)

C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 09-Jul-2004
C;Accession: E28027
R;Bauw, G.; De Loose, M.; Inze, D.; Van Montagu, M.; Vandekerckhove, J.
Proc. Natl. Acad. Sci. U.S.A. 84, 4806-4810, 1987
A;Title: Alterations in the phenotype of plant cells studied by NH2-terminal amino acid
A;Reference number: A94167
A;Accession: E28027
A;Molecule type: protein
A;Residues: 1-16 <BAU>
A;Cross-references: UNIPROT:Q7M1V7; UNIPARC:UPI000017B09F
A;Note: 10-Lys was also found

Query Match 20.4%; Score 16.5; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 1.6e+04;
Matches 5; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY 6 IVHSGNGN-TY 14
||| :|:|
DB 7 IVANDGSKTY 16

RESULT 12

C39509
mannose-specific lectin B-SJA-II chain b-1, bark - Japanese pagoda tree (fragment)
C;Species: Sophora japonica (Japanese pagoda tree)
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 31-Dec-2004
C;Accession: C39509
R;Ueno, M.; Ogawa, H.; Matsumoto, I.; Seno, N.
J. Biol. Chem. 266, 3146-3153, 1991
A;Title: A novel mannose-specific and sugar specifically aggregatable lectin from the b
A;Reference number: A39509; MUID:91131618; PMID:1993686
A;Accession: C39509
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-16 <UEN>
A;Cross-references: UNIPROT:P93537; UNIPARC:UPI000017B075
C;Superfamily: lectin

Query Match 19.8%; Score 16; DB 2; Length 16;
Best Local Similarity 40.0%; Pred. No. 1.9e+04;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 6 IVHSGNGNTYL 15
||| :|:
DB 5 IVAVEFDTVI 14

RESULT 13

G45681
orf 61.1 - phage T6 (fragment)
C;Species: phage T6
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994
C;Accession: G45681
R;Selick, H.B.; Stormo, G.D.; Dyson, R.L.; Alberts, B.M.
J. Virol. 67, 2305-2316, 1993
A;Title: Analysis of five presumptive protein-coding sequences clustered between the pr
A;Reference number: A45681; MUID:93188183; PMID:8383243
A;Accession: G45681
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-16 <SBL>
A;Cross-references: UNIPARC:UPI000017A83E
A;Note: sequence extracted from NCBI backbone (NCBIP:128349)

Query Match 19.8%; Score 16; DB 2; Length 16;
Best Local Similarity 11.1%; Pred. No. 1.9e+04;
Matches 1; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSSQSIVHS 9
:|:|:|:|
DB 6 KXSKNVINT 14

RESULT 14

S23184
redoxendonuclease (EC 4.2.99.-) - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Mar-1997 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
C;Accession: S23184
R;Hug, I.; Haukanes, B.I.; Helland, D.E.
Eur. J. Biochem. 206, 833-839, 1992
A;Title: Purification to homogeneity and characterization of a redoxendonuclease from calf thymus
A;Reference number: S23184; MUID:92299012; PMID:1376689
A;Accession: S23184
A;Molecule type: protein
A;Residues: 1-16 <HUQ>
A;Cross-references: UNIPARC:UPI000017C559
A;Experimental source: thymus
C;Function:
A;Description: recognizes and induces cleavage of DNA damaged by UV
C;Keywords: carbon-oxygen lyase

Query Match 19.8%; Score 16; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 1.9e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 SNGNTY 14
|:|
Db 1 SSGPAY 6

RESULT 15

A49226
major outer membrane protein - Haemophilus somnus (fragment)
C;Species: Haemophilus somnus
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A49226
R;Tagawa, Y.; Ishikawa, H.; Yuasa, N.
Infect. Immun. 61, 91-96, 1993
A;Title: Purification and partial characterization of the major outer membrane protein of Haemophilus somnus
A;Reference number: A49226; MUID:93114910; PMID:8418069
A;Contents: 8025
A;Accession: A49226
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-16 <TAG>
A;Cross-references: UNIPROT:Q9R5E9; UNIPARC:UPI00000BE2A7
A;Note: sequence extracted from NCBI backbone (NCBIP:121595)

Query Match 19.8%; Score 16; DB 2; Length 16;
Best Local Similarity 28.6%; Pred. No. 1.9e+04;
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 5 SIVHSNG 11
:::|
Db 2 TVINQNG 8

Search completed: December 30, 2005, 14:25:36
Job time : 24.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2005, 14:06:48 ; Search time 141.5 Seconds
(without alignments)
79.777 Million cell updates/sec

Title: US-10-735-916A-2
Perfect score: 81
Sequence: 1 RSSQSIVHSGNTYLQ 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 1144

Minimum DB seq length: 16
Maximum DB seq length: 16

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	29.6	16	Q8MUV9	SCHMA
2	22	27.2	16	Q9N235	9PRIM
3	21	25.9	16	Q7Y0M3	MAIZE
4	20	24.7	16	Q8MJT2	HORSE
5	20	24.7	16	Q9LAP2	ENTFC
6	20	24.7	16	Q89560	HV8
7	19	23.5	16	Q4YGP0	PLABE
8	19	23.5	16	Q8MBB6	PINTA
9	19	23.5	16	Q8MBE7	PINEL
10	19	23.5	16	Q9S8Y6	LUPAR
11	19	23.5	16	Q8MB85	PINEC
12	19	23.5	16	Q78377	GHV1
13	18	22.2	16	PPAC	BACHE
14	18	22.2	16	Q9UCR2	HUMAN
15	18	22.2	16	Q7RJ25	PLAYO
16	18	22.2	16	Q4YQ63	PLABE
17	18	22.2	16	Q9TR82	PIG
18	18	22.2	16	Q51950	92ZZZ
19	18	22.2	16	Q5DUAL	98TAP
20	18	22.2	16	Q7M0Z5	BACSP
21	18	22.2	16	Q6GB29	STAAS
22	18	22.2	16	Q6GI19	STAAR
23	18	22.2	16	Q7A6N0	STAAN
24	18	22.2	16	Q9VH9	STAM
25	17.5	21.6	16	Q9R4Z5	STRSU
26	17	21.0	16	C146	CYPDO
27	17	21.0	16	Q16183	HUMAN
28	17	21.0	16	Q9UC55	HOMO sapien
29	17	21.0	16	Q7PD45	PLAYO
30	17	21.0	16	Q4G403	MACCU
31	17	21.0	16	Q9S940	BETVU

32 17 21.0 16 2 Q80XZ9 9MURI
33 16.5 20.4 16 2 Q7M1V7 NICPL
34 16 19.8 16 1 CFAB BOVIN
35 16 19.8 16 1 NEP FVLJ3
36 16 19.8 16 2 P79034 EMENI
37 16 19.8 16 2 Q7S0C4 NEUCR
38 16 19.8 16 2 Q86UF7 HUMAN
39 16 19.8 16 2 Q9UC75 HUMAN
40 16 19.8 16 2 Q5C0J9 SCHJA
41 16 19.8 16 2 P79137 CERAE
42 16 19.8 16 2 Q6Q142 BOVIN
43 16 19.8 16 2 Q7JFV3 SHEEP
44 16 19.8 16 2 Q9TR88 BOVIN
45 16 19.8 16 2 Q9TSK2 VULVU

Q80XZ9 rattus sp.
Q7M1V7 nicotiana p
P81187 bos taurus
P12480 human immun
P79034 emericella
Q790C4 neurospora
Q86UF7 homo sapien
Q9UC75 homo sapien
Q5C0J9 schistosoma
P79137 cercopithec
Q6Q142 bos taurus
Q7JFV3 ovis aries
Q9TR88 bos taurus
Q9TSK2 vulpes vulp

ALIGNMENTS

RESULT 1

Q8MUV9 SCHMA
ID Q8MUV9 SCHMA PRELIMINARY; PRT; 16 AA.
AC Q8MUV9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Elastase 2a (Fragment).
GN NamesCE-2a;
OS Schistosoma mansoni (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatoidea; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6183;
RN [1]
RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=22086216; PubMed=11986325; DOI=10.1074/jbc.M202364200;
RA Salter J.P., Choe Y., Albrecht H., Franklin C., Lim K.C., Craik C.S.,
RA McKerrow J.H.;
RT "Cercarial elastase is encoded by a functionally conserved gene family
RT across multiple species of schistosomes";
RL J. Biol. Chem. 277:24618-24624(2002).
DR EMBL; AF510338; AAM43940.1; -; Genomic_DNA.
FT NON TER 16
SQ SEQUENCE 16 AA; 1910 MW; 88B1DFEAF61AE5 CRC64;
Query Match 29.6%; Score 24; DB 2; Length 16;
Best Local Similarity 66.7%; Pred. No. 4.1e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 NGNTYL 15
DB 3 NGRTFL 8

RESULT 2

Q9N235 9PRIM
ID Q9N235 9PRIM PRELIMINARY; PRT; 16 AA.
AC Q9N235;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cytochrome c oxidase polypeptide VIIa-heart (Fragment).
OS Nycticebus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Strepsirrhini; Loridae;
OC Nycticebus.
OX NCBI_TaxID=108082;
RN [1]
RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=9268136; PubMed=10335655;
RA Schmidt T.R., Goodman M., Grossman L.I.;
RA "Molecular evolution of the COX7A gene family in primates.";
RL Mol. Biol. Evol. 16:619-626(1999).
DR EMBL; AF127786; AAF72744.1; -; Genomic_DNA.

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FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1822 MW; E586241C602C15E8 CRC64;

Query Match
Best Local Similarity 27.2%; Score 22; DB 2; Length 16;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RSSQSIVHS 9
   |||::|
Db 5 RVSQLIRS 13

RESULT 3
QYOM3 MAIZE
ID Q7YOM3 MAIZE PRELIMINARY; PRT; 16 AA.
AC Q7YOM3;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Starch branching enzyme IIB (Fragment).
GN Name=ael;
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15377761; DOI=10.1105/tpc.104.025700;
RA Wilson L.M., Whitt S.R., Ibanez A.M., Rocheford T.R., Goodman M.M.,
RA Buckler E.S.;
RT "Dissection of maize kernel composition and starch production by
RT candidate gene association.";
RL Plant Cell 16:2719-2733(2004).
DR EMBL; AY290277; AAP44840.1; -; Genomic_DNA.
FT NON_TER 1 1
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1656 MW; AA2246F178DD5A4 CRC64;

Query Match
Best Local Similarity 25.9%; Score 21; DB 2; Length 16;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 HSNQNT 13
   |||::|
Db 1 HASSNT 6

RESULT 4
Q8MJT2 HORSE
ID Q8MJT2 HORSE PRELIMINARY; PRT; 16 AA.
AC Q8MJT2;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Laminin 5 gamma 2 (Fragment).
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Spirito F., Meneguzzi G.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF292647; RAM54459.1; -; mRNA.
DR InterPro; IPR000034; Laminin_B.
DR ProDom; PD003031; Laminin_B.1.
FT NON_TER 1 1
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1751 MW; 10CCECB38DCAB5C8 CRC64;

Query Match
Best Local Similarity 24.7%; Score 20; DB 2; Length 16;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 HSNQNT 12
   |||::|
Db 2 HSSGD 6

RESULT 5
Q9LAP2 ENTFC
ID Q9LAP2 ENTFC PRELIMINARY; PRT; 16 AA.
AC Q9LAP2;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE VanY (Fragment).
GN Name=vanYb;
OS Enterococcus faecium (Streptococcus faecium).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1352;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=TUH7-15;
RX MEDLINE=20307504; PubMed=10846225;
RA Dahl K.H., Lundblad E.W., Rokenes T.P., Olavik O., Sundsfjord A.;
RT "Genetic linkage of the vanB2 gene cluster to Tn5382 in vancomycin-
RT resistant enterococci and characterization of two novel insertion
RT sequences.";
RL Microbiology 146:1469-1479(2000).
DR EMBL; AF125554; AAP73102.1; -; Genomic_DNA.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1991 MW; 30402510516D5F9A CRC64;

Query Match
Best Local Similarity 24.7%; Score 20; DB 2; Length 16;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 QSVHNSGN 12
   |||::|
Db 3 KSNYHSNAD 11

RESULT 6
O89560 HHV8
ID O89560 HHV8 PRELIMINARY; PRT; 16 AA.
AC O89560;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Minor capsid protein (Fragment).
OS Human herpesvirus 8 (HHV-8) (Kaposi's sarcoma-associated herpesvirus).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=37296;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99034644; PubMed=9815212; DOI=10.1086/314514;
RA Labuca J.R., Love J.L., Abbott L.Z., Dube S., Freidman-Kien A.E.,
RA Poiesz B.J.;
RT "Detection of human herpesvirus 8 DNA sequences in tissues and bodily
RT fluids.";
RL J. Infect. Dis. 178:1610-1615(1998).
DR EMBL; AF042149; AAC25060.1; -; Genomic_DNA.
FT NON_TER 1 1
SQ SEQUENCE 16 AA; 1787 MW; 2B505B0137E39DFF CRC64;

Query Match
Best Local Similarity 24.7%; Score 20; DB 2; Length 16;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 IVHSNG 11
   |||::|
Db 1 VLESNG 6

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RESULT 7
QAYGPO PLABE
ID QAYGPO PLABE PRELIMINARY; PRT; 16 AA.
AC QAYGPO;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PB403344.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]_TaxID=5821;
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos P.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAI01005266; CAI02827.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 16 AA; 1971 MW; 9282A5EC21B7B5C1 CRC64;

Query Match 23.5%; Score 19; DB 2; Length 16;
Best Local Similarity 33.3%; Pred. No. 3.1e+04;
Matches 4; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 RSSQSIVHNGN 12
DB 3 RKINIFHPNIN 14

RESULT 8
Q8M8B6 PINTA
ID Q8M8B6 PINTA PRELIMINARY; PRT; 16 AA.
AC Q8M8B6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE NADH dehydrogenase subunit 3 (Fragment).
GN Name=nad3;
OS Pinus taeda (Loblolly pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
OX NCBI_TaxID=3352;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RA Chen J., Tauer C., Huang Y.;
RA Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF426453; AM21490.1; -; Genomic_DNA.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 16 AA; 1854 MW; FF3839987FD93A91 CRC64;

Query Match 23.5%; Score 19; DB 2; Length 16;
Best Local Similarity 57.1%; Pred. No. 3.1e+04;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 NGNTYLQ 16
DB '4 NGRRLVQ 10

RESULT 9
Q8M8B7 PINEL
ID Q8M8B7 PINEL PRELIMINARY; PRT; 16 AA.
AC Q8M8B7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE NADH dehydrogenase subunit 3 (Fragment).
GN Name=nad3;
OS Pinus elliotii (Slash pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
OX NCBI_TaxID=42064;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RA Chen J., Tauer C., Huang Y.;
RA Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF426452; AM21488.1; -; Genomic_DNA.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 16 AA; 1854 MW; FF3839987FD93A91 CRC64;

Query Match 23.5%; Score 19; DB 2; Length 16;
Best Local Similarity 57.1%; Pred. No. 3.1e+04;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 NGNTYLQ 16
DB 4 NGRRLVQ 10

RESULT 10
Q9S8Y6 LUPAR
ID Q9S8Y6 LUPAR PRELIMINARY; PRT; 16 AA.
AC Q9S8Y6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE L-asparaginase isoform A (EC 3.5.1.1) (Fragment).
OS Lupinus arboreus (Tree lupin).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Genisteae; Lupinus.
OX NCBI_TaxID=3872;
RN [1]_
RP PROTEIN SEQUENCE.
RA MEDLINE=92344803; PubMed=1368361; DOI=10.1016/0031-9422(92)83098-J;
RA Lough T.J., Chang K.S., Carne A., Monk B.C., Reynolds P.H.,
RA Farnden K.J.;
RA Phytochemistry 31:1519-1527(1992).
DR GO; GO:0004067; F:asparaginase activity; IEA.
SQ SEQUENCE 16 AA; 1499 MW; 90136390B527BF0B CRC64;

Query Match 23.5%; Score 19; DB 2; Length 16;
Best Local Similarity 66.7%; Pred. No. 3.1e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 VHSNGN 12
DB 7 VDSQGN 12

RESULT 11
Q8M8B5 PINEC
ID Q8M8B5 PINEC PRELIMINARY; PRT; 16 AA.
AC Q8M8B5;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE NADH dehydrogenase subunit 3 (Fragment).
OX NCBI_TaxID=3352;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RA Chen J., Tauer C., Huang Y.;
RA Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF426453; AM21490.1; -; Genomic_DNA.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 16 AA; 1854 MW; FF3839987FD93A91 CRC64;

Query Match 23.5%; Score 19; DB 2; Length 16;
Best Local Similarity 57.1%; Pred. No. 3.1e+04;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 NGNTYLQ 16
DB '4 NGRRLVQ 10
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GN Name=nad3;
OS Pinus echinata (Shortleaf pine).
OC Mitochondrion.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
OX NCBI_TaxID=71631;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Chen J., Tauer C., Huang Y.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF426454; AAM1492.1; -; Genomic_DNA.
DR GO: 0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 16 AA; 1854 MW; FF3839987FPD93A91 CRC64;

Query Match 23.5%; Score 19; DB 2; Length 16;
Best Local Similarity 57.1%; Pred. No. 3.1e+04;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 10 NGNTYLQ 16
|||
Db 4 NGRVLIQ 10

RESULT 12
ID Q78377_9HIV1 PRELIMINARY; PRT; 16 AA.
AC Q78377
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Immunodeficiency virus type 1, viral sample FLPBR4C (Florida patient
DE B), partial env cds, V4 region. (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retroviridae; Retroviridae; Lentivirus;
OC Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92271245; PubMed=1589796;
RA Ou C.-Y., Ciecielski C.A., Myers G., Bandea C.I., Luo C.C.,
RA Korber B.T.M., Mullins J.I., Schochetman G., Berkman R.L.,
RA Economou A.N., Witte J.J., Furman L.J., Satten G.A., Curran J.W.,
RA Jaffe H.W.;
RL "Molecular epidemiology of HIV transmission in a dental practice.";
RL Science 256:1165-1171(1992).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Zhang L.Q., Leigh-Brown A.J.;
RL Submitted (APR-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL: M92120; AAA44490.1; -; Genomic_RNA.
FT NON_TER 1
FT NON_TER 16
SQ SEQUENCE 16 AA; 1745 MW; 72260DC174FF6428 CRC64;

Query Match 23.5%; Score 19; DB 2; Length 16;
Best Local Similarity 37.5%; Pred. No. 3.1e+04;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 6 IVHSNGNT 13
: |||
Db 1 LFHTANTT 8

RESULT 13
FPAC_EACME
ID FPAC_EACME STANDARD; PRT; 16 AA.
AC P56948;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-FEB-2005 (Rel. 46, Last annotation update)
DE Manganese-dependent inorganic pyrophosphatase (EC 3.6.1.1)

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DE (Pyrophosphate phospho-hydrolase) (PPase) (Fragment).
GN Name=ppac;
OS Bacillus megaterium.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1404;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=98455825; PubMed=9782505;
RA Young T.W., Kuhn N.J., Wadeson A., Ward S., Burges D., Cooke G.D.;
RL "Bacillus subtilis ORF YyBQ encodes a manganese-dependent inorganic
RT pyrophosphatase with distinctive properties: the first of a new class
RT of soluble pyrophosphatase?";
RL Microbiology 144:2563-2571(1998).
CC -1- CATALYTIC ACTIVITY: Diphosphate + H(2)O = 2 phosphate.
CC -1- COFACTOR: Binds 2 manganese ions per subunit (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the PPase class C family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR HAMAP; MF_00207; -; 1.
KW Direct protein sequencing; Hydrolase; Manganese; Metal-binding.
FT METAL 8
FT METAL 12 12 Manganese 1 (By similarity).
FT METAL 14 14 Manganese 1 (By similarity).
FT METAL 16 16 Manganese 2 (By similarity).
FT NON_TER 16
SQ SEQUENCE 16 AA; 1828 MW; 3C0B6735D98B38A0 CRC64;

Query Match 22.2%; Score 18; DB 1; Length 16;
Best Local Similarity 50.0%; Pred. No. 4.7e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 8 HSNQNT 13
|||
Db 8 HKNPDT 13

RESULT 14
Q9UCR2_HUMAN
ID Q9UCR2_HUMAN PRELIMINARY; PRT; 16 AA.
AC Q9UCR2
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE AUTOTAXIN (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=92129337; PubMed=1733949;
RA Stracke M.L., Kruttsch H.C., Unsworth E.J., Arestad A., Cioce V.,
RA Schiffmann E., Liotta L.A.;
RL "Identification, purification, and partial sequence analysis of
RT autotaxin, a novel motility-stimulating protein.";
RL J. Biol. Chem. 267:2524-2529(1992).
FT NON_TER 1
FT NON_TER 16
SQ SEQUENCE 16 AA; 1775 MW; 0B851FF76214DBD6 CRC64;

Query Match 22.2%; Score 18; DB 2; Length 16;
Best Local Similarity 30.8%; Pred. No. 4.7e+04;
Matches 4; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 2 SSQSIHVSNGNTY 14
|||
Db 3 SMQIVFVGYGTFP 15

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RESULT 15
Q7RJ25 PLAYO
ID Q7RJ25 PLAYO PRELIMINARY; PRT; 16 AA.
AC Q7RJ25;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=PY03439;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=17XNL;
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shalom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaihi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL01000989; EAA23013.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 16 AA; 1892 MW; 711E4AA20D1D0958 CRC64;

Query Match 22.2%; Score 18; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.7e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 NTY 14
DB 3 NTY 5

Search completed: December 30, 2005, 14:24:46
Job time : 144.5 secs
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OM protein - protein search, using sw model

Run on: December 30, 2005, 14:25:05 ; Search time 110 Seconds
(without alignments)
60.775 Million cell updates/sec

Title: US-10-735-916A-2

Perfect score: 81

Sequence: 1 RSSQSIVHSNGNTYLQ 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 11256

Minimum DB seq length: 16

Maximum DB seq length: 16

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81	100.0	16	5	US-10-735-916A-2
2	78	96.3	16	3	US-09-995-529-32
3	78	96.3	16	3	US-09-947-839-30
4	78	96.3	16	3	US-09-995-529-32
5	78	96.3	16	4	US-10-226-795-28
6	78	96.3	16	4	US-10-470-045-53
7	78	96.3	16	6	US-11-070-697-1
8	76	93.8	16	3	US-09-563-222-29
9	76	93.8	16	4	US-10-783-950-29
10	76	93.8	16	5	US-10-810-881A-56
11	75	92.6	16	3	US-09-995-529-119
12	75	92.6	16	3	US-09-995-529-119
13	74	91.4	16	3	US-09-518-737-8
14	74	91.4	16	3	US-09-995-529-118
15	74	91.4	16	3	US-09-995-529-118
16	74	91.4	16	4	US-10-762-629-20
17	74	91.4	16	5	US-10-723-748-8
18	74	91.4	16	5	US-10-687-035-6
19	74	91.4	16	5	US-10-497-475-1
20	72	88.9	16	3	US-09-995-529-110
21	72	88.9	16	3	US-09-995-529-146
22	72	88.9	16	3	US-09-995-529-110
23	72	88.9	16	3	US-09-995-529-146
24	71	87.7	16	3	US-09-995-529-111
25	71	87.7	16	3	US-09-995-529-114
26	71	87.7	16	3	US-09-995-529-111
27	71	87.7	16	3	US-09-995-529-114

28 70 86.4 16 3 US-09-995-529-115 Sequence 115, App
29 70 86.4 16 3 US-09-995-529-117 Sequence 117, App
30 70 86.4 16 3 US-09-995-529-115 Sequence 115, App
31 70 86.4 16 3 US-09-995-529-117 Sequence 117, App
32 70 86.4 16 4 US-10-434-469-10 Sequence 10, Appl
33 70 86.4 16 5 US-10-846-981-3 Sequence 3, Appl
34 70 86.4 16 5 US-10-482-105-8 Sequence 8, Appl
35 70 86.4 16 5 US-10-409-611-79 Sequence 79, Appl
36 70 86.4 16 5 US-10-919-923-3 Sequence 3, Appl
37 70 86.4 16 5 US-10-409-608A-21 Sequence 21, Appl
38 70 86.4 16 5 US-10-500-207A-10 Sequence 10, Appl
39 69 85.2 16 3 US-09-972-636-5 Sequence 5, Appl
40 69 85.2 16 3 US-09-995-529-113 Sequence 113, App
41 69 85.2 16 3 US-09-995-529-113 Sequence 113, App
42 69 85.2 16 5 US-10-706-852-16 Sequence 16, Appl
43 69 85.2 16 5 US-10-723-441-4 Sequence 4, Appl
44 69 85.2 16 5 US-10-877-773-101 Sequence 101, App
45 69 85.2 16 5 US-10-877-774-101 Sequence 101, App

ALIGNMENTS

RESULT 1
US-10-735-916A-2
; Sequence 2, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10/735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-735-916A-2

Query Match 100.0%; Score 81; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSNGNTYLQ 16
Db 1 RSSQSIVHSNGNTYLQ 16

RESULT 2
US-09-995-529-32
; Sequence 32, Application US/09995529
; Publication No. US20030099655A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying

```

; TITLE OF INVENTION: Humanized Collagen Antibodies and
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-995-529-32

Query Match          96.3%; Score 78; DB 3; Length 16;
Best Local Similarity 93.8%; Pred. No. 3e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RSSQSIVHSNGNTYLQ 16
        |||||
Db      1 RSSQSIVHSNGNTYLE 16

RESULT 4
US-09-995-529-32
; Sequence 32, Application US/09995529
; Publication No. US20040091482A9
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; TITLE OF INVENTION: Related Methods
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-995-529-32

Query Match          96.3%; Score 78; DB 3; Length 16;
Best Local Similarity 93.8%; Pred. No. 3e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RSSQSIVHSNGNTYLQ 16
        |||||
Db      1 RSSQSIVHSNGNTYLE 16

RESULT 5
US-10-226-795-28
; Sequence 28, Application US/10226795
; Publication No. US20040053865A1
; GENERAL INFORMATION:
; APPLICANT: HART, MARY KATE
; APPLICANT: WILSON, JULIE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND COMPLEMENTARITY-DETERMINING
; TITLE OF INVENTION: REGIONS BINDING TO EBOLA GLYCOPROTEIN
; FILE REFERENCE: ARMY 166
; CURRENT APPLICATION NUMBER: US/10/226,795
; CURRENT FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic light
; OTHER INFORMATION: chain of Mab EGPd8-1-2 amino acid sequence
US-10-226-795-28

Query Match          96.3%; Score 78; DB 4; Length 16;
Best Local Similarity 93.8%; Pred. No. 3e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RSSQSIVHSNGNTYLQ 16
        |||||
Db      1 RSSQSIVHSNGNTYLE 16

RESULT 6
US-09-947-839-30
; TITLE OF INVENTION: Analogous Peptides With Broad
; TITLE OF INVENTION: Carcinoma Specificity, and Kit and
; FILE REFERENCE: Pretty, Schroeder & Poplawski
; CURRENT APPLICATION NUMBER: PC-DOS/MS-DOS 5.0
; CURRENT FILING DATE: 06-Sep-2001
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; SEQ ID NO 30
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-947-839-30

Query Match          96.3%; Score 78; DB 3; Length 16;
Best Local Similarity 93.8%; Pred. No. 3e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RSSQSIVHSNGNTYLQ 16
        |||||
Db      1 RSSQSIVHSNGNTYLE 16

RESULT 3
US-09-947-839-30
; Sequence 30, Application US/09947839
; Publication No. US20030138428A1
; GENERAL INFORMATION:
; APPLICANT: do Couto Dr., Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogous Peptides With Broad
; TITLE OF INVENTION: Carcinoma Specificity, and Kit and
; TITLE OF INVENTION: Diagnostic Vaccination and
; TITLE OF INVENTION: Therapeutic Methods
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder & Poplawski
; STREET: 444 South Flower St., 19th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/947,839
; FILING DATE: 06-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/976,288
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 07/977,696
; FILING DATE: No. US20030138428A1ember 16, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Anzel Ph.D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P6639938
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 622-7700
; TELEFAX: (213) 489-4210
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-947-839-30
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US-10-470-045-53
; Sequence 53, Application US/10470045
; Publication No. US20040146505A1
; GENERAL INFORMATION:
; APPLICANT: Scancell Limited
; APPLICANT: Durrant, Linda Gillian
; APPLICANT: Parsons, Tina
; TITLE OF INVENTION: Substances
; FILE REFERENCE: P32181WO/NUL
; CURRENT APPLICATION NUMBER: US/10/470,045
; CURRENT FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: GB 0102145.0
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-470-045-53

Query Match 96.3%; Score 78; DB 4; Length 16;
Best Local Similarity 93.8%; Pred. No. 3e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSNGNTYLQ 16
|||||:|||||:
DB 1 RSSQSIVHSNGNTYL 16

RESULT 7
US-11-070-697-1
; Sequence 1, Application US/11070697
; Publication No. US20050169926A1
; GENERAL INFORMATION:
; APPLICANT: OU, ZHENGXING
; APPLICANT: HANSEN, HANS
; APPLICANT: GOLDENBERG, DAVID M.
; TITLE OF INVENTION: CHIMERIC, HUMAN AND HUMANIZED ANTI-CSAP MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 018733/1064
; CURRENT APPLICATION NUMBER: US/11/070,697
; CURRENT FILING DATE: 2005-03-03
; PRIOR APPLICATION NUMBER: US/10/116,116
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 09/823,746
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 09/337,756
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/104,156
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/090,142
; PRIOR FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-11-070-697-1

Query Match 96.3%; Score 78; DB 6; Length 16;
Best Local Similarity 93.8%; Pred. No. 3e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSNGNTYLQ 16
|||||:|||||:
DB 1 RSSQSIVHSNGNTYL 16

RESULT 8
US-09-563-222-29
; Sequence 29, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Hein, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; TITLE OF INVENTION: EUKARYOTIC CELLS
; FILE REFERENCE: 310098.406
; CURRENT APPLICATION NUMBER: US/09/563,222
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-563-222-29

Query Match 93.8%; Score 76; DB 3; Length 16;
Best Local Similarity 87.5%; Pred. No. 6.5e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSNGNTYLQ 16
|||||:|||||:
DB 1 RSSQSIVHSNGNTYL 16

RESULT 9
US-10-783-950-29
; Sequence 29, Application US/10783950
; Publication No. US20040199945A1
; GENERAL INFORMATION:
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICHAEL
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT APPLICATION NUMBER: US/10/783,950
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US/09/563,222
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-783-950-29

Query Match 93.8%; Score 76; DB 4; Length 16;
Best Local Similarity 87.5%; Pred. No. 6.5e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIVHSNGNTYLQ 16
|||||:|||||:
DB 1 RSSQSIVHSNGNTYL 16

RESULT 10
US-10-810-881A-56
; Sequence 56, Application US/10810881A
; Publication No. US20050129695A1
; GENERAL INFORMATION:
; APPLICANT: Mercken, Marc; Benson, Jacqueline M.
; TITLE OF INVENTION: ANTI-AMYLOID ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN5021 NP
; CURRENT APPLICATION NUMBER: US/10/810,881A

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; CURRENT FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US 60/458,474
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/458,469
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/458,509
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/458,510
; PRIOR FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 56
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(16)
; OTHER INFORMATION: LC CDR1
US-10-810-881A-56
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```
Query Match          93.8%; Score 76; DB 5; Length 16;
Best Local Similarity 87.5%; Pred. No. 6.5e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 RSSQSIVHSNGNTYLQ 16
   |||||:|||||:
Db 1 RSSQSLVHSNGNTYLE 16
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RESULT 11

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US-09-995-529-119
; Sequence 119, Application US/09995529
; Publication No. US20030099655A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 119
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody mutation
US-09-995-529-119
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```
Query Match          92.6%; Score 75; DB 3; Length 16;
Best Local Similarity 87.5%; Pred. No. 9.5e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 RSSQSIVHSNGNTYLQ 16
   |||||:|||||:
Db 1 RSSQSLVHSNGNTYLE 16
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RESULT 12

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US-09-995-529-119
; Sequence 119, Application US/09995529
; Publication No. US20040091482A9
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; FILE REFERENCE: P-IX 4976
```

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; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 119
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody mutation
US-09-995-529-119
```

```
Query Match          92.6%; Score 75; DB 3; Length 16;
Best Local Similarity 87.5%; Pred. No. 9.5e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 RSSQSIVHSNGNTYLQ 16
   |||||:|||||:
Db 1 RSSQSLVHSNGNTYLE 16
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RESULT 13

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US-09-518-737-8
; Sequence 8, Application US/09518737
; Publication No. US20030008321A1
; GENERAL INFORMATION:
; APPLICANT: FUKUI, YASUHIKA
; APPLICANT: SHIRAI, RYUICHI
; APPLICANT: SAITO, NAOAKI
; TITLE OF INVENTION: MONOCLONAL ANTIBODY RECOGNIZING
; FILE REFERENCE: 1965/49618
; CURRENT APPLICATION NUMBER: US/09/518,737
; CURRENT FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: JP 1999-250209
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-518-737-8
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Query Match          91.4%; Score 74; DB 3; Length 16;
Best Local Similarity 93.3%; Pred. No. 1.4e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 RSSQSIVHSNGNTYL 15
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Db 1 RSSQSLVHSNGNTYL 15
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RESULT 14

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US-09-995-529-118
; Sequence 118, Application US/09995529
; Publication No. US20030099655A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Tang, Ying
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 118
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
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; FEATURES:
; OTHER INFORMATION: synthetic antibody mutation
US-09-995-529-118

Query Match 91.4%; Score 74; DB 3; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.4e-05;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGTYLQ 16
||| ||||| :
Db 1 RSSQSIVHSGNGTYFE 16

RESULT 15

US-09-995-529-118
; Sequence 118, Application US/09995529
; Publication No. US20040091482A9
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffery D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; TITLE OF INVENTION: Related Methods
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 118
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody mutation
US-09-995-529-118

Query Match 91.4%; Score 74; DB 3; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.4e-05;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSSQSIVHSGNGTYLQ 16
||| ||||| :
Db 1 RSSQSIVHSGNGTYFE 16

Search completed: December 30, 2005, 14:43:48
Job time : 111 secs

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OM protein - protein search, using sw model

Run on: December 30, 2005, 14:25:45 ; Search time 8 Seconds
(without alignments)
14.978 Million cell updates/sec

Title: US-10-735-916A-2
Perfect score: 81
Sequence: 1 RSSQSIHVSNGNTYLQ 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues
Total number of hits satisfying chosen parameters: 602

Minimum DB seq length: 16
Maximum DB seq length: 16

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pap:
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pap:
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pap:
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pap:
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pap:
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pap:
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pap:
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81	100.0	16	7 US-11-012-353-2	Sequence 2, Appli
2	71	87.7	16	7 US-11-125-837-13	Sequence 13, Appli
3	70	86.4	16	7 US-11-102-743-3	Sequence 3, Appli
4	69	85.2	16	6 US-10-932-334-4	Sequence 4, Appli
5	68	81.5	16	7 US-11-125-837-1	Sequence 1, Appli
6	61	75.3	16	7 US-11-009-939-18	Sequence 18, Appli
7	59	72.8	16	7 US-11-105-708-17	Sequence 17, Appli
8	25	30.9	16	6 US-10-726-554-13	Sequence 13, Appli
9	25	30.9	16	6 US-10-507-662-5	Sequence 5, Appli
10	22	27.2	16	6 US-10-999-866-59	Sequence 59, Appli
11	22	27.2	16	7 US-11-055-163-20	Sequence 20, Appli
12	21	25.9	16	7 US-11-010-748A-77	Sequence 77, Appli
13	21	25.9	16	7 US-11-010-748A-89	Sequence 89, Appli
14	21	25.9	16	7 US-11-010-748A-126	Sequence 126, App
15	21	25.9	16	7 US-11-010-748A-138	Sequence 138, App
16	21	25.9	16	7 US-11-060-646-10	Sequence 10, Appli
17	20	24.7	16	7 US-11-087-812-92	Sequence 92, Appli
18	19	23.5	16	7 US-11-009-939-24	Sequence 24, Appli
19	18.5	22.8	16	7 US-11-127-677-87	Sequence 87, Appli
20	18	22.2	16	6 US-10-507-662-6	Sequence 6, Appli
21	18	22.2	16	6 US-10-467-657-9175	Sequence 9175, Ap
22	18	22.2	16	6 US-10-485-788A-495	Sequence 495, App
23	18	22.2	16	6 US-10-919-492-3	Sequence 3, Appli
24	18	22.2	16	6 US-10-919-492-10	Sequence 10, Appli
25	18	22.2	16	7 US-11-052-168A-32	Sequence 32, Appli

26	18	22.2	16	7 US-11-090-908-5	Sequence 5, Appli
27	18	22.2	16	7 US-11-060-005-34	Sequence 34, Appli
28	18	22.2	16	7 US-11-167-710-12	Sequence 12, Appli
29	17	21.0	16	7 US-11-089-764-3	Sequence 3, Appli
30	17	21.0	16	7 US-11-089-764-4	Sequence 4, Appli
31	17	21.0	16	7 US-11-089-764-7	Sequence 7, Appli
32	17	21.0	16	7 US-11-089-764-10	Sequence 10, Appli
33	17	21.0	16	7 US-11-089-764-11	Sequence 11, Appli
34	17	21.0	16	7 US-11-089-764-12	Sequence 12, Appli
35	17	21.0	16	7 US-11-089-764-33	Sequence 33, Appli
36	17	21.0	16	7 US-11-054-515-2728	Sequence 2728, Ap
37	17	21.0	16	7 US-11-054-515-2868	Sequence 2868, Ap
38	17	21.0	16	7 US-11-054-515-3212	Sequence 3212, Ap
39	17	21.0	16	7 US-11-060-646-4	Sequence 4, Appli
40	17	21.0	16	7 US-11-044-899-44	Sequence 44, Appli
41	17	21.0	16	7 US-11-009-939-34	Sequence 34, Appli
42	16	19.8	16	6 US-10-467-657-8935	Sequence 8935, Ap
43	16	19.8	16	6 US-10-467-657-9115	Sequence 9115, Ap
44	16	19.8	16	6 US-10-649-229-18	Sequence 18, Appli
45	16	19.8	16	6 US-10-929-988-281	Sequence 281, Appli

ALIGNMENTS

RESULT 1
US-11-012-353-2
; Sequence 2, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION: GORTSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFILOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 2
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-012-353-2

Query Match 100.0%; Score 81; DB 7; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSQSIHVSNGNTYLQ 16
| | | | | | | | | | | | | | | |
Db 1 RSSQSIHVSNGNTYLQ 16

RESULT 2
US-11-125-837-13
; Sequence 13, Application US/11125837

```
; Publication No. US20050266003A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Rong-Hwa
; APPLICANT: Chang, Chung Nan
; APPLICANT: Chen, Pei-Jiun
; APPLICANT: Huang, Chiu-Chen
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 13062-011001
; CURRENT APPLICATION NUMBER: US/11/125,837
; CURRENT FILING DATE: 2005-05-10
; PRIOR APPLICATION NUMBER: US 60/569,892
; PRIOR FILING DATE: 2004-05-10
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-125-837-13

Query Match      87.7%; Score 71; DB 7; Length 16;
Best Local Similarity 87.5%; Pred. No. 6.5e-07;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSNGNTYLQ 16
Db 1 RSSQSIVHSNGNTYLE 16

RESULT 3
US-11-102-743-3
; Sequence 3, Application US/11/102743
; Publication No. US20050266002A1
; GENERAL INFORMATION:
; APPLICANT: Siegall, Clay
; APPLICANT: Wahi, Alan
; APPLICANT: Francisco, Joseph
; APPLICANT: Fell, H. Perry
; TITLE OF INVENTION: RECOMBINANT ANTI-CD40 ANTIBODY AND USES THEREOF
; FILE REFERENCE: 9632-005
; CURRENT APPLICATION NUMBER: US/11/102,743
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US/09/328,296
; PRIOR FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-102-743-3

Query Match      86.4%; Score 70; DB 7; Length 16;
Best Local Similarity 86.7%; Pred. No. 9.8e-07;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSNGNTYL 15
Db 1 RSSQSLVHSNGNTFL 15

RESULT 4
US-10-932-334-4
; Sequence 4, Application US/10932334
; Publication No. US20050249728A1
; GENERAL INFORMATION:
; APPLICANT: ImmunoGen, Inc.
; TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
; FILE REFERENCE: A8689
; CURRENT APPLICATION NUMBER: US/10/932,334
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US/10/729,441
; PRIOR FILING DATE: 2003-12-08

; Publication No. US20050266003A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Rong-Hwa
; APPLICANT: Chang, Chung Nan
; APPLICANT: Chen, Pei-Jiun
; APPLICANT: Huang, Chiu-Chen
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 13062-011001
; CURRENT APPLICATION NUMBER: US/11/125,837
; CURRENT FILING DATE: 2005-05-10
; PRIOR APPLICATION NUMBER: US 60/569,892
; PRIOR FILING DATE: 2004-05-10
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-125-837-13

Query Match      85.2%; Score 69; DB 6; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.5e-06;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSNGNTYLQ 16
Db 1 RSSQSIVHSNVNTYLE 16

RESULT 5
US-11-125-837-1
; Sequence 1, Application US/11/125837
; Publication No. US20050266003A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Rong-Hwa
; APPLICANT: Chang, Chung Nan
; APPLICANT: Chen, Pei-Jiun
; APPLICANT: Huang, Chiu-Chen
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 13062-011001
; CURRENT APPLICATION NUMBER: US/11/125,837
; CURRENT FILING DATE: 2005-05-10
; PRIOR APPLICATION NUMBER: US 60/569,892
; PRIOR FILING DATE: 2004-05-10
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-125-837-1

Query Match      81.5%; Score 66; DB 7; Length 16;
Best Local Similarity 75.0%; Pred. No. 4.9e-06;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RSSQSIVHSNGNTYLQ 16
Db 1 RSSQSIVHNDGNTYFE 16

RESULT 6
US-11-009-939-18
; Sequence 18, Application US/11009939
; Publication No. US20050265998A1
; GENERAL INFORMATION:
; APPLICANT: Elson, Greg Christopher Andrew
; TITLE OF INVENTION: Neutralizing Antibodies and Methods of Use Thereof
; FILE REFERENCE: 23135-402
; CURRENT APPLICATION NUMBER: US/11/009,939
; CURRENT FILING DATE: 2005-12-10
; PRIOR APPLICATION NUMBER: 60/528,811
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 60/528,812
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 60/528,962
; PRIOR FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 16
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TYPE: PRT
ORGANISM: Mus musculus
US-11-009-939-18

Query Match 75.3%; Score 61; DB 7; Length 16;
Best Local Similarity 80.0%; Pred. No. 3.7e-05;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSSQSIVHNGNTYL 15
DB 1 RSSQSLENGNTYL 15

RESULT 7
US-11-105-708-17
Sequence 17, Application US/11105708
Publication No. US20050281821A1
GENERAL INFORMATION:
APPLICANT: Pernaesetti, Bruce
APPLICANT: Freimark, Bruce
APPLICANT: Van Epps, Dennis
APPLICANT: Brooks, Peter C
TITLE OF INVENTION: Method and Composition for Angiogenesis Inhibition
FILE REFERENCE: 30797-704.501
CURRENT APPLICATION NUMBER: US/11/105,708
CURRENT FILING DATE: 2005-04-13
PRIOR APPLICATION NUMBER: 09/478,977
PRIOR FILING DATE: 2000-01-06
PRIOR APPLICATION NUMBER: 60/152,496
PRIOR FILING DATE: 1999-09-02
PRIOR APPLICATION NUMBER: 60/143,534
PRIOR FILING DATE: 1999-09-02
PRIOR APPLICATION NUMBER: 60/114,878
PRIOR FILING DATE: 1999-01-06
PRIOR APPLICATION NUMBER: 60/114,877
PRIOR FILING DATE: 1999-01-06
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.2
SEQ ID NO 17
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic peptide
US-11-105-708-17

Query Match 72.8%; Score 59; DB 7; Length 16;
Best Local Similarity 81.2%; Pred. No. 8.2e-05;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RSSQSIVHNGNTYLQ 16
DB 1 RSSQSIVSSWGNTYLE 16

RESULT 8
US-10-726-554-13
Sequence 13, Application US/10726554
Publication No. US20050249753A1
GENERAL INFORMATION:
APPLICANT: LEE, Jong Wook et al.
TITLE OF INVENTION: A VARIABLE REGION OF THE MONOCLONAL ANTIBODY AGAINST
TITLE OF INVENTION: THE HBV S-SURFACE
TITLE OF INVENTION: ANTIGEN AND A GENE ENCODING THE SAME
FILE REFERENCE: 1599-0197P
CURRENT APPLICATION NUMBER: US/10/726,554
CURRENT FILING DATE: 2003-12-04
PRIOR APPLICATION NUMBER: US/09/865,483
PRIOR FILING DATE: PRIOR FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
LENGTH: 16

TYPE: PRT
ORGANISM: Escherichia coli
US-10-726-554-13

Query Match 30.9%; Score 25; DB 6; Length 16;
Best Local Similarity 50.0%; Pred. No. 72;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 IVHSGNT 13
DB 1 VIWSGNT 8

RESULT 9
US-10-507-662-5
Sequence 5, Application US/10507662
Publication No. US20050255102A1
GENERAL INFORMATION:
APPLICANT: BIOGEN, INC.
TITLE OF INVENTION: ANTI-ALPHA-V BETA-6 ANTIBODIES
FILE REFERENCE: A136PCT
CURRENT APPLICATION NUMBER: US/10/507,662
CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: 60/364,991
PRIOR FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: 60/426,286
PRIOR FILING DATE: 2002-11-13
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 16
TYPE: PRT
ORGANISM: Homo sapiens
US-10-507-662-5

Query Match 30.9%; Score 25; DB 6; Length 16;
Best Local Similarity 50.0%; Pred. No. 72;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 VHSNGNTY 14
DB 2 ISSGGSTY 9

RESULT 10
US-10-999-866-59
Sequence 59, Application US/10999866
Publication No. US20050266004A1
GENERAL INFORMATION:
APPLICANT: GILES-KONAR, Jill; SCALLON, Bernard J.; CAI, Ann
TITLE OF INVENTION: ANTI-HUMAN LYMPHOTOXIN ALPHA ANTIBODIES, COMPOSITIONS, METHODS A
FILE REFERENCE: CEN5042NP
CURRENT APPLICATION NUMBER: US/10/999,866
CURRENT FILING DATE: 2004-11-30
PRIOR APPLICATION NUMBER: 60/527,794
PRIOR FILING DATE: 2003-12-08
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn version 3.3
SEQ ID NO 59
LENGTH: 16
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1)-(16)
OTHER INFORMATION: HC CDR 2
US-10-999-866-59

Query Match 27.2%; Score 22; DB 6; Length 16;
Best Local Similarity 37.5%; Pred. No. 2.4e+02;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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QY      6 IVHNGNT 13
      : : : |||
Db      1 VIVAGNT 8

RESULT 11
US-11-055-163-20
; Sequence 20, Application US/11055163
; Publication No. US20050271655A1
; GENERAL INFORMATION:
; APPLICANT: LEE, DANIEL H. S.
; APPLICANT: PEPINSKY, R. BLAKE
; APPLICANT: LI, WEIWEI
; APPLICANT: RABACCHI, SYLVIA A.
; APPLICANT: RELTON, JANE K.
; APPLICANT: WORLEY, DANE S.
; APPLICANT: STRITTMATTER, STEPHEN M.
; APPLICANT: SAH, DINAH Y.W.
; TITLE OF INVENTION: NOGO RECEPTOR ANTAGONISTS
; FILE REFERENCE: A170 CON (00455.271)
; CURRENT APPLICATION NUMBER: US/11/055.163
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: PCT/US03/25004
; PRIOR FILING DATE: 2003-08-07
; PRIOR APPLICATION NUMBER: 60/402,866
; PRIOR FILING DATE: 2002-08-10
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: heavy chain peptide sequence
US-11-055-163-20

Query Match      27.2%; Score 22; DB 7; Length 16;
Best Local Similarity 33.3%; Pred. No. 2.4e+02;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      6 IVHNGNTY 14
      : : : ||| |
Db      1 LIYSNDRKY 9

RESULT 12
US-11-010-748A-77
; Sequence 77, Application US/11010748A
; Publication No. US2005024421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMATTER, Wolfgang
; APPLICANT: MOLL, Heidrun
; APPLICANT: SCHARM, Burkhard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CD15 peptide fragment
US-11-010-748A-77

Query Match      25.9%; Score 21; DB 7; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 TYLQ 16
      : : : |||
Db      2 TYLQ 5

RESULT 13
US-11-010-748A-89
; Sequence 89, Application US/11010748A
; Publication No. US2005024421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMATTER, Wolfgang
; APPLICANT: MOLL, Heidrun
; APPLICANT: SCHARM, Burkhard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 89
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CD15 peptide fragment
US-11-010-748A-89

Query Match      25.9%; Score 21; DB 7; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 TYLQ 16
      : : : |||
Db      2 TYLQ 5

RESULT 14
US-11-010-748A-126
; Sequence 126, Application US/11010748A
; Publication No. US2005024421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMATTER, Wolfgang
; APPLICANT: MOLL, Heidrun
; APPLICANT: SCHARM, Burkhard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 126
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CD15 peptide fragment
US-11-010-748A-126

Query Match      25.9%; Score 21; DB 7; Length 16;
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Best Local Similarity 100.0%; Pred. No. 3.6e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 13 TYLQ 16
 ||||
Db 2 TYLQ 5

RESULT 15
US-11-010-748A-138
; Sequence 138, Application US/11010748A
; Publication No. US2005024421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMAYER, Wolfgang
; APPLICANT: MOLL, Heidrun
; APPLICANT: SCHARM, Burkhard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 138
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CD15 peptide fragment
US-11-010-748A-138

Query Match 25.9%; Score 21; DB 7; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.6e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 13 TYLQ 16
 ||||
Db 2 TYLQ 5

Search completed: December 30, 2005, 14:44:10
Job time : 9 secs

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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:02:01 ; Search time 62.2097 Seconds
(without alignments)
49.440 Million cell updates/sec

Title: US-10-735-916A-4

Perfect score: 35

Sequence: 1 KVSFRLY 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: Geneseqp1980s.*

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3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	7	ADJ76838	Adj76838 CDR seque
2	35	100.0	7	ADZ67008	Adz67008 Murine in
3	35	100.0	112	ADJ76888	Adj76888 Anti-IGF-
4	35	100.0	112	ADJ76899	Adj76899 Anti-IGF-
5	35	100.0	112	ADJ76895	Adj76895 Anti-IGF-
6	35	100.0	112	ADZ67058	Adz67058 Murine in
7	35	100.0	112	ADZ67069	Adz67069 Human ant
8	35	100.0	112	ADZ67065	Adz67065 Human ant
9	35	100.0	122	ADJ76883	Adj76883 Anti-IGF-
10	35	100.0	122	ADZ67053	Adz67053 Murine in
11	35	100.0	111	ADJ76901	Adj76901 Anti-IGF-
12	35	100.0	131	ADJ76897	Adj76897 Anti-IGF-
13	35	100.0	131	ADZ67071	Adz67071 Human ant
14	35	100.0	131	ADZ67067	Adz67067 Human ant
15	35	100.0	841	ADQ08646	Adq08646 Clona int
16	34	97.1	435	AAG09372	Aag09372 Arabidops
17	34	97.1	571	AAG09371	Aag09371 Arabidops
18	34	97.1	576	AAG09370	Aag09370 Arabidops
19	31	88.6	374	ABR53373	AbR53373 Protein s
20	31	88.6	374	ADK63348	Adk63348 Disease t
21	31	88.6	687	AAy58997	Aay58997 Soybean s
22	30	85.7	176	ADT56879	Adt56879 Plant pol
23	30	85.7	323	ADA33883	Ada33883 Acinetoba
24	30	85.7	380	ABM73096	Abm73096 Staphyloc

25	30	85.7	388	5	ABP38975	Abp38975 Staphyloc
26	30	85.7	388	8	ADJ06741	Adj06741 Staphyloc
27	30	85.7	419	6	ABJ26662	Abj26662 Human pro
28	30	85.7	439	5	ABB75887	Abb75887 Human dip
29	30	85.7	463	2	AAW04360	Aaw04360 Human cat
30	30	85.7	463	2	AAW04360	Aaw04360 Human cat
31	30	85.7	463	4	AAW04360	Aaw04360 Human cat
32	30	85.7	463	5	AAO21724	Aao21724 Human all
33	30	85.7	463	5	ADZ58744	Adz58744 Human cat
34	30	85.7	463	6	ABP71988	Abp71988 Human cat
35	30	85.7	463	6	ABU57625	Abu57625 Different
36	30	85.7	463	7	ADN95622	Adn95622 Human BEC
37	30	85.7	463	7	ABO84400	AbO84400 Human cat
38	30	85.7	463	7	ADP65152	Adp65152 Human cat
39	30	85.7	463	8	ADZ67989	Adz67989 Human pro
40	30	85.7	463	8	ADJ75482	Adj75482 Marker ge
41	30	85.7	463	8	ADJ75390	Adj75390 Marker ge
42	30	85.7	463	8	ADN03739	Adn03739 Antipeori
43	30	85.7	463	8	ADO55149	Ado55149 Protein #
44	30	85.7	463	8	ADO20355	Ado20355 Human PRO
45	30	85.7	463	8	ADR67272	Adr67272 Human bla
						Adr97344 Human CTS

ALIGNMENTS

RESULT 1

ADJ76838	ADJ76838 standard; peptide; 7 AA.
ID	ADJ76838
XX	ADJ76838;
AC	
XX	
DT	06-MAY-2004 (first entry)
XX	
DE	CDR sequence for anti-IGF-1R antibody.
XX	
KW	cytostatic; antiproliferative; antibody;
KW	insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;
KW	or epidermal growth factor receptor; EGFR; signal transduction pathway;
KW	ligand; tumor; cancer; osteosarcoma; complementarity determining region;
XX	CDR.
OS	Mus musculus.
XX	
PN	WO2003059951-A2.
XX	
PD	24-JUL-2003.
XX	
PF	20-JAN-2003; 2003WO-FR000178.
XX	
PR	18-JAN-2002; 2002FR-00000653.
PR	18-JAN-2002; 2002FR-00000654.
PR	07-MAY-2002; 2002FR-00005753.
XX	
PA	(FABR) FABRE MEDICAMENT SA PIERRE.
XX	
PI	Goetsch L, Corvaia N, Leger O;
XX	
DR	WPI; 2003-569653/53.
DR	N-PSDB; ADJ76837.
PT	New antibodies that bind to human insulin-like growth factor receptor,
PT	useful for treatment, prevention and diagnosis of cancers.
XX	
XX	Claim 1; SEQ ID NO 4; 164pp; French.
XX	
CC	The invention relates to an isolated antibody (Ab), and its functional
CC	fragments, that bind to human insulin-like growth factor-1 receptor (IGF-
CC	1R) and optionally: (i) inhibit natural binding of insulin-like growth
CC	factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine
CC	kinase activity of IGF-1R. Ab and its fragments are used to prevent or
CC	treat diseases associated with overexpression and/or abnormal activity of
CC	IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with

CC hyperactivity of signal transduction pathways mediated by interaction of
 CC these receptors with their ligands. Especially they inhibit
 CC transformation of normal cells to tumor cells, inhibit growth and/or
 CC proliferation of tumor cells, so are useful against cancers of the
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused
 CC by abnormal expression of IGF-IR and/or EGFR. This sequence represents an
 CC CDR sequence used to generate the Ab of the invention.

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 35; DB 7; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSNNRLY 7
 |||||
 DB 1 KVSNNRLY 7

RESULT 2

ADZ67008
 ID ADZ67008 standard; peptide; 7 AA.

XX AC ADZ67008;

DT 30-JUN-2005 (first entry)

DE Murine insulin-like growth factor T receptor IGF-IR CDR SEQ ID NO:4.

XX Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
 KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;
 KW musculoskeletal disease; respiratory disease; lung tumor;
 KW endocrine disease; gynecology and obstetrics; breast tumor;
 KW endometroid carcinoma; gastrointestinal disease; colon tumor;
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder.

XX OS Mus musculus.

PN US2005084906-A1.

XX 21-APR-2005.

PF 16-DEC-2003; 2003US-00735916.

XX 18-JAN-2002; 2002FR-00000653.

PR 18-JAN-2002; 2002FR-00000654.

PR 07-MAY-2002; 2002FR-00005753.

PR 20-JAN-2003; 2003WO-FR000178.

PR 11-JUL-2003; 2003FR-00008538.

XX (GOET/) GOETSCH L.

PA (CORV/) CORVAIA N.

PA (LEGE/) LEGER O.

PA (DUFL/) DUFIOS A.

PA (HAEU/) HAEUW J.

XX (BECK/) BECK A.

PI Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;

XX WPI; 2005-321968/33.

DR N-PSDB; ADZ67007.

XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)
 PT antibody or its functional fragment, being capable of binding human IGF-
 PT IR and specifically inhibiting tyrosine kinase activity of receptor,
 PT useful for treating cancer.

XX Claim 1; SEQ ID NO 4; 125pp; English.

XX The invention relates to a novel isolated anti-insulin-like growth factor
 CC I receptor (IGF-IR) antibody (I) or its functional fragment, being
 CC capable of binding to human IGF-IR and, if necessary, capable of

CC specifically inhibiting tyrosine kinase activity of the receptor,
 CC comprising a light or heavy chain having at least one complementary
 CC determining region (CDR) consisting of one of two fully defined 16 amino
 CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in
 CC the preparation of a medicament intended for the prevention or treatment
 CC of an illness connected with an overexpression and/or an abnormal
 CC activation of the IGF-IR and/or EGFR, and/or connected with a
 CC hyperactivation of the transduction pathway of the signal mediated by the
 CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where
 CC the administration of the medicament does not induce or only slightly
 CC induces secondary effects connected with inhibition of the insulin
 CC receptor. The antibody is useful for preparation of a medicament intended
 CC to inhibit the transformation of normal cells into cells with tumoral
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is
 CC useful for preparation of a medicament intended to inhibit the growth
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a
 CC medicament intended for prevention or for the treatment of cancer, where
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the
 CC preparation of a medicament intended for the prevention or for the
 CC treatment of psoriasis. (I) is useful in preparation of a medicament
 CC intended for the specific targeting of a biologically active compound to
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)
 CC is useful for in vitro diagnosis of illnesses induced by an
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor
 CC starting from a biological sample in which the abnormal presence, of IGF-
 CC IR and/or EGFR receptor is suspected, which involves contacting the
 CC biological sample with (I), which is optionally labeled. The present
 CC sequence is used in the exemplification of the invention.

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 35; DB 9; Length 7;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSNNRLY 7
 |||||
 DB 1 KVSNNRLY 7

RESULT 3

ADJ76888

ID ADJ76888 standard; protein; 112 AA.

XX AC ADJ76888;

XX 06-MAY-2004 (first entry)

DT Anti-IGF-IR related protein #5.

XX cytostatic; antipsoriatic; antibody;
 DE insulin-like growth factor-1 receptor; IGF-IR; tyrosine kinase activity;
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;
 KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;
 KW CDR.

XX Mus musculus.

OS WO2003059951-A2.

PN 24-JUL-2003.

PD 20-JAN-2003; 2003WO-FR000178.

PR 18-JAN-2002; 2002FR-00000653.

PR 18-JAN-2002; 2002FR-00000654.

PR 07-MAY-2002; 2002FR-00005753.

XX (FABR) FABRE MEDICAMENT SA PIERRE.

XX PI Goetsch L, Corvaia N, Leger O;
 XX WPI; 2003-569653/53.
 XX New antibodies that bind to human insulin-like growth factor receptor,
 XX useful for treatment, prevention and diagnosis of cancers.
 XX Disclosure; SEQ ID NO 54; 164pp; French.
 XX The invention relates to an isolated antibody (Ab), and its functional
 XX fragments, that bind to human insulin-like growth factor-1 receptor (IGF-
 XX 1R) and optionally: (i) inhibit natural binding of insulin-like growth
 XX factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine
 XX kinase activity of IGF-1R. Ab and its fragments are used to prevent or
 XX treat diseases associated with overexpression and/or abnormal activity of
 XX IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with
 XX hyperactivity of signal transduction pathways mediated by interaction of
 XX these receptors with their ligands. Especially they inhibit
 XX transformation of normal cells to tumor cells, inhibit growth and/or
 XX proliferation of tumor cells, so are useful against cancers of the
 XX prostate, lung, breast, endometrium and colon, also osteosarcoma, and
 XX also for treating psoriasis. Ab are also used to diagnose diseases caused
 XX by abnormal expression of IGF-1R and/or EGFR. This sequence represents a
 XX protein sequence used to generate the Ab of the invention.
 XX SQ Sequence 112 AA;
 Query Match 100.0%; Score 35; DB 7; Length 112;
 Best Local Similarity 100.0%; Pred. No. 7.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVSNNRLY 7
 DB 55 KVSNNRLY 61
 RESULT 4
 ADJ76899
 ID ADJ76899 standard; protein; 112 AA.
 AC ADJ76899;
 XX 06-MAY-2004 (first entry)
 DT Anti-IGF-1R related protein #14.
 DE Cytostatic; antipsoriatic; antibody;
 XX insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;
 KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;
 KW CDR.
 XX Homo sapiens.
 OS WO2003059951-A2.
 XX 24-JUL-2003.
 XX 20-JAN-2003; 2003WO-FR000178.
 XX 18-JAN-2002; 2002FR-00000653.
 XX 18-JAN-2002; 2002FR-00000654.
 XX 07-MAY-2002; 2002FR-00005753.
 XX (FABR) FABRE MEDICAMENT SA PIERRE.
 XX Goetsch L, Corvaia N, Leger O;
 XX WPI; 2003-569653/53.
 XX New antibodies that bind to human insulin-like growth factor receptor,
 XX useful for treatment, prevention and diagnosis of cancers.

XX Disclosure; SEQ ID NO 65; 164pp; French.
 XX The invention relates to an isolated antibody (Ab), and its functional
 XX fragments, that bind to human insulin-like growth factor-1 receptor (IGF-
 XX 1R) and optionally: (i) inhibit natural binding of insulin-like growth
 XX factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine
 XX kinase activity of IGF-1R. Ab and its fragments are used to prevent or
 XX treat diseases associated with overexpression and/or abnormal activity of
 XX IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with
 XX hyperactivity of signal transduction pathways mediated by interaction of
 XX these receptors with their ligands. Especially they inhibit
 XX transformation of normal cells to tumor cells, inhibit growth and/or
 XX proliferation of tumor cells, so are useful against cancers of the
 XX prostate, lung, breast, endometrium and colon, also osteosarcoma, and
 XX also for treating psoriasis. Ab are also used to diagnose diseases caused
 XX by abnormal expression of IGF-1R and/or EGFR. This sequence represents a
 XX protein sequence used to generate the Ab of the invention.
 XX SQ Sequence 112 AA;
 Query Match 100.0%; Score 35; DB 7; Length 112;
 Best Local Similarity 100.0%; Pred. No. 7.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVSNNRLY 7
 DB 55 KVSNNRLY 61
 RESULT 5
 ADJ76895
 ID ADJ76895 standard; protein; 112 AA.
 AC ADJ76895;
 XX 06-MAY-2004 (first entry)
 DT Anti-IGF-1R related protein #12.
 DE Cytostatic; antipsoriatic; antibody;
 XX insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;
 KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;
 KW CDR.
 XX Homo sapiens.
 OS WO2003059951-A2.
 XX 24-JUL-2003.
 XX 20-JAN-2003; 2003WO-FR000178.
 XX 18-JAN-2002; 2002FR-00000653.
 XX 18-JAN-2002; 2002FR-00000654.
 XX 07-MAY-2002; 2002FR-00005753.
 XX (FABR) FABRE MEDICAMENT SA PIERRE.
 XX Goetsch L, Corvaia N, Leger O;
 XX WPI; 2003-569653/53.
 XX New antibodies that bind to human insulin-like growth factor receptor,
 XX useful for treatment, prevention and diagnosis of cancers.
 XX Disclosure; SEQ ID NO 61; 164pp; French.
 XX The invention relates to an isolated antibody (Ab), and its functional
 XX fragments, that bind to human insulin-like growth factor-1 receptor (IGF-
 XX 1R) and optionally: (i) inhibit natural binding of insulin-like growth
 XX factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine

CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or
 CC treat diseases associated with overexpression and/or abnormal activity of
 CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with
 CC hyperactivity of signal transduction pathways mediated by interaction of
 CC these receptors with their ligands. Especially they inhibit
 CC transformation of normal cells to tumor cells, inhibit growth and/or
 CC proliferation of tumor cells, so are useful against cancers of the
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a
 CC protein sequence used to generate the Ab of the invention.

XX SQ Sequence 112 AA;

Query Match 100.0%; Score 35; DB 7; Length 112;
 Best Local Similarity 100.0%; Pred. No. 7.7; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0;

Qy 1 KVSNNRLY 7
 |||||
 Db 55 KVSNNRLY 61

RESULT 6
 ADZ67058
 ID ADZ67058 standard; protein; 112 AA.

AC ADZ67058;

XX 30-JUN-2005 (first entry)

XX Murine immunoglobulin light chain variable region 7C10 VL SEQ ID NO:54.

XX Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
 KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;
 KW musculoskeletal disease; respiratory disease; lung tumor;
 KW endocrine disease; gynecology and obstetrics; breast tumor;
 KW endometrial carcinoma; gastrointestinal disease; colon tumor;
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder;
 KW immunoglobulin; light chain variable region.

XX Mus musculus.

XX US2005084906-A1.

XX 21-APR-2005.

XX 16-DEC-2003; 2003US-00735916.

XX 18-JAN-2002; 2002FR-00000653.

XX 18-JAN-2002; 2002FR-00000654.

XX 07-MAY-2002; 2002FR-00005753.

XX 20-JAN-2003; 2003WO-FR000178.

XX 11-JUL-2003; 2003FR-00008538.

XX (GOET/) GOETSCH L.

XX (CORV/) CORVAIA N.

XX (LEGE/) LEGER O.

XX (DUFLO/) DUFLOS A.

XX (HAEU/) HAEUW J.

XX (BECK/) BECK A.

XX Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;

XX WPI; 2005-321968/33.

XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)
 PT antibody or its functional fragment, being capable of binding human IGF-
 PT IR and specifically inhibiting tyrosine kinase activity of receptor,
 PT useful for treating cancer.

XX Example 12; SEQ ID NO 54; 125pp; English.

CC The invention relates to a novel isolated anti-insulin-like growth factor
 CC I receptor (IGF-IR) antibody (I) or its functional fragment, being
 CC capable of binding to human IGF-IR and, if necessary, capable of
 CC specifically inhibiting tyrosine kinase activity of the receptor,
 CC comprising a light or heavy chain having at least one complementary
 CC determining region (CDR) consisting of one of two fully defined 16 amino
 CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in
 CC the preparation of a medicament intended for the prevention or treatment
 CC of an illness connected with an overexpression and/or an abnormal
 CC activation of the IGF-IR and/or EGFR, and/or connected with a
 CC hyperactivation of the transduction pathway of the signal mediated by the
 CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where
 CC the administration of the medicament does not induce or only slightly
 CC induces secondary effects connected with inhibition of the insulin
 CC receptor. The antibody is useful for preparation of a medicament intended
 CC to inhibit the transformation of normal cells into cells with tumoral
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is
 CC useful for preparation of a medicament intended to inhibit the growth
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a
 CC medicament intended for prevention or for the treatment of cancer, where
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the
 CC preparation of a medicament intended for the prevention or for the
 CC treatment of psoriasis. (I) is useful in preparation of a medicament
 CC intended for the specific targeting of a biologically active compound to
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)
 CC is useful for in vitro diagnosis of illnesses induced by an
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor
 CC starting from a biological sample in which the abnormal presence, of IGF-
 CC IR and/or EGFR receptor is suspected, which involves contacting the
 CC biological sample with (I), which is optionally labeled. The present
 CC sequence is used in the exemplification of the invention.

XX SQ Sequence 112 AA;

Query Match 100.0%; Score 35; DB 9; Length 112;
 Best Local Similarity 100.0%; Pred. No. 7.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNNRLY 7
 |||||
 Db 55 KVSNNRLY 61

RESULT 7
 ADZ67069

ID ADZ67069 standard; protein; 112 AA.

AC ADZ67069;

XX 30-JUN-2005 (first entry)

XX Human antibody 7C10 2 light chain variable region SEQ ID NO:65.

XX Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
 KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;
 KW musculoskeletal disease; respiratory disease; lung tumor;
 KW endocrine disease; gynecology and obstetrics; breast tumor;
 KW endometrial carcinoma; gastrointestinal disease; colon tumor;
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder;
 KW light chain variable region.

XX Homo sapiens.

XX US2005084906-A1.

XX 21-APR-2005.

XX 16-DEC-2003; 2003US-00735916.

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PR 18-JAN-2002; 2002FR-00000653.
PR 18-JAN-2002; 2002FR-00000654.
PR 07-MAY-2002; 2002FR-00005753.
PR 20-JAN-2003; 2003WO-FR000178.
PR 11-JUL-2003; 2003FR-00008538.
XX
XX (GOET/) GOETSCH L.
XX (CORV/) CORVAIA N.
XX (LEGE/) LEGER O.
XX (DUFLO/) DUFLOS A.
XX (HAEU/) HAEUW J.
XX (BECK/) BECK A.
XX
XX Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;
XX WPI; 2005-321968/33.
XX
XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)
XX antibody or its functional fragment, being capable of binding human IGF-
XX IR and specifically inhibiting tyrosine kinase activity of receptor,
XX useful for treating cancer.
XX
XX Example 12; SEQ ID NO 65; 125pp; English.
XX
XX The invention relates to a novel isolated anti-insulin-like growth factor
XX I receptor (IGF-IR) antibody (I) or its functional fragment, being
XX capable of binding to human IGF-IR and, if necessary, capable of
XX specifically inhibiting tyrosine kinase activity of the receptor,
XX comprising a light or heavy chain having at least one complementary
XX determining region (CDR) consisting of one of two fully defined 16 amino
XX acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in
XX the preparation of a medicament intended for the prevention or treatment
XX of an illness connected with an overexpression and/or an abnormal
XX activation of the IGF-IR and/or EGFR, and/or connected with a
XX hyperactivation of the transduction pathway of the signal mediated by the
XX interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where
XX the administration of the medicament does not induce or only slightly
XX induces secondary effects connected with inhibition of the insulin
XX receptor. The antibody is useful for preparation of a medicament intended
XX to inhibit the transformation of normal cells into cells with tumoral
XX character, preferably IGF-dependent, especially IGF1 and/or IGF2-
XX dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is
XX useful for preparation of a medicament intended to inhibit the growth
XX and/or the proliferation of tumor cells, preferably IGF-dependent,
XX especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or
XX HER2/neu-dependent cells. (I) is useful in the preparation of a
XX medicament intended for prevention or for the treatment of cancer, where
XX the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,
XX breast cancer, endometrial cancer or colon cancer. (I) is useful in the
XX preparation of a medicament intended for the prevention or for the
XX treatment of psoriasis. (I) is useful in preparation of a medicament
XX intended for the specific targeting of a biologically active compound to
XX cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)
XX is useful for in vitro diagnosis of illnesses induced by an
XX overexpression or an underexpression of the IGF-IR and/or EGFR receptor
XX starting from a biological sample in which the abnormal presence, of IGF-
XX IR and/or EGFR receptor is suspected, which involves contacting the
XX biological sample with (I), which is optionally labeled. The present
XX sequence is used in the exemplification of the invention.
XX
XX Query Match 100.0%; Score 35; DB 9; Length 112;
XX Best Local Similarity 100.0%; Pred. No. 7.7;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 KVSNNRLY 7
XX 55 KVSNNRLY 61
XX
XX RESULT 8
XX ADZ67065

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ID ADZ67065 standard; protein; 112 AA.
XX
XX AC ADZ67065;
XX
XX DT 30-JUN-2005 (first entry)
XX
XX DE Human antibody 7C10 1 light chain variable region SEQ ID NO:61.
XX
XX KW Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
XX neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;
XX musculoskeletal disease; respiratory disease; lung tumor;
XX endocrine disease; gynecology and obstetrics; breast tumor;
XX endometrial carcinoma; psoriasis; gastrointestinal disease; colon tumor;
XX antipsoriatic; psoriasis; dermatological disease; immune disorder;
XX light chain variable region.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX Region 24..39
XX FT /note= "CDR1"
XX FT 55..61
XX FT /note= "CDR2"
XX FT 94..102
XX FT /note= "CDR3"
XX
XX US2005084906-A1.
XX
XX PD 21-APR-2005.
XX
XX PF 16-DEC-2003; 2003US-00735916.
XX
XX PR 18-JAN-2002; 2002FR-00000653.
XX PR 18-JAN-2002; 2002FR-00000654.
XX PR 07-MAY-2002; 2002FR-00005753.
XX PR 20-JAN-2003; 2003WO-FR000178.
XX PR 11-JUL-2003; 2003FR-00008538.
XX
XX (GOET/) GOETSCH L.
XX (CORV/) CORVAIA N.
XX (LEGE/) LEGER O.
XX (DUFLO/) DUFLOS A.
XX (HAEU/) HAEUW J.
XX (BECK/) BECK A.
XX
XX Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;
XX WPI; 2005-321968/33.
XX
XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)
XX antibody or its functional fragment, being capable of binding human IGF-
XX IR and specifically inhibiting tyrosine kinase activity of receptor,
XX useful for treating cancer.
XX
XX Example 12; SEQ ID NO 61; 125pp; English.
XX
XX The invention relates to a novel isolated anti-insulin-like growth factor
XX I receptor (IGF-IR) antibody (I) or its functional fragment, being
XX capable of binding to human IGF-IR and, if necessary, capable of
XX specifically inhibiting tyrosine kinase activity of the receptor,
XX comprising a light or heavy chain having at least one complementary
XX determining region (CDR) consisting of one of two fully defined 16 amino
XX acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in
XX the preparation of a medicament intended for the prevention or treatment
XX of an illness connected with an overexpression and/or an abnormal
XX activation of the IGF-IR and/or EGFR, and/or connected with a
XX hyperactivation of the transduction pathway of the signal mediated by the
XX interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where
XX the administration of the medicament does not induce or only slightly
XX induces secondary effects connected with inhibition of the insulin
XX receptor. The antibody is useful for preparation of a medicament intended
XX to inhibit the transformation of normal cells into cells with tumoral
XX character, preferably IGF-dependent, especially IGF1 and/or IGF2-
XX dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is
XX useful for preparation of a medicament intended to inhibit the growth
XX and/or the proliferation of tumor cells, preferably IGF-dependent,
XX especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or
XX HER2/neu-dependent cells. (I) is useful in the preparation of a
XX medicament intended for prevention or for the treatment of cancer, where
XX the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,
XX breast cancer, endometrial cancer or colon cancer. (I) is useful in the
XX preparation of a medicament intended for the prevention or for the
XX treatment of psoriasis. (I) is useful in preparation of a medicament
XX intended for the specific targeting of a biologically active compound to
XX cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)
XX is useful for in vitro diagnosis of illnesses induced by an
XX overexpression or an underexpression of the IGF-IR and/or EGFR receptor
XX starting from a biological sample in which the abnormal presence, of IGF-
XX IR and/or EGFR receptor is suspected, which involves contacting the
XX biological sample with (I), which is optionally labeled. The present
XX sequence is used in the exemplification of the invention.
XX
XX Query Match 100.0%; Score 35; DB 9; Length 112;
XX Best Local Similarity 100.0%; Pred. No. 7.7;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 KVSNNRLY 7
XX 55 KVSNNRLY 61
XX
XX RESULT 8
XX ADZ67065

```

CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is
 CC useful for preparation of a medicament intended to inhibit the growth
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a
 CC medicament intended for prevention or for the treatment of cancer, where
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the
 CC preparation of a medicament intended for the prevention or for the
 CC treatment of psoriasis. (I) is useful in preparation of a medicament
 CC intended for the specific targeting of a biologically active compound to
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)
 CC is useful for in vitro diagnosis of illnesses induced by an
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor
 CC starting from a biological sample in which the abnormal presence, of IGF-
 CC IR and/or EGFR receptor is suspected, which involves contacting the
 CC biological sample with (I), which is optionally labeled. The present
 CC sequence is used in the exemplification of the invention.
 XX
 SQ Sequence 112 AA;

Query Match 100.0%; Score 35; DB 9; Length 112;
 Best Local Similarity 100.0%; Pred. No. 7.7; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0;

Qy 1 KVSNNLY 7
 Db 55 KVSNNLY 61
 |||||

RESULT 9

ADJ76883
 ID ADJ76883 standard; protein; 122 AA.

AC ADJ76883;

DT 06-MAY-2004 (first entry)

DE Anti-IGF-IR related protein #3.

XX cytostatic; antipsoriatic; antibody;

KW insulin-like growth factor-1 receptor; IGF-IR; tyrosine kinase activity;
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;
 KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;
 KW CDR.

XX Mus musculus.

XX WO2003059951-A2.

XX 24-JUL-2003.

XX 20-JAN-2003; 2003WO-FR000178.

XX 18-JAN-2002; 2002FR-00000653.

XX 18-JAN-2002; 2002FR-00000654.

XX 07-MAY-2002; 2002FR-00005753.

XX (FABR) FABRE MEDICAMENT SA PIERRE.

XX Goetsch L, Corvaia N, Leger O;

XX WPI; 2003-569653/53.

XX New antibodies that bind to human insulin-like growth factor receptor,
 FT useful for treatment, prevention and diagnosis of cancers.

XX Disclosure; SEQ ID NO 49; 164pp; French.

XX The invention relates to an isolated antibody (Ab), and its functional
 CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-
 CC IR) and optionally: (i) inhibit natural binding of insulin-like growth

CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine
 CC kinase activity of IGF-IR. Ab and its fragments are used to prevent or
 CC treat diseases associated with overexpression and/or abnormal activity of
 CC IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with
 CC hyperactivity of signal transduction pathways mediated by interaction of
 CC these receptors with their ligands. Especially they inhibit
 CC transformation of normal cells to tumor cells, inhibit growth and/or
 CC proliferation of tumor cells, so are useful against cancers of the
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused
 CC by abnormal expression of IGF-IR and/or EGFR. This sequence represents a
 CC protein sequence used to generate the Ab of the invention.

SQ Sequence 122 AA;

Query Match 100.0%; Score 35; DB 7; Length 122;
 Best Local Similarity 100.0%; Pred. No. 8.4;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNNLY 7
 Db 65 KVSNNLY 71
 |||||

RESULT 10

ADZ67053
 ID ADZ67053 standard; protein; 122 AA.

AC ADZ67053;

DT 30-JUN-2005 (first entry)

DE Murine immunoglobulin light chain variable region 7C10 VL SEQ ID NO:49.

XX Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
 KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;
 KW musculoskeletal disease; respiratory disease; lung tumor;
 KW endocrine disease; gynecology and obstetrics; breast tumor;
 KW endometrial carcinoma; gastrointestinal disease; colon tumor;
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder;
 KW immunoglobulin; light chain variable region.

XX Mus musculus.

XX Key Location/Qualifiers
 FH Peptide 1..10
 FT /note= "leader peptide"

FT Region 34..49
 FT /note= "CDR1"

FT Region 65..71
 FT /note= "CDR2"

FT Region 104..111
 FT /note= "CDR3"

XX US2005084906-A1.

XX 21-APR-2005.

XX 16-DEC-2003; 2003US-00735916.

XX 18-JAN-2002; 2002FR-00000653.

XX 18-JAN-2002; 2002FR-00000654.

XX 07-MAY-2002; 2002FR-00005753.

XX 20-JAN-2003; 2003WO-FR000178.

XX 11-JUL-2003; 2003FR-00008538.

XX (GOET/) GOETSCH L.

XX (CORV/) CORVAIA N.

XX (LEGE/) LEGER O.

XX (DUFL/) DUFLOS A.

XX (HAEU/) HAEUW J.

XX (BECK/) BECK A.

PI Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;
 XX WPI; 2005-321968/33.
 DR N-PSDB; AD267052.
 XX
 XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)
 PT antibody or its functional fragment, being capable of binding human IGF-
 PT IR and specifically inhibiting tyrosine kinase activity of receptor,
 PT useful for treating cancer.
 XX
 XX Example 8; SEQ ID NO 49; 125pp; English.
 XX
 XX The invention relates to a novel isolated anti-insulin-like growth factor
 CC I receptor (IGF-IR) antibody (I) or its functional fragment, being
 CC capable of binding to human IGF-IR and, if necessary, capable of
 CC specifically inhibiting tyrosine kinase activity of the receptor,
 CC comprising a light or heavy chain having at least one complementary
 CC determining region (CDR) consisting of one of two fully defined 16 amino
 CC acids (AD267006 and AD267014). An antibody of the invention is useful in
 CC the preparation of a medicament intended for the prevention or treatment
 CC of an illness connected with an overexpression and/or an abnormal
 CC activation of the IGF-IR and/or EGFR, and/or connected with a
 CC hyperactivation of the transduction pathway of the signal mediated by the
 CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where
 CC the administration of the medicament does not induce or only slightly
 CC induces secondary effects connected with inhibition of the insulin
 CC receptor. The antibody is useful for preparation of a medicament intended
 CC to inhibit the transformation of normal cells into cells with tumoral
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is
 CC useful for preparation of a medicament intended to inhibit the growth
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,
 CC especially IGF1- and/or IGF2-dependent and/or EGF-dependent and/or
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a
 CC medicament intended for prevention or for the treatment of cancer, where
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the
 CC preparation of a medicament intended for the prevention or for the
 CC treatment of psoriasis. (I) is useful in preparation of a medicament
 CC intended for the specific targeting of a biologically active compound to
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)
 CC is useful for in vitro diagnosis of illnesses induced by an
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor
 CC starting from a biological sample in which the abnormal presence, of IGF-
 CC IR and/or EGFR receptor is suspected, which involves contacting the
 CC biological sample with (I), which is optionally labeled. The present
 CC sequence is used in the exemplification of the invention.

XX SQ Sequence 122 AA;

Query Match 100.0%; Score 35; DB 9; Length 122;
 Best Local Similarity 100.0%; Pred. No. 8.4;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNNLY 7
 |||||
 Db 65 KVSNNLY 71

RESULT 11
 ADJ76901
 ID ADJ76901 standard; protein; 131 AA.

XX AC ADJ76901;

XX DT 06-MAY-2004 (first entry)

XX DE Anti-IGF-1R related protein #15.

XX KW cytosolic; antipsoriatic; antibody;
 KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;
 KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;

KW CDR.

XX Homo sapiens.

XX PN WO2003059951-A2.

XX PD 24-JUL-2003.

XX PF 20-JAN-2003; 2003WO-FR000178.

XX PR 18-JAN-2002; 2002FR-00000653.

XX PR 18-JAN-2002; 2002FR-00000654.

XX PR 07-MAY-2002; 2002FR-00005753.

XX (FAER) FABRE MEDICAMENT SA PIERRE.

XX PI Goetsch L, Corvaia N, Leger O;

XX WPI; 2003-569653/53.

XX New antibodies that bind to human insulin-like growth factor receptor,
 PT useful for treatment, prevention and diagnosis of cancers.

XX Disclosure; SEQ ID NO 67; 164pp; French.

XX The invention relates to an isolated antibody (Ab), and its functional
 CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-
 CC IR) and optionally: (i) inhibit natural binding of insulin-like growth
 CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine
 CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or
 CC treat diseases associated with overexpression and/or abnormal activity of
 CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with
 CC hyperactivity of signal transduction pathways mediated by interaction of
 CC these receptors with their ligands. Especially they inhibit
 CC transformation of normal cells to tumor cells, inhibit growth and/or
 CC proliferation of tumor cells, so are useful against cancers of the
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a
 CC protein sequence used to generate the Ab of the invention.

XX SQ Sequence 131 AA;

Query Match 100.0%; Score 35; DB 7; Length 131;
 Best Local Similarity 100.0%; Pred. No. 9.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNNLY 7
 |||||
 Db 74 KVSNNLY 80

RESULT 12
 ADJ76897

ID ADJ76897 standard; protein; 131 AA.

XX AC ADJ76897;

XX DT 06-MAY-2004 (first entry)

XX DE Anti-IGF-1R related protein #13.

XX KW cytosolic; antipsoriatic; antibody;
 KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;
 KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;
 KW CDR.

XX OS Homo sapiens.

XX PN WO2003059951-A2.

XX PD 24-JUL-2003.

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XX PF 20-JAN-2003; 2003WO-FR000178.
XX PR 18-JAN-2002; 2002FR-00000653.
XX PR 18-JAN-2002; 2002FR-00000654.
XX PR 07-MAY-2002; 2002FR-00005753.
XX (FABR ) FABRE MEDICAMENT SA PIERRE.
XX Goetsch L, Corvaia N, Leger O;
XX WPI; 2003-569653/53.
XX New antibodies that bind to human insulin-like growth factor receptor,
XX useful for treatment, prevention and diagnosis of cancers.
XX Disclosure; SEQ ID NO 63; 164pp; French.
XX The invention relates to an isolated antibody (Ab), and its functional
XX fragments, that bind to human insulin-like growth factor-1 receptor (IGF-
XX IR) and optionally: (i) inhibit natural binding of insulin-like growth
XX factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine
XX kinase activity of IGF-1R. Ab and its fragments are used to prevent or
XX treat diseases associated with overexpression and/or abnormal activity of
XX IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with
XX hyperactivity of signal transduction pathways mediated by interaction of
XX these receptors with their ligands. Especially they inhibit
XX transformation of normal cells to tumor cells, inhibit growth and/or
XX proliferation of tumor cells, so are useful against cancers of the
XX prostate, lung, breast, endometrium and colon, also osteosarcoma, and
XX also for treating psoriasis. Ab are also used to diagnose diseases caused
XX by abnormal expression of IGF-1R and/or EGFR. This sequence represents a
XX protein sequence used to generate the Ab of the invention.
XX Sequence 131 AA;
XX
Query Match 100.0%; Score 35; DB 7; Length 131;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVSNNRLY 7
DB 74 KVSNNRLY 80
|||||||
RESULT 13
ADZ67071
ID ADZ67071 standard; protein; 131 AA.
XX AC ADZ67071;
XX 30-JUN-2005 (first entry)
XX Human antibody 7C10 2 light chain variable region SEQ ID NO:67.
XX Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
XX neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;
XX musculoskeletal disease; respiratory disease; lung tumor;
XX endocrine disease; gynecology and obstetrics; breast tumor;
XX endometrial carcinoma; gastrointestinal disease; colon tumor;
XX antipsoriatic; psoriasis; dermatological disease; immune disorder;
XX light chain variable region.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..19 /note= "leader peptide"
XX Region 43..58 /note= "CDR1"
XX Region 74..80 /note= "CDR2"
XX Region 113..121 /note= "CDR3"

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FT /note= "CDR3"
XX US2005084906-A1.
XX 21-APR-2005.
XX 16-DEC-2003; 2003US-00735916.
XX 18-JAN-2002; 2002FR-00000653.
XX 18-JAN-2002; 2002FR-00000654.
XX 07-MAY-2002; 2002FR-00005753.
XX 20-JAN-2003; 2003WO-FR000178.
XX 11-JUL-2003; 2003FR-00008538.
XX (GOET/) GOETSCH L.
XX (CORV/) CORVAIA N.
XX (LEGE/) LEGER O.
XX (DUFL/) DUFLOS A.
XX (HAEU/) HAEUW J.
XX (BECK/) BECK A.
XX Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;
XX WPI; 2005-321968/33.
XX N-FSDB; ADZ67070.
XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)
XX antibody or its functional fragment, being capable of binding human IGF-
XX IR and specifically inhibiting tyrosine kinase activity of receptor,
XX useful for treating cancer.
XX Example 12; SEQ ID NO 67; 125pp; English.
XX The invention relates to a novel isolated anti-insulin-like growth factor
XX I receptor (IGF-IR) antibody (I) or its functional fragment, being
XX capable of binding to human IGF-IR and, if necessary, capable of
XX specifically inhibiting tyrosine kinase activity of the receptor,
XX comprising a light or heavy chain having at least one complementary
XX determining region (CDR) consisting of one of two fully defined 16 amino
XX acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in
XX the preparation of a medicament intended for the prevention or treatment
XX of an illness connected with an overexpression and/or an abnormal
XX activation of the IGF-IR and/or EGFR, and/or connected with a
XX hyperactivation of the transduction pathway of the signal mediated by the
XX interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where
XX the administration of the medicament does not induce or only slightly
XX induces secondary effects connected with inhibition of the insulin
XX receptor. The antibody is useful for preparation of a medicament intended
XX to inhibit the transformation of normal cells into cells with tumoral
XX character, preferably IGF-dependent, especially IGF1 and/or IGF2-
XX dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is
XX useful for preparation of a medicament intended to inhibit the growth
XX and/or the proliferation of tumor cells, preferably IGF-dependent,
XX especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or
XX HER2/neu-dependent cells. (I) is useful in the preparation of a
XX medicament intended for prevention or for the treatment of cancer, where
XX the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,
XX breast cancer, endometrial cancer or colon cancer. (I) is useful in the
XX preparation of a medicament intended for the prevention or for the
XX treatment of psoriasis. (I) is useful in preparation of a medicament
XX intended for the specific targeting of a biologically active compound to
XX cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)
XX is useful for in vitro diagnosis of illnesses induced by an
XX overexpression or an underexpression of the IGF-IR and/or EGFR receptor
XX starting from a biological sample in which the abnormal presence, of IGF-
XX IR and/or EGFR receptor is suspected, which involves contacting the
XX biological sample with (I), which is optionally labeled. The present
XX sequence is used in the exemplification of the invention.
XX Sequence 131 AA;
XX
Query Match 100.0%; Score 35; DB 9; Length 131;
Best Local Similarity 100.0%; Pred. No. 9.1;

```

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSRLY 7
 DB 74 KVSRLY 80

RESULT 14
 ID ADZ67067 standard; protein; 131 AA.
 AC ADZ67067;
 DT 30-JUN-2005 (first entry)
 XX Human antibody 7C10 1 light chain variable region SEQ ID NO:63.
 XX Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
 KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;
 KW musculoskeletal disease; respiratory disease; lung tumor;
 KW endocrine disease; gynecology and obstetrics; breast tumor;
 KW endometrial carcinoma; gastrointestinal disease; colon tumor;
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder;
 KW light chain variable region.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FH Peptide 1..19
 FT /note= "leader peptide"
 FT Region 43..62
 FT /note= "CDR1"
 FT Region 74..80
 FT /note= "CDR2"
 FT Region 113..121
 FT /note= "CDR3"
 XX US2005084906-A1.
 XX 21-APR-2005.
 XX 16-DEC-2003; 2003US-00735916.
 XX 18-JAN-2002; 2002FR-00000653.
 XX 18-JAN-2002; 2002FR-00000654.
 XX 07-MAY-2002; 2002FR-00005753.
 XX 20-JAN-2003; 2003WO-FR000178.
 XX 11-JUL-2003; 2003FR-00008538.
 XX (GOET/) GOETSCH L.
 XX (CORV/) CORVAIA N.
 XX (LEGE/) LEGER O.
 XX (DUFL/) DUFLOS A.
 XX (HAEU/) HAEUW J.
 XX (BECK/) BECK A.
 XX Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;
 XX WPI; 2005-321968/33.
 XX N-PSDB; ADZ67066.
 XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)
 XX antibody or its functional fragment, being capable of binding human IGF-
 XX IR and specifically inhibiting tyrosine kinase activity of receptor,
 XX useful for treating cancer.
 XX Example 12; SEQ ID NO 63; 125pp; English.
 XX The invention relates to a novel isolated anti-insulin-like growth factor
 XX I receptor (IGF-IR) antibody (I) or its functional fragment, being
 XX capable of binding to human IGF-IR and, if necessary, capable of
 XX specifically inhibiting tyrosine kinase activity of the receptor,
 XX comprising a light or heavy chain having at least one complementary

determining region (CDR) consisting of one of two fully defined 16 amino acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in the preparation of a medicament intended for the prevention or treatment of an illness connected with an overexpression and/or an abnormal activation of the IGF-IR and/or EGFR, and/or connected with a hyperactivation of the IGF-IR and/or EGFR, and/or of EGF with EGFR, where interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where the administration of the medicament does not induce or only slightly induces secondary effects connected with inhibition of the insulin receptor. The antibody is useful for preparation of a medicament intended to inhibit the transformation of normal cells into cells with tumoral character, preferably IGF-dependent, especially IGF1 and/or IGF2-dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is useful for the preparation of a medicament intended to inhibit the growth and/or the proliferation of tumor cells, preferably IGF-dependent, especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is useful in the preparation of a medicament intended for prevention or for the treatment of cancer, where the cancer is chosen from prostate cancer, osteosarcoma, lung cancer, breast cancer, endometrial cancer or colon cancer. (I) is useful in the preparation of a medicament intended for the prevention or for the treatment of psoriasis. (I) is useful in preparation of a medicament intended for the specific targeting of a biologically active compound to cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I) is useful for in vitro diagnosis of illnesses induced by an overexpression or an underexpression of the IGF-IR and/or EGFR receptor starting from a biological sample in which the abnormal presence, of IGF-IR and/or EGFR receptor is suspected, which involves contacting the biological sample with (I), which is optionally labeled. The present sequence is used in the exemplification of the invention.

Sequence 131 AA;
 Query Match 100.0%; Score 35; DB 9; Length 131;
 Best Local Similarity 100.0%; Pred. No. 9.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSRLY 7
 DB 74 KVSRLY 80

RESULT 15
 ADQ08646
 ID ADQ08646 standard; protein; 841 AA.
 XX AC ADQ08646;
 XX DT 26-AUG-2004 (first entry)
 XX Ciona intestinalis nervous system associated protein SeqID48.
 XX gene cluster; nervous system; sea-squirt tailbud; embryo; larva;
 XX nervous system disease.
 XX Ciona intestinalis.
 XX JP2004057127-A.
 XX 26-FEB-2004.
 XX 31-JUL-2002; 2002JP-00222532.
 XX 31-JUL-2002; 2002JP-00222532.
 XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 XX WPI; 2004-208712/20.
 XX N-PSDB; ADQ08645.
 XX Novel genes derived from Ciona intestinalis (sea squirt), expressed in nervous system in the tailbud embryo or larva, useful for studying the development of nervous system.

XX PS Claim 4; SEQ ID NO 48; 897pp; Japanese.
XX CC This invention relates to a novel gene cluster, where the encoded
CC proteins are expressed in the nervous system of sea-squirt tailbud embryo
CC or larva. The invention is useful for studying the development of the
CC nervous system of the sea-squirt and for research purposes. The genes may
CC be used for determining the disease-development mechanisms in the nervous
CC system. In addition, novel gene clusters expressed in nervous system of
CC sea-squirt tailbud embryo or larva allows development of diagnostics and
CC therapeutics related to nervous system diseases. The present sequence is
CC that of a protein encoded by a C intestinalis gene of the invention.

XX SQ Sequence 841 AA;
Query Match 100.0%; Score 35; DB 8; Length 841;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVSRLY 7
Db 801 KVSRLY 807
|||||

Search completed: December 30, 2005, 13:23:57
Job time : 64.2097 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:11:41 ; Search time 9.93548 Seconds
(without alignments)
67.789 Million cell updates/sec

Title: US-10-735-916A-4

Perfect score: 35

Sequence: 1 KVSNNLY 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80.*

1: Pir1.*

2: Pir2.*

3: Pir3.*

4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	31	88.6	108	E32530	Ig kappa chain V r
2	31	88.6	112	D28195	Ig kappa chain V r
3	31	88.6	374	A57583	histone acetyltran
4	30	85.7	64	JS0299	cytotoxin homolog
5	30	85.7	216	PQ0299	hypothetical prote
6	30	85.7	305	A12079	hypothetical prote
7	30	85.7	375	G89972	conserved hypotet
8	30	85.7	405	A41252	heat shock protein
9	30	85.7	435	E69820	conserved hypotet
10	30	85.7	463	S66504	dipeptidyl-peptida
11	30	85.7	600	A12454	ATP-binding protei
12	30	85.7	845	I48176	synaptonemal compl
13	30	85.7	993	S49461	synaptonemal compl
14	30	85.7	1102	AD2136	microcytin synthet
15	29	82.9	184	G97182	hypothetical secre
16	29	82.9	264	E90500	lipopate-protein li
17	29	82.9	293	D90153	cobalamin biosynth
18	29	82.9	329	T04710	peroxidase (EC 1.1
19	29	82.9	379	A42421	leukocyte elastase
20	29	82.9	379	S27383	elastase inhibitor
21	29	82.9	407	I39859	germination respon
22	29	82.9	528	A12321	hypothetical prote
23	29	82.9	566	S07508	DNA primase - phag
24	29	82.9	588	E71802	penicillin-binding
25	29	82.9	588	E64715	penicillin-binding
26	29	82.9	809	S33533	heat shock protein
27	29	82.9	832	E71492	hypothetical prote
28	29	82.9	1003	C71139	hypothetical prote
29	29	82.9	2144	T21712	hypothetical prote

hypothetical prote
Ig kappa chain V r
conserved hypotet
hypothetical prote
hypothetical prote
ORF MSV146 hypotet
repressor - Staphy
ribose-phosphate d
ribose-phosphate d
phosphoribosylpyro
ribose-phosphate d
phosphoribosylpyro
ribose-phosphate d
class I histocompa
membrane associate
hypothetical prote

ALIGNMENTS

RESULT 1

E32530
Ig kappa chain V region (DB3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 09-Jul-2004
C:Accession: E32530
R:Deverson, E.; Berek, C.; Taussig, M.; Feinstein, A.
Eur. J. Immunol. 17, 9-13, 1987
A:Title: Monoclonal BALB/c anti-progesterone antibodies use family IX variable region h
A:Reference number: A32530; MUID:87133855; PMID:3102254
A:Accession: E32530
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-108 <DEV>
A:Cross-references: UNIPROT:Q8VC16; UNIPARC:UPI0000176B00; GB:M27587
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
P:16-95/Domain: immunoglobulin homology <IMM>

Query Match 88.6%; Score 31; DB 2; Length 108;
Best Local Similarity 85.7%; Pred. No. 7.4;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVSNNLY 7
DB 55 KVSNNRY 61
|||||

RESULT 2

D28195
Ig kappa chain V region (anti-haloperidol antibody D) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C:Accession: D28195
R:Sherman, M.A.; Deans, R.J.; Bolger, M.B.
J. Biol. Chem. 263, 4059-4063, 1988
A:Title: Haloperidol binding to monoclonal antibodies. Hypervariable region amino acid
A:Reference number: A28195; MUID:88153717; PMID:3267217
A:Accession: D28195
A:Molecule type: mRNA
A:Residues: 1-112 <SHE>
A:Cross-references: UNIPROT:Q99M37; UNIPARC:UPI0000176B01; GB:M19769
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
P:16-95/Domain: immunoglobulin homology <IMM>

Query Match 88.6%; Score 31; DB 2; Length 112;
Best Local Similarity 85.7%; Pred. No. 7.7;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVSNNLY 7
|||||

Db 55 KVSNNRFP 61

RESULT 3
A57583
histone acetyltransferase (EC 2.3.1.48) HAT1 - yeast (Saccharomyces cerevisiae)
N|Alternate names: protein LPA15w; protein YP8132.12; protein YPL001w
C|Species: Saccharomyces cerevisiae
C|Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C|Accession: A57583; S52530; S59692
R|Kleff, S.; Andrusis, E.D.; Anderson, C.W.; Sternglanz, R.
J. Biol. Chem. 270, 24674-24677, 1995
A|Title: Identification of a gene encoding a yeast histone H4 acetyltransferase.
A|Reference number: A57583; MUID:96027552; PMID:7559580
A|Accession: A57583
A|Status: nucleic acid sequence not shown
A|Molecule type: DNA
A|Residues: 1-374 <KLB>
A|Cross-references: UNIPROT:Q12341; UNIPARC:UPI00000530B2; GB:Z48483; NID:9683777; PIDN:
R|Badcock, K.; Churcher, C.
submitted to the EMBL Data Library, February 1995
A|Reference number: S52519
A|Accession: S52530
A|Molecule type: DNA
A|Residues: 1-374 <BAD>
A|Cross-references: UNIPARC:UPI00000530B2; EMBL:Z48483; NID:9683777; PIDN:CAA88385.1; PI
R|Hall, J.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Storms, R.K.; Vo, D.H.; Wa
submitted to the EMBL Data Library, August 1995
A|Description: The sequence of Saccharomyces cerevisiae chromosome XVI left arm.
A|Reference number: S59677
A|Accession: S59692
A|Molecule type: DNA
A|Residues: 1-374 <HAL>
A|Cross-references: UNIPARC:UPI00000530B2; EMBL:U33335; NID:9565076; PIDN:AAB68104.1; PI
C|Genetics:
A|Gene: SGD:HAT1
A|Cross-references: SGD:S0005922; MIPS:YPL001w
A|Map position: 16L
C|Keywords: acyltransferase; coenzyme A

Query Match 88.6%; Score 31; DB 2; Length 374;
Best Local Similarity 85.7%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVSNNRFP 7
|||
326 KVSNNRFP 332

Db 326 KVSNNRFP 332

RESULT 4
JS0299
cytotoxin homolog S4C8 - shield snake
C|Species: Aspidelaps scutatus (shield snake)
C|Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C|Accession: JS0299
R|Joubert, F.J.
Int. J. Biochem. 20, 337-345, 1988
A|Title: Snake venom toxins II. The primary structures of cytotoxin homologues S3C2 and
A|Reference number: JS0299; MUID:88185648; PMID:3356299
A|Accession: JS0299
A|Molecule type: protein
A|Residues: 1-64 <JOU>
A|Cross-references: UNIPROT:P19004; UNIPARC:UPI00001287FC
A|Experimental source: venom
C|Superfamily: snake toxin
C|Keywords: cytotoxin

Query Match 85.7%; Score 30; DB 2; Length 64;
Best Local Similarity 71.4%; Pred. No. 7.4;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNNRFP 7

Db 24 KVSNNRFP 30

RESULT 5
PQ0299
hypothetical protein 5 (gldA 3' region) - Bacillus stearothermophilus (fragment)
C|Species: Bacillus stearothermophilus
C|Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Oct-2004
C|Accession: PQ0299
R|Mallinder, P.R.; Pritchard, A.; Moir, A.
Gene 110, 9-16, 1992
A|Title: Cloning and characterization of a gene from Bacillus stearothermophilus var. n.
A|Reference number: JQ1474; MUID:92184120; PMID:1339360
A|Accession: PQ0299
A|Molecule type: DNA
A|Residues: 1-216 <MAL>
A|Cross-references: UNIPROT:P32815; UNIPARC:UPI000013B0F1; GB:M65289; NID:gl42976; PIDN:
A|Experimental source: strain var. non-diataticus
F|20-94/Domain: ferredoxin 2[4Fe-4S] homology <FER>

Query Match 85.7%; Score 30; DB 2; Length 216;
Best Local Similarity 71.4%; Pred. No. 26;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVSNNRFP 7
|||
71 KVSNNRFP 77

Db 71 KVSNNRFP 77

RESULT 6
AI2079
hypothetical protein alr2191 [imported] - Nostoc sp. (strain PCC 7120)
C|Species: Nostoc sp. PCC 7120
A|Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C|Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C|Accession: AI2079
R|Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A|Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A|Reference number: AB1807; MUID:21595285; PMID:11759840
A|Accession: AI2079
A|Status: preliminary
A|Molecule type: DNA
A|Residues: 1-305 <KUR>
A|Cross-references: UNIPROT:Q8YU20; UNIPARC:UPI00000CE359; GB:BA000019; PIDN:BA073890.1;
A|Experimental source: strain PCC 7120
C|Genetics:
A|Gene: alr2191

Query Match 85.7%; Score 30; DB 2; Length 305;
Best Local Similarity 71.4%; Pred. No. 37;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVSNNRFP 7
|||
49 KVSNNRFP 55

Db 49 KVSNNRFP 55

RESULT 7
G89972
conserved hypothetical protein SA1673 [imported] - Staphylococcus aureus (strain N315)
C|Species: Staphylococcus aureus
C|Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 05-Oct-2004
C|Accession: G89972
R|Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A|Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A|Reference number: AB9758; MUID:21311952; PMID:11418146
A|Accession: G89972

A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-375 <KUR>
 A;Cross-references: UNIPROT:Q99T22; UNIPARC:UPI00000CACF6; GB:BA000018; PID:g13701649; F
 A;Experimental source: strain N315
 C;Genetics:
 A;Gene: SA1673

Query Match 85.7%; Score 30; DB 2; Length 375;
 Best Local Similarity 71.4%; Pred. No. 45;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVSNNLY 7
 |: |||||

DB 232 KIGNRLY 238

RESULT 8

A41252
 heat shock protein 47 precursor - chicken
 C;Species: Gallus gallus (chicken)
 C;Date: 03-Apr-1992 #sequence revision 12-Apr-1996 #text_change 05-Oct-2004
 C;Accession: A41252; A27656; S16673
 R;Hirayoshi, K.; Kudo, H.; Takechi, H.; Nakai, A.; Yamada, K.M.; Nagata, K.
 Mol. Cell. Biol. 11, 4036-4044, 1991
 A;Title: HSP47: a tissue-specific, transformation-sensitive, collagen-binding heat shock
 A;Reference number: A41252; MUID:91304395; PMID:2072906
 A;Accession: A41252
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-405 <HIR>
 A;Cross-references: UNIPROT:P13731; UNIPARC:UPI000012CC27; GB:X57157; NID:g63510; PID:N
 R;Nagata, K.; Saga, S.; Yamada, K.M.
 Biochem. Biophys. Res. Commun. 153, 428-434, 1988
 A;Title: Characterization of a novel transformation-sensitive heat-shock protein (HSP47)
 A;Reference number: A27656; MUID:88240438; PMID:3377793
 A;Accession: A27656
 A:Molecule type: protein
 A:Residues: 16-51 <NAG>
 A;Cross-references: UNIPARC:UPI00001731PD
 R;Nagata, K.

Trends Biochem. Sci. 21, 23-26, 1996
 A;Title: Hsp47: a collagen-specific molecular chaperone.
 A;Reference number: A57864
 A;Contents: annotation; review article
 C;Comment: This stress-induced glycoprotein of the ER lumen lacks protease inhibitor act
 C;Genetics:
 A;Gene: HSP47
 C;Function:
 A;Description: Hsp47 associates transiently with procollagen to assist as a molecular ch
 and is induced by stresses such as heat shock.
 C;Superfamily: serpin
 C;Keywords: collagen binding; endoplasmic reticulum; glycoprotein; heat shock; molecular
 F;1-15/Domain: signal sequence #status predicted <SIG>
 F;16-405/Product: heat shock protein 47 #status predicted <MAT>
 F;402-405/Region: endoplasmic reticulum retention signal
 F;107,112/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 85.7%; Score 30; DB 1; Length 405;
 Best Local Similarity 71.4%; Pred. No. 49;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVSNNLY 7
 |: |||||

DB 116 KIGNRLY 122

RESULT 9

E69820
 conserved hypothetical protein yhbA - Bacillus subtilis
 C;Species: Bacillus subtilis
 C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-Oct-2004
 C;Accession: E69820

R;Kunst, P.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
 C.; Bron, S.; Brummet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
 A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
 Nature 390, 249-256, 1997
 A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle
 iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Hoisappel, S.; Hosono, S.; Hullo, M.F
 Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
 A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauee
 Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelli
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon
 A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero
 akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpsira, P.; Tognoni, A.; Tosato, V.; Uchiyama
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida,
 A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.

A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
 A;Reference number: A69580; MUID:98044033; PMID:9384377

A;Accession: E69820

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-435 <KUN>

A;Cross-references: UNIPROT:P97030; UNIPARC:UPI0000060111; GB:Z99108; GB:AL009126; NID:.

A;Experimental source: strain 168

C;Genetics:

A;Gene: yhbA

F;230-304/Domain: ferredoxin 2[4Fe-4S] homology <PER>

Query Match 85.7%; Score 30; DB 2; Length 435;

Best Local Similarity 71.4%; Pred. No. 53;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVSNNLY 7
 |: |||||

DB 281 KIGNRLY 287

RESULT 10

S66504
 dipeptidyl-peptidase I (EC 3.4.14.1) precursor - human
 C;Species: Homo sapiens (man)
 C;Date: 19-Mar-1997 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004
 C;Accession: S66504
 R;Paris, A.; Strukelj, B.; Pungercar, J.; Renko, M.; Dolenc, I.; Turk, V.
 FEBS Lett. 369, 326-330, 1995
 A;Title: Molecular cloning and sequence analysis of human preprocathepsin C.
 A;Reference number: S66504; MUID:95377428; PMID:7649281
 A;Accession: S66504
 A>Status: preliminary
 A:Molecule type: mRNA
 A;Residues: 1-463 <PAR>
 A;Cross-references: UNIPROT:PS3634; UNIPARC:UPI0000127099; EMBL:X87212; NID:gl006656; P

C;Genetics:
 A;Gene: GDB:CTSC
 A;Cross-references: GDB:642234
 A;Map position: 8p22-8p22
 C;Superfamily: papain
 C;Keywords: dipeptidylpeptidase hydrolase
 F;258,405,427/Active site: Cys, His, Asn #status predicted

Query Match 85.7%; Score 30; DB 2; Length 463;
 Best Local Similarity 85.7%; Pred. No. 56;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVSNNLY 7
 |: |||||

DB 162 KVSNNLY 168

RESULT 11

AI2454
 ATP-binding protein of ABC transporter all5193 [imported] - Nostoc sp. (strain PCC 7120
 C;Species: Nostoc sp. PCC 7120
 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C;Accession: A12454
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpō, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: A12454
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-600 <KUR>
A;Cross-references: UNIPROT:O8YLW3; UNIPARC:UPI00000CEDBE; GB:BA000019; PIDN:BA076892.1;
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all5193
C;Superfamily: Escherichia coli ABC transporter mlaA; ATP-binding cassette homology

Query Match 85.7%; Score 30; DB 2; Length 600;
Best Local Similarity 85.7%; Pred. No. 74;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVSNNLY 7
|||
115 KVSNNLY 121

RESULT 12
I48176
synaptonemal complex protein - golden hamster (fragment)
C;Species: Mesocricetus auratus (Golden hamster)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
A;Accession: I48176
R;Dobson, M.J.; Pearlman, R.E.; Karaizakis, A.; Spyropoulos, B.; Moens, P.B.
J. Cell Sci. 107, 2749-2760, 1994
A;Title: Synaptonemal complex proteins: occurrence, epitope mapping and chromosome disju
A;Reference number: I48176; MUID:95181577; PMID:7876343
A;Accession: I48176
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-845 <RES>
A;Cross-references: UNIPROT:Q60563; UNIPARC:UPI000013567E; GB:IL32978; NID:G598124; PIDN:
C;Genetics:
A;Gene: syn1

Query Match 85.7%; Score 30; DB 2; Length 845;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNNLY 7
|||
781 EISNNLY 787

RESULT 13
S49461
synaptonemal complex protein 1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
A;Accession: S49461; S59599
R;Julien, S.; Luc, M.; Francois, C.
submitted to the EMBL Data Library, October 1994
A;Description: Cloning and sequencing of the murine SCP1 cDNA.
A;Reference number: S49461
A;Accession: S49461
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-993 <JUN>
A;Cross-references: UNIPROT:Q62209; UNIPARC:UPI0000028B49; EMBL:Z38118; NID:G1360015; PI
R;Sage, J.; Martin, L.; Cuzin, F.; Rassoulizadegan, M.
Biochim. Biophys. Acta 1263, 258-260, 1995
A;Title: cDNA sequence of the murine synaptonemal complex protein 1 (SCP1).
A;Reference number: S59599; MUID:96004899; PMID:7548215
A;Accession: S59599
A;Status: preliminary

A;Molecule type: mRNA
A;Residues: 1-993 <SAG>
A;Cross-references: UNIPARC:UPI0000028B49; EMBL:Z38118; NID:G1360015; PIDN:CAA86262.1; P
Query Match 85.7%; Score 30; DB 2; Length 993;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSNRLY 7
|||||
927 VSNRLY 932

RESULT 14
AD2136
microcystin synthetase B [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
A;Accession: AD2136
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpō, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AD2136
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1102 <KUR>
A;Cross-references: UNIPROT:Q8YTS0; UNIPARC:UPI00000CE4E9; GB:BA000019; PIDN:BA074342.1;
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all2643
C;Superfamily: peptide synthetase ppsB; acetate-CoA ligase homology; acyl carrier protei
C;Keywords: carrier protein

Query Match 85.7%; Score 30; DB 2; Length 1102;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSNRLY 7
|||||
639 VSNRLY 644

RESULT 15
G97182
hypothetical secreted protein [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
A;Accession: G97182
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: G97182
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-184 <KUR>
A;Cross-references: UNIPROT:Q97GS2; UNIPARC:UPI00000CA495; GB:AE001437; PIDN:AAK80250.1;
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC2293

Query Match 82.9%; Score 29; DB 2; Length 184;
Best Local Similarity 71.4%; Pred. No. 37;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNNLY 7
|||||
60 KVSNNLY 66

Search completed: December 30, 2005, 13:34:53
Job time : 10.9355 secs

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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:11:26 ; Search time 63 Seconds
(without alignments)
78.392 Million cell updates/sec

Title: US-10-735-916A-4
Perfect score: 35
Sequence: 1 KVSRLY 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	97.1	404	Q90420 BRARE	Q90420 brachydanio
2	34	97.1	405	Q6IQV2 BRARE	Q6IQV2 brachydanio
3	34	97.1	406	Q5DW60 ONCMY	Q5DW60 oncorhynchu
4	34	97.1	576	G6PD1 ARATH	Q43727 arabidopsis
5	32	91.4	355	Q8KKD3 HELPY	Q8KKD3 helicobacte
6	32	91.4	614	Q6BSM3 DEBHA	Q6BSM3 debaryomyce
7	32	91.4	1220	Q4PFH3 USTWA	Q4PFH3 ustilago ma
8	31	88.6	374	HAT1 YEAST	Q12341 saccharomyc
9	31	88.6	573	Q9AWB2 SOYEN	Q9AWB2 glycine max
10	31	88.6	685	Q75NZ0 PEA	Q75NZ0 pisum sativ
11	30	85.7	64	CKH48 ASPSC	P19004 aspidelaps
12	30	85.7	130	Q6FSG5 CANGA	Q6FSG5 candida gla
13	30	85.7	161	Q747U3 GEOSL	Q747U3 geobacter s
14	30	85.7	189	Q4U9D3 THEAN	Q4U9D3 theileria a
15	30	85.7	216	YGL5 BACST	P32815 bacillus st
16	30	85.7	219	Q90XR7 BRARE	Q90XR7 brachydanio
17	30	85.7	219	Q567K6 BRARE	Q567K6 brachydanio
18	30	85.7	238	Q4WH23 ASPFU	Q4WH23 aspergillus
19	30	85.7	238	Q4WH44 ASPFU	Q4WH44 aspergillus
20	30	85.7	248	Q9AJU8 SHIFL	Q9AJU8 shigella fl
21	30	85.7	248	Q8VSA9 SHIFL	Q8VSA9 shigella fl
22	30	85.7	301	Q9AFK9 SHIFL	Q9AFK9 shigella fl
23	30	85.7	305	Q8YU20 ANASP	Q8YU20 anabaena sp
24	30	85.7	331	Q9M425 SPIOL	Q9M425 spinacia ol
25	30	85.7	356	Q50Q58 ENTHI	Q50Q58 entamoeba h
26	30	85.7	375	Q4L7G0 STAHJ	Q4L7G0 staphylococ
27	30	85.7	375	Q6G877 STAA5	Q6G877 staphylococ
28	30	85.7	375	Q6GPK0 STAA8	Q6GPK0 staphylococ
29	30	85.7	375	Q7A4U3 STAA8	Q7A4U3 staphylococ
30	30	85.7	375	Q8NVV0 STAAW	Q8NVV0 staphylococ
31	30	85.7	375	Q99T22 STAAW	Q99T22 staphylococ

32 30 85.7 375 2 QSHER8 STAA8 Q5HER8 staphylococ
33 30 85.7 376 2 Q5HN80 STAEQ Q5HN80 staphylococ
34 30 85.7 380 2 Q8CRX0 STAEQ Q8CRX0 staphylococ
35 30 85.7 380 2 Q5L2R3 GEOKA Q5L2R3 geobacillus
36 30 85.7 385 2 Q5OME4 ENTHI Q5OME4 entamoeba h
37 30 85.7 405 1 HSP47 CHICK P13731 gallus gall
38 30 85.7 435 2 P97030 BACSU P97030 bacillus su
39 30 85.7 456 2 Q526J5 MAGGR Q526J5 magnaporthe
40 30 85.7 463 1 CATC HUMAN P53634 h dipeptidyl
41 30 85.7 463 1 CATC HUMAN Q60HG6 m dipeptidyl
42 30 85.7 463 2 Q53G93 HUMAN Q53G93 homo sapien
43 30 85.7 463 2 Q71E76 HUMAN Q71E76 homo sapien
44 30 85.7 463 2 Q8WY99 HUMAN Q8WY99 homo sapien
45 30 85.7 463 2 Q5RB02 PONPY Q5RB02 pongo pygma

ALIGNMENTS

RESULT 1
ID Q90420 BRARE PRELIMINARY; PRT; 404 AA.
AC Q90420;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE 47 kDa heat shock protein.
GN Name-hsp47; Synonymshsp;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=9626405; PubMed=8634155;
RA Pearson D.S., Kulyk W.M., Kelly G.M., Krone P.H.;
RT "Cloning and characterization of a cDNA encoding the collagen-binding
RT stress protein hsp47 in zebrafish.",
RL DNA Cell Biol. 15:263-272(1996).
CC -!- SIMILARITY: Belongs to the serpin family.
DR EMBL; U31079; AAB06193.1; -; mRNA.
DR HSSP; P01012; IOVA.
DR Ensembl; ENSDARG0000019949; Danio rerio.
DR ZFIN; ZDB-GENE-990415-93; hsp47.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR000886; P:response to unfolded protein; IEA.
DR InterPro; IPR000215; Prot_inh_serpin.
DR Pfam; PF00079; Serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
DR PROSITE; PS00284; SERPIN; 1.
KW Heat shock; Serpin.
SQ SEQUENCE 404 AA; 5225D331FBCFA0F7 CRC64;

Query Match 97.1%; Score 34; DB 2; Length 404;
Best Local Similarity 85.7%; Pred. No. 42;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSRLY 7
|:|||||
Db 115 KISRLY 121

RESULT 2
ID Q6IQV2 BRARE PRELIMINARY; PRT; 405 AA.
AC Q6IQV2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Hsp47 protein.
GN Name=hsp47;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_taxid=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler N.K.,
RA Altschul S.F., Collins B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the serpin family.
DE EMBL; BC071301; AAH71301.1; -; mRNA.
DR ZFIN; ZDB-GENE-990415-93; hsp47.
DR GO; GO:0004867; P:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR000886; ER_target_S.
DR InterPro; IPR000215; Prot_inh_serpin.
DR Pfam; PF00079; Serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
DR PROSITE; PS00284; SERPIN; 1.
KW Serpin.
SQ SEQUENCE 405 AA; 45593 MW; 0083BE0AC435184B CRC64;
Query Match 97.1%; Score 34; DB 2; Length 405;
Best Local Similarity 85.7%; Pred. No. 42;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVSNNLY 7
DB 116 KISNNLY 122
RESULT 3
QSDW60_ONCMY QSDW60_ONCMY PRELIMINARY; PRT; 406 AA.
ID QSDW60;
AC QSDW60;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Heat shock protein 47.
GN Name=HSP47;
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_taxid=8022;
RN [1]

RP NUCLEOTIDE SEQUENCE.
RX PubMed=15721272; DOI=10.1016/j.bbrc.2005.01.097;
RA Ojima N., Yamashita M., Watabe S.;
RT "Quantitative mRNA expression profiling of heat-shock protein families
in rainbow trout cells.";
RL Biochem. Biophys. Res. Commun. 329:51-57 (2005).
CC -1- SIMILARITY: Belongs to the serpin family.
DR EMBL; AB196463; FAD90029.1; -; mRNA.
DR GO; GO:0004867; P:serine-type endopeptidase inhibitor activity; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IRA.
DR InterPro; IPR000886; ER_target_S.
DR InterPro; IPR000215; Prot_inh_serpin.
DR Pfam; PF00079; Serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
DR PROSITE; PS00284; SERPIN; 1.
KW Heat shock; Serpin.
SQ SEQUENCE 406 AA; 45451 MW; 897A18B5B427877C CRC64;
Query Match 97.1%; Score 34; DB 2; Length 406;
Best Local Similarity 85.7%; Pred. No. 42;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVSNNLY 7
DB 117 KISNNLY 123
RESULT 4
G6PD1_ARATH G6PD1_ARATH STANDARD; PRT; 576 AA.
ID G6PD1_ARATH
AC Q43727; O65577; Q9FFM5;
DT 15-DEC-1998 (Rel. 37, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Glucose-6-phosphate 1-dehydrogenase 1, chloroplast precursor
(EC 1.1.1.49) (G6PD1) (G6PDH1).
GN Name=APG1; OrderedLocusNames=At5g35790; ORFNames=MIK22.2, MWP19.3;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=9364543; PubMed=10437832; DOI=10.1023/A:1006257230779;
RA Wendt U.K., Hauschild R., Lange C., Pietersma M., Wenderoth I.,
RA von Schaewen A.;
RT "Evidence for functional convergence of redox regulation in G6PDH
isoforms of cyanobacteria and higher plants.";
RL Plant Mol. Biol. 40:487-494 (1999).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=cv. Columbia;
RX MEDLINE=97471969; PubMed=9330910;
RA Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,
RA Miyajima N., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence
features of the 1.6 Mb regions covered by twenty physically assigned
P1 clones.";
RL DNA Res. 4:215-230 (1997).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=cv. Columbia;
RX MEDLINE=22954850; PubMed=14593172; DOI=10.1126/science.1088305;
RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J., Yu G.,
RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
RA Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
Chen M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,
Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,

RA Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,
 RA Khan S., Koesena E., Ishida J., Jiang P.X., Jones T., Kawai J.,
 RA Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
 RA Satou M., Tame R., Vayaberg M., Wallender E.K., Wong C., Yamamura Y.,
 RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Becker J.R.;
 RT "Empirical analysis of transcriptional activity in the Arabidopsis
 genome.";
 RL Science 302:842-846(2003).
 RN [4]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RP Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
 RA Fink A., Greppin H., Tacchini P.;
 RT "Nucleotide sequence of a cDNA encoding the glucose-6-phosphate
 RT dehydrogenase from Arabidopsis thaliana.";
 RL (er) Plant Gene Register FGR95-021.
 CC -!- FUNCTION: Catalyzes the rate-limiting step of the oxidative
 CC pentose-phosphate pathway, which represents a route for the
 CC dissimilation of carbohydrates besides glycolysis. The main
 CC function of this enzyme is to provide reducing power (NADPH) and
 CC pentose phosphates for fatty acid and nucleic acid synthesis which
 CC are involved in membrane synthesis and cell division.
 CC -!- CATALYTIC ACTIVITY: D-glucose 6-phosphate + NADP(+) = D-glucono-
 CC 1,5-lactone 6-phosphate + NADPH.
 CC -!- ENZYME REGULATION: Regulated by metabolites. Posttranslationally
 CC inactivated by cysteine-mediated redox modification via the
 CC ferredoxin-thioredoxin system in the light and this avoids futile
 CC cycles with photosynthetic CO2 fixation (by similarity).
 CC -!- PATHWAY: Pentose phosphate pathway; first step.
 CC -!- SUBUNIT: Homodimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Chloroplast.
 CC -!- DEVELOPMENTAL STAGE: Increase of activity in the apex linked to
 CC the early stages of the transition from vegetative to reproductive
 CC growth.
 CC -!- MISCELLANEOUS: There are 6 glucose-6-phosphate 1-dehydrogenase
 CC genes in A.thaliana.
 CC -!- SIMILARITY: Belongs to the glucose-6-phosphate dehydrogenase
 CC family.
 CC -!- CAUTION: Ref.5 sequence differs from that shown due to a
 CC frameshift in position 65.
 CC
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 CC EMBL; AJ001359; CAA04696.1; -; mRNA.
 CC EMBL; AB005236; BAB09918.1; -; Genomic_DNA.
 CC EMBL; AY099561; AM20413.1; -; mRNA.
 CC EMBL; BT002133; AAN72144.1; -; mRNA.
 CC EMBL; AY086213; AAM64291.1; -; mRNA.
 CC EMBL; X84230; CAA59012.1; ALT_FRAME; mRNA.
 CC HSSP; P11413; 1OKI.
 CC InterPro; IPR001282; G6PD.
 CC PANTHER; PTHR10097; G6PD; 1.
 CC Pfam; PF02781; G6PD_C; 1.
 CC Pfam; PF00479; G6PD_N; 1.
 CC PRINTS; PIRSF000110; G6PD; 1.
 CC PRODOM; PD001129; G6PD; 1.
 CC TIGRFAMs; TIGR00871; zwf; 1.
 CC PROSITE; PS00069; G6P_DEHYDROGENASE; 1.
 CC Carbohydrate metabolism; Chloroplast; Glucose metabolism;
 CC KW Multi-subunit family; NADP; Oxidoreductase; Transit peptide.
 CC TRANSIT 1 50
 CC CHAIN 51 576 Glucose-6-phosphate 1-dehydrogenase 1.

FT ACT_SITE 326 Proton acceptor (By similarity).
 FT BINDING 99 NADP (By similarity).
 FT BINDING 131 NADP (By similarity).
 FT BINDING 284 Substrate; phosphate group (By
 FT BINDING 268 similarity).
 FT BINDING 268 Substrate; phosphate group (By
 FT similarity).
 FT DISULFID 149 Redox modulation (By similarity).
 FT CONFLICT 110 A -> D (in Ref. 5).
 FT CONFLICT 205 IPPNIFVDV -> STPKLLVDE (in Ref. 1).
 FT CONFLICT 297 Q -> E (in Ref. 5).
 FT CONFLICT 383 G -> A (in Ref. 5).
 FT CONFLICT 485 RS -> PR (in Ref. 1).
 FT CONFLICT 514 G -> A (in Ref. 1).
 FT CONFLICT 530 D -> E (in Ref. 1).
 FT CONFLICT 539 L -> R (in Ref. 1).
 SQ SEQUENCE 576 AA; 65428 MW; 6559FFCCF76F44DF CRC64;
 Query Match 97.1%; Score 34; DB 1; Length 576;
 Best Local Similarity 85.7%; Pred. No. 61;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVSNNLY 7
 Db 195 KISNNLY 201
 RESULT 5
 Q8KKD3 HELPY
 ID Q8KKD3 HELPY PRELIMINARY; PRT; 355 AA.
 AC Q8KKD3;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein orf58.
 GN Name=orf58;
 OS Helicobacter pylori (Campylobacter pylori).
 OG Plasmid pHel5.
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
 OC Helicobacteraceae; Helicobacter.
 ON NCBI_TaxID=210;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21972792; PubMed=11976306;
 RX DOI=10.1128/JB.184.10.2755-2766.2002;
 RA Hofreuter D., Haas R.;
 RT "Characterization of two cryptic Helicobacter pylori plasmids: a
 RT putative source for horizontal gene transfer and gene shuffling.";
 RL J. Bacteriol. 184:2755-2766(2002).
 DR EMBL; AF469113; AAM22664.1; -; Genomic_DNA.
 KW Hypothetical protein; Plasmid.
 SQ SEQUENCE 355 AA; 41561 MW; C9090A779A04693F CRC64;
 Query Match 91.4%; Score 32; DB 2; Length 355;
 Best Local Similarity 85.7%; Pred. No. 1.1e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVSNNLY 7
 Db 345 KLSNNLY 351
 RESULT 6
 Q6BSM3 DEBHA
 ID Q6BSM3 DEBHA PRELIMINARY; PRT; 614 AA.
 AC Q6BSM3;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Similar to CA3237[CaSPB4 Candida albicans CaSPB4.
 GN OrderedLocusNames=DEHA008470g;
 OS Debaryomyces hansenii (Yeast) (Torulaspora hansenii).
 OS Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Debaryomycetes.
 OX NCBI_TaxID=4959;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=ATCC 36239 / CBS 767; DOI=10.1038/nature02579;
 RX PubMed=1529592; DOI=10.1038/nature02579;
 RA DuJon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marck C., Neveglise C., Talia E.,
 RA Goffard N., Franchuel L., Aigle M., Anthouard V., Babour A., Barbe V.,
 RA Barnay S., Blanchin S., Beckerich J.-M., Beyne M., Bleykasten C.,
 RA Besrane A., Boyer J., Cattolico L., Confanioli E., de Daruvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hertray F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Nicola J.-M., Nikolski M., Ozas S., Ozier-Kalogeropoulos O.,
 RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
 RA Swennen D., Tekala F., Weslowski-Louvel M., Westhof E., Wirth B.,
 RA Zenlou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
 RA Wincker P., Souciet J.-L.;
 RT "Genome evolution in yeasts.";
 RL Nature 430:35-44(2004).
 CC -1- SIMILARITY: Belongs to the DEAD box helicase family.
 DR EMBL; CR382136; CAG86941.1; -; Genomic_DNA.
 DR GO; GO:000524; F:ATP binding; IEA.
 DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
 DR GO; GO:0016787; F:hydrolyase activity; IEA.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR InterPro; IPR001410; DEAD.
 DR InterPro; IPR011545; DEAD/DEAH_N.
 DR InterPro; IPR000629; DEAD box.
 DR InterPro; IPR001650; Helicase_C.
 DR Pfam; PF00270; DEAD; 1.
 DR Pfam; PF00271; Helicase_C; 1.
 DR SMART; SM00487; DEXDC; 1.
 DR SMART; SM00490; HELIC; 1.
 DR PROSITE; PS00039; DEAD ATP HELICASE; 1.
 KW ATP-binding; Complete proteome; Helicase; Hydrolase;
 KW Nucleotide-binding; RNA-binding.
 SQ SEQUENCE 614 AA; 70369 MW; 9AB5F7CC840C5D1B CRC64;
 Query Match 91.4%; Score 32; DB 2; Length 614;
 Best Local Similarity 85.7%; Pred. No. 1.9e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVSRLY 7
 DB 71 KLSRLY 77
 RESULT 7
 Q4PFH3 USTMA PRELIMINARY; PRT; 1220 AA.
 ID Q4PFH3 USTMA PRELIMINARY; PRT; 1220 AA.
 AC Q4PFH3;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DE Hypothetical protein.
 GN ORFNames=U001140.1;
 OS Ustilago maydis 521.
 OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
 OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
 OX NCBI_TaxID=237631;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=521;
 RA Birren B., Nussbaum C., Abebe A., Abouelheil A., Adekoya E.,
 RA Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
 RA Arachchi H., Armbruster J., Bachstang P., Baldwin J., Barry A.,
 RA Bayul T., Biletskevych B., Bloom T., Blye J., Boguslavskiy L.,
 RA Borowsky M., Bouthgater B., Brunache A., Butler J., Calixte N.,
 RA Calvo S., Camarata J., Campo K., Chang J., Cheehatsang Y., Citroen M.,
 RA Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,

RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
 RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
 RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
 RA Fitzgerald M., Foley K., Gage D., Galaan J., Gearin G., Gnarre S.,
 RA Girke A., Coyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
 RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
 RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
 RA Jaffe D., Jones C., Kamal M., Kamat A., Kamvasselis M., Karlsson E.,
 RA Kells C., Kieu A., Kisner P., Kodira C., Kulbokas E., Labutti K.,
 RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
 RA Lindblad-toh K., Liu X., Lokviteang T., Lokviteang Y., Lucien O.,
 RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
 RA Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,
 RA McCarthy M., McDonough S., Mcghee T., Meldrim J., Meneus L.,
 RA Mesirov J., Mihalev A., Mihova T., Mikkelson T., Menga V., Moru K.,
 RA Mozes J., Mulrain L., Munson G., Naylor J., Neves C., Nguyen C.,
 RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
 RA Norbu N., O'donnell P., Okoawo O., O'leary S., Omotosho B.,
 RA O'Neill K., Osman S., Parker S., Perrin D., Phunkhang P., Piquani B.,
 RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
 RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
 RA Rutman M., Schupbach R., Seaman C., Settupalli S., Sharpe T.,
 RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,
 RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
 RA Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuanga P.,
 RA Tenzing P., Testaye S., Theodore J., Thoultsang Y., Topham K.,
 RA Towey S., Tsamla T., Tsomo N., Vallee D., Vassiliev H.,
 RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
 RA Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
 RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
 RA Zimmer A., Zody M., Lander E.;
 RT "The genome sequence of Ustilago maydis.";
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AACP0100040; EAK81699.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 1220 AA; 130516 MW; 588850F6ACA5C65C CRC64;
 Query Match 91.4%; Score 32; DB 2; Length 1220;
 Best Local Similarity 85.7%; Pred. No. 3.8e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVSRLY 7
 DB 1082 KLSRLY 1088
 RESULT 8
 HAT1 YEAST STANDARD; PRT; 374 AA.
 ID HAT1 YEAST STANDARD; PRT; 374 AA.
 AC Q12341; O6Q515;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE Histone acetyltransferase type B catalytic subunit (EC 2.3.1.48).
 GN Name=HAT1; OrderedLocusNames=YPL001W; ORFNames=LPA16W, YP8132.12;
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP NUCLEOTIDE SEQUENCE, PARTIAL PROTEIN SEQUENCE, AND CHARACTERIZATION.
 RX MEDLINE=97011141; PubMed=8958151; DOI=10.1016/S0092-8674(00)81325-2;
 RA Parthun M.R., Widom J., Gottschling D.E.;
 RT "The major cytoplasmic histone acetyltransferase in yeast: links to
 RL chromatin replication and histone metabolism.";
 RL Cell 87:85-94(1996).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=7559580; DOI=10.1074/jbc.270.42.24674;
 RA Kleff S., Andrusis E.D., Anderson C.W., Sternglanz R.;

RT "Identification of a gene encoding a yeast histone H4
RT acetyltransferase."; J. Biol. Chem. 270:24674-24677(1995).
RL [3]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=S288C / AB972;
RX MEDLINE=97313271; PubMed=9169875;
RA Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Anseorge W.,
RA Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V., Cherry J.M.,
RA Botstein D., Bowman S., Bruckner M., Carpenter J., Davis R.W.,
RA Chung E., Churcher C.M., Coster F., Davis K., Davis R.W.,
RA Dietrich F.S., Delius H., DiPaolo T., Dubois E., Duesterhoeft A.,
RA Duncan M., Floeth M., Fortin N., Friesen J.D., Fritz C., Goffeau A.,
RA Hall J., Hebling U., Heumann K., Hilbert H., Hillier L.W.,
RA Hunnicke-Smith S., Hyman R.W., Johnston M., Kaiman S., Kleine K.,
RA Komp C., Kurdi O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J.,
RA Marathe R., Messenguy F., Mewes H.-W., Mirtipati S., Moestl D.,
RA Mueller-Auer S., Namath A., Nentwich U., Oefner P., Pearson D.,
RA Petel F.X., Pohl T.M., Purnelle B., Rajandream M.A., Rehmann S.,
RA Rieger M., Riles L., Roberts D., Schaefer M., Scharfe M., Scherens B.,
RA Schramm S., Schroeder M., Sidcu A.-M., Tettelin H., Urrestarazu L.A.,
RA Ushinsky S., Vierendeels F., Viessers S., Voss H., Walsh S.V.,
RA Wambutt R., Wang Y., Wedler E., Wedler H., Winnett E., Zhong W.-W.,
RA Zollner A., Vo D.H., Hani J.;
RT "The nucleotide sequence of *Saccharomyces cerevisiae* chromosome XVI";
RL Nature 387:103-105(1997).
RN [4]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX STRAIN=S288C;
RA Marsischky G., Rolfs A., Richardson A., Kane M., Baqui M., Taycher E.,
RA Hu Y., Vannberg F., Weger J., Kramer J., Moreira D., Kelley P.,
RA Zuo D., Raphael J., Hogle C., Jepson D., Williamson J., Camargo A.,
RA Gonzaga L., Vasconcelos A.T., Simpson A., Kolodner R., Harlow E.,
RA LaBaer J.;
RT "Creation of the YLEX clone resource: cloning of *Saccharomyces*
RT *cerevisiae* ORFs in the Gateway recombinational cloning system.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
RN [5]
RX X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 1-320.
RP MEDLINE=9839469; PubMed=9727486; DOI=10.1016/S0092-8674(00)81584-6;
RA Duttall R.N., Tafrov S.T., Sternglanz R., Ramakrishnan V.;
RT "Structure of the histone acetyltransferase Hat1: a paradigm for the
RT GCNS-related N-acetyltransferase superfamily.";
RL Cell 94:427-438(1998).
CC -1- FUNCTION: Acetylates the lysine at residue 12 of free histone H4
CC but does not modify histone H4 when packaged in chromatin. Hat1
CC has intrinsic substrate specificity that modifies lysine in
CC recognition sequence GXGKG.
CC -1- CATALYTIC ACTIVITY: Acetyl-CoA + histone = CoA + acetylhistone.
CC -1- SUBUNIT: Oligomer (>200 kDa) of Hat1 and Hat2 subunits.
CC -1- INTERACTION: P39984:HAT2; NDEXP=1; INACT=EBI-8176, EBI-8185;
CC P39861:INL230C; NDEXP=1; INACT=EBI-8176, EBI-20191;
CC -1- SUBCELLULAR LOCATION: Cytoplasmic, also detected in nuclear
CC extracts.
CC -1- SIMILARITY: To *S.pombe* SPAC139.06.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; Z48493; CAA8385.1; -; Genomic DNA.
CC EMBL; Z71255; CAA95040.1; -; Genomic DNA.
CC EMBL; U33335; AAB68104.1; -; Genomic DNA.
CC EMBL; AY558042; AAS56368.1; -; Genomic DNA.
CC PIR; A57583; A57583.
CC PDB; 1BOB; X-ray; 0=1-320.
CC IntAct; Q12341; -.
CC GeneOnline; 143983; -.
CC Ensembl; YPL001W; *Saccharomyces cerevisiae*.
CC SGD; S00005922; HAT1.

DR GO; GO:0005737; C:cytoplasm; IDA.
DR GO; GO:000123; C:histone acetyltransferase complex; IPI.
DR GO; GO:0005634; C:nucleus; IDA.
DR GO; GO:0004406; F:H3/H4 histone acetyltransferase activity; IMP.
DR GO; GO:0006348; P:chromatin silencing at telomere; IMP.
DR GO; GO:0016573; P:histone acetylation; IDA.
KW 3D-structure; Acetyltransferase; Complete proteome;
KW Direct protein sequencing; Nuclear protein; Transferase.
FT COMPIAS 314 317 Poly-Leu.
FT CONFLICT 87 87 L -> V (in Ref. 4).
FT HELIX 8 10
FT STRAND 12 14
FT HELIX 15 18
FT STRAND 19 24
FT STRAND 28 31
FT HELIX 37 40
FT TURN 41 44
FT STRAND 45 47
FT STRAND 49 50
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FT STRAND 65 70
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FT TURN 78 79
FT HELIX 83 88
FT TURN 89 90
FT TURN 93 94
FT STRAND 97 98
FT HELIX 101 114
FT TURN 117 120
FT STRAND 122 129
FT TURN 130 131
FT STRAND 132 139
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FT HELIX 259 275
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FT HELIX 278 281
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FT TURN 285 286
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FT HELIX 304 317
FT TURN 318 318
SQ SEQUENCE 374 AA; 43873 MW; 8DECA134274413E6 CRC64;

Query Match 88.6%; Score 31; DB 1; Length 374;
Best Local Similarity 85.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVSRLY 7
Db 326 KVKRLY 332

RESULT 9
Q9AWB2_SOYBN
ID Q9AWB2_SOYBN PRELIMINARY; PRT; 573 AA.
AC Q9AWB2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)

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DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ferredoxin:sulfite reductase precursor (Fragment).
GN Name=sir;
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
OC Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Keaton M.A., Cannon G.C., Heinhorst S.;
RT "cDNA sequence for soybean ferredoxin:sulfite reductase.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY017473; AAG59996.1; -; mRNA.
DR HSSP; P17846; 4AOP.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006066; Nir_Si.
DR InterPro; IPR006067; Nir_Sir_4Fe4S.
DR InterPro; IPR005117; Nir_Sir_beta_fer.
DR InterPro; IPR011787; Sir.
DR Pfam; PF01077; NIR_SIR; 1.
DR Pfam; PF03460; NIR_SIR_ferr; 2.
DR PRINTS; PR00397; SIROHAM.
DR TIGRFAMs; TIGR02042; sir; 1.
DR PROSITE; PS00365; NIR_SIR; 1.
KW Signal.
FT SIGNAL.
FT CHAIN.
FT NON_TER.
SQ SEQUENCE 573 AA; 63821 MW; FD02A907B746B2D9 CRC64;

Query Match      88.6%; Score 31; DB 2; Length 573;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSNNRLY 7
Db 135 KVSNNQLY 141

RESULT 10
ID Q75NZO_PEA PRELIMINARY; PRT; 685 AA.
AC Q75NZO.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Sulfite reductase precursor.
GN Name=sir;
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sekine K., Sato N.;
RT "Cloning of pea sulfite reductase.";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB168112; BAB12837.1; -; mRNA.
DR HSSP; P17846; 1AOP.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006066; Nir_Si.
DR InterPro; IPR006067; Nir_Sir_4Fe4S.
DR InterPro; IPR005117; Nir_Sir_beta_fer.
DR InterPro; IPR011787; Sir.
DR Pfam; PF01077; NIR_SIR; 2.
DR Pfam; PF03460; NIR_SIR_ferr; 2.
DR PRINTS; PR00397; SIROHAM.
DR TIGRFAMs; TIGR02042; sir; 1.
DR PROSITE; PS00365; NIR_SIR; 1.
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KW Transit peptide.
FT TRANSIT 1 51 Potential.
FT CHAIN 52 685 sulfite reductase.
SQ SEQUENCE 685 AA; 76839 MW; 170660B32867D40 CRC64;

Query Match      88.6%; Score 31; DB 2; Length 685;
Best Local Similarity 85.7%; Pred. No. 3.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSNNRLY 7
Db 133 KVSNNQLY 139

RESULT 11
CXH48 ASPSC
ID CXH48 ASPSC STANDARD; PRT; 64 AA.
AC P19004;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Cytotoxin homolog S4C8.
OS Aspidelaps scutatus (Shield-nose snake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophiinae; Aspidelaps.
OX NCBI_TaxID=8607;
RN [1]
RP PROTEIN SEQUENCE, AND LETHAL DOSE.
RC TISSUE=venom;
RX MEDLINE=88185648; PubMed=3356299; DOI=10.1016/0020-711X(88)90361-8;
RA Joubert F.J.;
RT "Snake venom toxins -- II. The primary structures of cytotoxin
RT homologues S9C2 and S4C8 from Aspidelaps scutatus (shield or shield-
RT nose snake) venom.";
RL Int. J. Biochem. 20:337-345(1988).
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -|- TOXIC DOSE: LD(50) is 9.4 mg/kg by intravenous injection.
CC -|- SIMILARITY: Belongs to the snake toxin family. Orphan group XIII
CC subfamily.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; J50299; J50299.
CC HSSP; P07525; 1CHV.
CC InterPro; IPR003572; Cytotoxin.
CC Pfam; PF00087; Toxin_1_1.
CC PRINTS; PR00282; CYTOTOXIN.
CC ProDom; PD000206; Snake_toxin; 1.
CC PROSITE; PS00272; SNAKE_TOXIN; 1.
KW Cardiotoxin; Direct protein sequencing; Multigene family; Toxin.
FT DISULFID 3 22 By similarity.
FT DISULFID 15 40 By similarity.
FT DISULFID 44 55 By similarity.
FT DISULFID 56 62 By similarity.
SQ SEQUENCE 64 AA; 7317 MW; 2AC8FEE8B6BEE092 CRC64;

Query Match      85.7%; Score 30; DB 1; Length 64;
Best Local Similarity 71.4%; Pred. No. 52;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSNNRLY 7
Db 24 KVSNNRMV 30

RESULT 12
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QY      1 KVSNNRLY 7
      | : |||||
      92 KIQNNRLY 98

Db

RESULT 13
Q747U3 GEOSL
ID Q747U3_GEOSL PRELIMINARY; PRT; 161 AA.
AC Q747U3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=GSU3172;
OS Geobacter sulfurreducens.
OC Bacteria; Proteobacteria;
OC Geobacteraceae; Geobacter.
OX NCBI_TaxID=35554;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PCA / ATCC 51573;
RX PubMed=14671304; DOI=10.1126/science.1088727;
RA Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,
RA Heidelberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J.,
RA Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
RA Gattung M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
RA Davidesen T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,
RA Weidman J.P., Khouri H.M., Feldblyum T.V., Utterback T.R.,
RA Van Aken S.E., Lovley D.R., Fraser C.M.;
RT "Genome of Geobacter sulfurreducens: metal reduction in subsurface
RT environments."
RL Science 302:1967-1969(2003) .
DR EMBL: AE017180; AAR36563.1; -; Genomic DNA.

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100

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CC use as long as its content is in no way modified and this statement is not
CC removed.

CC EMBL; M65289; AAA22480.1; -; Genomic_DNA.
DR PIR; PQ0299; PQ0299.
DR InterPro; IPR001450; 4Fe4S_Fe_S_bd.
DR InterPro; IPR011989; ARM-like.
DR InterPro; IPR004155; PBS_lyase_HEAT.
DR Pfam; PF00037; Fer4; 1.
DR Pfam; PF03130; HEAT_PBS; 2.
DR PROSITE; PS00198; 4Fe4S_FERREDOXIN; 1.
KW 4Fe-4S; Hypothetical protein; Iron; Iron-sulfur; Metal-binding.
FT METAL 27 27 Iron-sulfur 1 (4Fe-4S) (Potential).
FT METAL 30 30 Iron-sulfur 1 (4Fe-4S) (Potential).
FT METAL 33 33 Iron-sulfur 1 (4Fe-4S) (Potential).
FT METAL 37 37 Iron-sulfur 2 (Potential).
FT METAL 79 79 Iron-sulfur 2 (Potential).
FT METAL 82 82 Iron-sulfur 2 (Potential).
FT METAL 86 86 Iron-sulfur 1 (4Fe-4S) (Potential).
FT NON_TER 1
SQ SEQUENCE 216 AA; 24210 MW; 0A95D704B2CA0695 CRC64;

Query Match 85.7%; Score 30; DB 1; Length 216;
Best Local Similarity 71.4%; Pred.No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVSRLY 7
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Db 71 KIGNRLY 77

Search completed: December 30, 2005, 13:33:23
Job time : 66 secs

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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:14:26 ; Search time 15.6935 Seconds
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Title: US-10-735-916A-4
Perfect score: 35
Sequence: 1 KVSNNLY 7

Scoring table: BLOSUM62
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Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	88.6	113	2	US-09-232-290-20
2	31	88.6	687	2	US-09-720-524-4
3	31	88.6	687	2	US-10-757-114-4
4	30	85.7	323	2	US-09-328-352-5170
5	30	85.7	365	2	US-09-230-586A-25
6	30	85.7	388	2	US-09-134-001C-3820
7	30	85.7	463	1	US-08-426-428-2
8	30	85.7	463	2	US-08-871-314-2
9	30	85.7	463	2	US-09-886-319A-73
10	30	85.7	463	2	US-09-919-039-154
11	30	85.7	463	2	US-09-949-016-6132
12	30	85.7	474	2	US-09-949-016-7306
13	30	85.7	3025	6	5223423-3
14	29	82.9	267	1	US-08-667-809B-2
15	29	82.9	274	1	US-08-307-499-27
16	29	82.9	274	2	US-09-239-268-27
17	29	82.9	375	1	US-08-121-714-8
18	29	82.9	375	1	US-08-477-108A-8
19	29	82.9	375	1	US-08-477-112-8
20	29	82.9	375	4	PCT-US93-08322-8
21	29	82.9	378	2	US-09-543-681A-4604
22	29	82.9	379	1	US-08-121-714-4
23	29	82.9	379	1	US-08-477-108A-4
24	29	82.9	379	1	US-08-477-112-4
25	29	82.9	379	2	US-10-094-944-9
26	29	82.9	379	4	PCT-US93-08322-4
27	29	82.9	540	2	US-09-248-796A-15935

28	28	80.0	56	2	US-09-513-999C-6825	Sequence 6825, Ap
29	28	80.0	100	2	US-09-840-459-26	Sequence 26, Appl
30	28	80.0	100	2	US-09-497-625A-26	Sequence 26, Appl
31	28	80.0	343	2	US-09-489-039A-10330	Sequence 10330, A
32	28	80.0	352	2	US-09-816-028A-21	Sequence 21, Appl
33	28	80.0	352	2	US-10-303-162-21	Sequence 21, Appl
34	28	80.0	352	2	US-10-303-134-21	Sequence 21, Appl
35	28	80.0	352	2	US-10-303-118-21	Sequence 21, Appl
36	28	80.0	352	2	US-10-303-128-21	Sequence 21, Appl
37	28	80.0	395	2	US-09-252-991A-30497	Sequence 30497, A
38	28	80.0	443	2	US-09-248-796A-19547	Sequence 19547, A
39	28	80.0	496	2	US-09-248-796A-18957	Sequence 18957, A
40	28	80.0	621	2	US-09-059-522-1	Sequence 1, Appl
41	28	80.0	621	2	US-09-382-027-1	Sequence 1, Appl
42	28	80.0	658	2	US-09-248-796A-17674	Sequence 17674, A
43	28	80.0	1287	2	US-09-252-991A-29606	Sequence 29606, A
44	27	77.1	138	2	US-09-489-039A-9722	Sequence 9722, Ap
45	27	77.1	166	2	US-08-916-576B-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-09-232-290-20
; Sequence 20, Application US/09232290A
; Patent No. 6815540
; GENERAL INFORMATION:
; APPLICANT: PLUCKTHUN, ANDREAS
; APPLICANT: NIEBA, LARS
; APPLICANT: HONEGGER, ANNEMARIE
; TITLE OF INVENTION: IMMUNOGLOBULIN SUPER FAMILY DOMAINS AND FRAGMENTS WITH
; FILE REFERENCE: MORPHO/7
; CURRENT APPLICATION NUMBER: US/09/232,290A
; CURRENT FILING DATE: 1999-01-15
; EARLIER APPLICATION NUMBER: PCT/EP96/02230
; EARLIER FILING DATE: 1996-05-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Murine
US-09-232-290-20

Query Match 88.6%; Score 31; DB 2; Length 113;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVSNNLY 7
Db 55 KVSNNRY 61

RESULT 2
US-09-720-524-4
; Sequence 4, Application US/09720524
; Patent No. 6720172
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Genes Encoding Sulfate Assimilation Proteins
; FILE REFERENCE: BB-1167-D
; CURRENT APPLICATION NUMBER: US/09/720,524
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/092,833
; PRIOR FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 4
; LENGTH: 687
; TYPE: PRT
; ORGANISM: Glycine max

US-09-720-524-4

Query Match 88.6%; Score 31; DB 2; Length 687;
Best Local Similarity 85.7%; Pred. No. 97;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNNLY 7
|:|:|:|
Db 135 KVSNNLY 141

RESULT 3

US-10-757-114-4
; Sequence 4, Application US/10757114
; Patent No. 6939710

; GENERAL INFORMATION:

; APPLICANT: E. I. du Pont de Nemours and Company

; TITLE OF INVENTION: Genes Encoding Sulfate Assimilation Proteins

; FILE REFERENCE: BB-1167-D

; CURRENT APPLICATION NUMBER: US/10/757,114

; CURRENT FILING DATE: 2004-01-14

; PRIOR APPLICATION NUMBER: US/09/720,524

; PRIOR FILING DATE: 2001-05-10

; PRIOR APPLICATION NUMBER: 60/092,833

; PRIOR FILING DATE: 1998-07-14

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 4

; LENGTH: 687

; TYPE: PRT

; ORGANISM: Glycine max

US-10-757-114-4

Query Match 88.6%; Score 31; DB 2; Length 687;
Best Local Similarity 85.7%; Pred. No. 97;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNNLY 7
|:|:|:|
Db 135 KVSNNLY 141

RESULT 4

US-09-328-352-5170

; Sequence 5170, Application US/09328352

; Patent No. 6562958

; GENERAL INFORMATION:

; APPLICANT: Gary L. Breton et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

; FILE REFERENCE: GTC99-03PA

; CURRENT APPLICATION NUMBER: US/09/328,352

; CURRENT FILING DATE: 1999-06-04

; NUMBER OF SEQ ID NOS: 8252

; SEQ ID NO 5170

; LENGTH: 323

; TYPE: PRT

; ORGANISM: Acinetobacter baumannii

US-09-328-352-5170

Query Match 85.7%; Score 30; DB 2; Length 323;
Best Local Similarity 71.4%; Pred. No. 75;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNNLY 7
|:|:|:|
Db 241 KVSNNLY 247

RESULT 5

US-09-290-586A-25

; Sequence 25, Application US/09290586A

; Patent No. 6800473

; GENERAL INFORMATION:

; APPLICANT: SANTAMARIA, Ignacio

; APPLICANT: VELASCO, Gloria

; APPLICANT: CAZORLA, Maite

; APPLICANT: FUEYO, Antonio

; APPLICANT: CAMPO, Elias

; APPLICANT: LOPEZ-OTIN, Carlos

; APPLICANT: AOKI, Takanori

; APPLICANT: IWATA, Kazushi

; TITLE OF INVENTION: NOVEL HUMAN CATHEPSIN L2 PROTEIN, GENE ENCODING SAID

; FILE REFERENCE: 99-410A/WMC/01332

; CURRENT APPLICATION NUMBER: US/09/290,586A

; CURRENT FILING DATE: 1999-04-13

; PRIOR APPLICATION NUMBER: JP 10-172147

; PRIOR FILING DATE: 1998-06-05

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 25

; LENGTH: 365

; TYPE: PRT

; ORGANISM: Human

US-09-290-586A-25

Query Match 85.7%; Score 30; DB 2; Length 365;
Best Local Similarity 85.7%; Pred. No. 85;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVSNNLY 7
|:|:|:|
Db 65 KVSNNLY 71

RESULT 6

US-09-134-001C-3820

; Sequence 3820, Application US/09134001C

; Patent No. 6380370

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

; FILE REFERENCE: GTC-007

; CURRENT APPLICATION NUMBER: US/09/134,001C

; CURRENT FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/064,964

; PRIOR FILING DATE: 1997-11-08

; PRIOR APPLICATION NUMBER: US 60/055,779

; PRIOR FILING DATE: 1997-08-14

; NUMBER OF SEQ ID NOS: 5674

; SEQ ID NO 3820

; LENGTH: 388

; TYPE: PRT

; ORGANISM: Staphylococcus epidermidis

US-09-134-001C-3820

Query Match 85.7%; Score 30; DB 2; Length 388;
Best Local Similarity 71.4%; Pred. No. 91;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVSNNLY 7
|:|:|:|
Db 243 KVSNNLY 249

RESULT 7

US-08-426-428-2

; Sequence 2, Application US/08426428

; Patent No. 5637462

; GENERAL INFORMATION:

; APPLICANT: Coleman, Roger

; APPLICANT: Braxton, Scott M.

; APPLICANT: Seilhamer, Jeffrey J.

; TITLE OF INVENTION: NEW CATHEPSIN C HOMOLOG

```
;
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3330 Hillview Avenue
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/426,428
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J.
; REGISTRATION NUMBER: 33954
; REFERENCE/DOCKET NUMBER: PF-0032 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 463 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-426-428-2
;
; Query Match 85.7%; Score 30; DB 1; Length 463;
; Best Local Similarity 85.7%; Pred. No. 1.1e+02;
; Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 1 KYSNRLY 7
; DB 162 KYSNRLY 168
;
; RESULT 8
; US-08-871-314-2
; Sequence 2, Application US/08871314
; Patent No. 6068488
; GENERAL INFORMATION:
; APPLICANT: Coleman, Roger
; APPLICANT: Braxton, Scott M.
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: NEW CATHEPSIN C HOMOLOG
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3330 Hillview Avenue
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/871,314
; FILING DATE: 6/9/1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/426,428
; FILING DATE: 04/19/1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J.
; REGISTRATION NUMBER: 33954
;
; REFERENCE/DOCKET NUMBER: PF-0032 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 463 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-871-314-2
;
; Query Match 85.7%; Score 30; DB 2; Length 463;
; Best Local Similarity 85.7%; Pred. No. 1.1e+02;
; Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 1 KYSNRLY 7
; DB 162 KYSNRLY 168
;
; RESULT 9
; US-09-886-319A-73
; Sequence 73, Application US/09886319A
; Patent No. 6586185
; GENERAL INFORMATION:
; APPLICANT: Wolf, Eckard
; APPLICANT: Werner, Sabine
; APPLICANT: Hallie, Jorn-Peter
; APPLICANT: Regenbogen, Johannes
; APPLICANT: Goppelt, Andreas
; TITLE OF INVENTION: Use of Polypeptides or Nucleic Acids for
; TITLE OF INVENTION: the Diagnosis or Treatment of Skin Disorders and Wound
; TITLE OF INVENTION: Healing and for the Identification of Pharmacologically
; TITLE OF INVENTION: Active Substances
; FILE REFERENCE: 50125/014002
; CURRENT APPLICATION NUMBER: US/09/886,319A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 60/222,081
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: DE 10030149.5
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 73
; LENGTH: 463
; TYPE: PRI
; ORGANISM: Homo sapiens
; US-09-886-319A-73
;
; Query Match 85.7%; Score 30; DB 2; Length 463;
; Best Local Similarity 85.7%; Pred. No. 1.1e+02;
; Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 1 KYSNRLY 7
; DB 162 KYSNRLY 168
;
; RESULT 10
; US-09-919-039-154
; Sequence 154, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
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; SEQ ID NO 154
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6727066 014284CD1
US-09-919-039-154

Query Match      85.7%; Score 30; DB 2; Length 463;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVSNNRLY 7
Db 162 KYSNNRLY 168

RESULT 11
US-09-949-016-6132
; Sequence 6132, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6132
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6132

Query Match      85.7%; Score 30; DB 2; Length 463;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVSNNRLY 7
Db 162 KYSNNRLY 168

RESULT 12
US-09-949-016-7306
; Sequence 7306, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7306
; LENGTH: 474
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; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7306

Query Match      85.7%; Score 30; DB 2; Length 474;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVSNNRLY 7
Db 173 KYSNNRLY 179

RESULT 13
5223423-3
; Patent No. 5223423
; APPLICANT: FRANCHINI, GENOVEPPA;WONG-STAAAL, FLOSSIE;
; GALLO, ROBERT
; TITLE OF INVENTION: CHARACTERIZATION OF REPLICATION COMPETENT
; HUMAN IMMUNODEFICIENCY TYPE 2 PROVIRAL CLONE HIV-2 SBL/ISY
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/331,212
; FILING DATE: 03-31-1989
; SEQ ID NO:3
; LENGTH: 3025
5223423-3

Query Match      85.7%; Score 30; DB 6; Length 3025;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSNRLY 7
Db 2030 VSNRLY 2035

RESULT 14
US-08-667-809B-2
; Sequence 2, Application US/08667809B
; Patent No. 5986174
; GENERAL INFORMATION:
; APPLICANT: Barbour, Eric
; APPLICANT: Baszczyński, Chris
; APPLICANT: Rosichan, Jeffrey L.
; APPLICANT: Horowitz, Jeanine
; TITLE OF INVENTION: MAIZE PROMOTER SEQUENCE FOR LEAF- AND
; TITLE OF INVENTION: STALK-PREFERRED GENE EXPRESSION
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC.
; STREET: Darwin Building, 7100 N.W. 62nd Ave., P.O.
; CITY: Johnston
; STATE: Iowa
; COUNTRY: USA
; ZIP: 50131
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/667,809B
; FILING DATE: 21-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sweeney, Patricia A.
; REGISTRATION NUMBER: 32,733
; REFERENCE/DOCKET NUMBER: 0530
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (515) 248-4800
; TELEFAX: (515) 248-4844
; INFORMATION FOR SEQ ID NO: 2:
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SEQUENCE CHARACTERISTICS:
 LENGTH: 267 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-667-809B-2

Query Match 82.9%; Score 29; DB 1; Length 267;
 Best Local Similarity 71.4%; Pred. No. 1e+02; 0; Indels 0; Gaps 0;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSRLY 7
 DB 18 KISRLH 24

RESULT 15
 US-08-307-499-27
 ; Sequence 27, Application US/08307499
 ; Patent No. 5651972
 ; GENERAL INFORMATION:
 ; APPLICANT: Moyer, Richard W.
 ; APPLICANT: Vi uela, Eladio
 ; APPLICANT: Gibbs, E.P.J.
 ; TITLE OF INVENTION: Use of Recombinant Swine Poxvirus as a
 ; TITLE OF INVENTION: Live Vaccine Vector
 ; NUMBER OF SEQUENCES: 60
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: David R. Saliwanchik
 ; STREET: 2421 N.W. 41st Street, Suite A-1
 ; CITY: Gainesville
 ; STATE: Florida
 ; COUNTRY: U.S.A.
 ; ZIP: 32606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/307,499
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA: US 07/908,241
 ; FILING DATE: 1-JUL-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/908,630
 ; FILING DATE: 29-JUN-1992
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/342,212
 ; FILING DATE: 21-APR-1992
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Saliwanchik, David R.
 ; REGISTRATION NUMBER: 31,794
 ; REFERENCE/DOCKET NUMBER: UF35.1.FWCC1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 904-375-8100
 ; TELEFAX: 904-372-5800
 ; INFORMATION FOR SEQ ID NO: 27:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 274 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-307-499-27

Query Match 82.9%; Score 29; DB 1; Length 274;
 Best Local Similarity 71.4%; Pred. No. 1.1e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSRLY 7
 DB 229 RVNRLY 235

Search completed: December 30, 2005, 13:37:17
 Job time : 16.6935 secs

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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:33:42 ; Search time 52.0484 Seconds
(without alignments)
56.194 Million cell updates/sec

Title: US-10-735-916A-4

Perfect score: 35

Sequence: 1 KVSNNLY 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications_AA_Main:*
- 1: /cgn2_6/ptodata1/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata1/pubpaa/US08_PUBCOMB.pep.*
 - 3: /cgn2_6/ptodata1/pubpaa/US09_PUBCOMB.pep.*
 - 4: /cgn2_6/ptodata1/pubpaa/US10A_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata1/pubpaa/US10B_PUBCOMB.pep.*
 - 6: /cgn2_6/ptodata1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	7	5	US-10-735-916A-4
2	35	100.0	112	5	US-10-735-916A-54
3	35	100.0	112	5	US-10-735-916A-61
4	35	100.0	112	5	US-10-735-916A-65
5	35	100.0	122	5	US-10-735-916A-49
6	35	100.0	131	5	US-10-735-916A-63
7	35	100.0	131	5	US-10-735-916A-67
8	32	91.4	214	4	US-10-425-115-303579
9	31	88.6	92	4	US-10-425-115-264792
10	31	88.6	223	4	US-10-424-599-283409
11	31	88.6	687	4	US-10-424-599-283410
12	31	88.6	687	4	US-10-757-114-4
13	30	85.7	71	4	US-10-424-599-225929
14	30	85.7	176	5	US-10-739-930-6956
15	30	85.7	223	4	US-10-425-115-336315
16	30	85.7	269	4	US-10-437-963-134241
17	30	85.7	388	4	US-10-724-972A-6036
18	30	85.7	419	5	US-10-480-988-16
19	30	85.7	439	4	US-10-297-509-1
20	30	85.7	463	3	US-09-886-319A-73
21	30	85.7	463	3	US-09-974-298-66
22	30	85.7	463	3	US-09-919-039-154
23	30	85.7	463	4	US-10-204-752-29
24	30	85.7	463	4	US-10-376-564-73
25	30	85.7	463	5	US-10-287-436A-393
26	30	85.7	463	5	US-10-287-436A-1093
27	30	85.7	463	5	US-10-631-467-642

ALIGNMENTS

RESULT 1

US-10-735-916A-4
; Sequence 4, Application US/10735916A

; Publication No. US20050084906A1

; GENERAL INFORMATION:

; APPLICANT: GOETTSCH, Liliane

; APPLICANT: CORVAIA, Nathalie

; APPLICANT: LEGER, Olivier

; APPLICANT: DUFLOS, Alain

; APPLICANT: BECK, Alain

; APPLICANT: HAEUW, Jean-Francois

; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF

; FILE REFERENCE: 017753-183

; CURRENT APPLICATION NUMBER: US/10/735,916A

; CURRENT FILING DATE: 2003-12-16

; PRIOR APPLICATION NUMBER: FR 03/08 538

; PRIOR FILING DATE: 2003-07-11

; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178

; PRIOR FILING DATE: 2003-01-20

; PRIOR APPLICATION NUMBER: FR 02/00 653

; PRIOR FILING DATE: 2002-01-18

; PRIOR APPLICATION NUMBER: FR 02/00 654

; PRIOR FILING DATE: 2002-01-18

; PRIOR APPLICATION NUMBER: FR 02/05 753

; PRIOR FILING DATE: 2002-05-07

; NUMBER OF SEQ ID NOS: 156

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 4

; LENGTH: 7

; TYPE: PRT

; ORGANISM: Mus musculus

US-10-735-916A-4

Query Match 100.0%; Score 35; DB 5; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.7e+06;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSNNLY 7

Db 1 KVSNNLY 7

RESULT 2

US-10-735-916A-54

; Sequence 54, Application US/10735916A

; Publication No. US20050084906A1

; GENERAL INFORMATION:

; APPLICANT: GOETTSCH, Liliane

; APPLICANT: CORVAIA, Nathalie

; APPLICANT: LEGER, Olivier

; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10/735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 54
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-735-916A-54

Query Match 100.0%; Score 35; DB 5; Length 112;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSRLY 7
|||
Db 55 KVSRLY 61

RESULT 3
US-10-735-916A-61
; Sequence 61, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10/735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 61
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-735-916A-61

Query Match 100.0%; Score 35; DB 5; Length 112;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSRLY 7
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Db 55 KVSRLY 61

Db 55 KVSRLY 61
RESULT 4
US-10-735-916A-65
; Sequence 65, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10/735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 65
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-735-916A-65

Query Match 100.0%; Score 35; DB 5; Length 112;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSRLY 7
|||
Db 55 KVSRLY 61

RESULT 5
US-10-735-916A-49
; Sequence 49, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10/735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 49

; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178									
; PRIOR FILING DATE: 2003-01-20									
; PRIOR APPLICATION NUMBER: FR 02/00 653									
; PRIOR FILING DATE: 2002-01-18									
; PRIOR APPLICATION NUMBER: FR 02/00 654									
; PRIOR FILING DATE: 2002-01-18									
; PRIOR APPLICATION NUMBER: FR 02/05 753									
; PRIOR FILING DATE: 2002-05-07									
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; SEQ ID NO 67									
; LENGTH: 131									
; TYPE: PRT									
; ORGANISM: Homo sapiens									
US-10-735-916A-67									
Query Match 100.0%; Score 35; DB 5; Length 131;									
Best Local Similarity 100.0%; Pred. No. 14;									
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	KVSNRLY	7						
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RESULT 8									
US-10-425-115-303579									
; Sequence 303579, Application US/10425115									
; Publication No. US20040214272A1									
; GENERAL INFORMATION:									
; APPLICANT: La Rosa, Thomas J.									
; APPLICANT: Kovalic, David K.									
; APPLICANT: Zhou, Yihua									
; APPLICANT: Cao, Yongwei									
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With									
; TITLE OF INVENTION: Plants									
; FILE REFERENCE: 38-21(53222)B									
; CURRENT APPLICATION NUMBER: US/10/425,115									
; CURRENT FILING DATE: 2003-04-28									
; NUMBER OF SEQ ID NOS: 369326									
; SEQ ID NO 303579									
; LENGTH: 214									
; TYPE: PRT									
; ORGANISM: Zea mays									
; FEATURE:									
; OTHER INFORMATION: Clone ID: MRT4577_39938C.1.pcp									
US-10-425-115-303579									
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Best Local Similarity 85.7%; Pred. No. 1e+02;									
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	KVSNRLY	7						
Db	116	KVSNRLY	122						
RESULT 9									
US-10-425-115-264792									
; Sequence 264792, Application US/10425115									
; Publication No. US20040214272A1									
; GENERAL INFORMATION:									
; APPLICANT: La Rosa, Thomas J.									
; APPLICANT: Kovalic, David K.									
; APPLICANT: Zhou, Yihua									
; APPLICANT: Cao, Yongwei									
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With									
; TITLE OF INVENTION: Plants									
; FILE REFERENCE: 38-21(53222)B									
; CURRENT APPLICATION NUMBER: US/10/425,115									
; CURRENT FILING DATE: 2003-04-28									
; NUMBER OF SEQ ID NOS: 369326									
; SEQ ID NO 264792									

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; LENGTH: 92
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(92)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_17309C.1.pgp
US-10-425-115-264792

Query Match      88.6%; Score 31; DB 4; Length 92;
Best Local Similarity 71.4%; Pred. No. 68;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSRLY 7
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Db 85 KISNKL 91

RESULT 10
US-10-424-599-283409
; Sequence 283409, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 283409
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(223)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_97941C.1.pgp
US-10-424-599-283409

Query Match      88.6%; Score 31; DB 4; Length 223;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSRLY 7
   :|:|:|
Db 136 KVSQNL 142

RESULT 11
US-10-424-599-283410
; Sequence 283410, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 283410
; LENGTH: 687
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(687)
; OTHER INFORMATION: Clone ID: PAT_MRT3847_97942C.1.pgp
US-10-424-599-283410

Query Match      88.6%; Score 31; DB 4; Length 687;
Best Local Similarity 85.7%; Pred. No. 5.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSRLY 7
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Db 135 KVSQNL 141

RESULT 12
US-10-757-114-4
; Sequence 4, Application US/10757114
; Publication No. US20040137496A1
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Genes Encoding Sulfate Assimilation Proteins
; FILE REFERENCE: BB-1167-D
; CURRENT APPLICATION NUMBER: US/10/757,114
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US/09/720,524
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/092,833
; PRIOR FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 4
; LENGTH: 687
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(687)
; OTHER INFORMATION: Clone ID: PAT_MRT3847_46044C.1.pgp
US-10-757-114-4

Query Match      88.6%; Score 31; DB 4; Length 687;
Best Local Similarity 85.7%; Pred. No. 5.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSRLY 7
   :|:|:|
Db 135 KVSQNL 141

RESULT 13
US-10-424-599-225929
; Sequence 225929, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 225929
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(71)
; OTHER INFORMATION: Clone ID: PAT_MRT3847_46044C.1.pgp
US-10-424-599-225929

Query Match      85.7%; Score 30; DB 4; Length 71;
Best Local Similarity 71.4%; Pred. No. 85;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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Qy 1 KVSRLY 7
|:|:|:|
Db 32 KISRLY 38

RESULT 14

US-10-739-930-6956
; Sequence 6956, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 6956
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Brassica napus
; FEATURE:
; OTHER INFORMATION: Clone ID: BRANA-23APR03-C27607_1.p
US-10-739-930-6956

Query Match 85.7%; Score 30; DB 5; Length 176;
Best Local Similarity 71.4%; Pred. No. 2.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVSRLY 7
|:|:|:|
Db 47 KISRLY 53

RESULT 15

US-10-425-115-336315
; Sequence 336315, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 336315
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_69828C.1.p
US-10-425-115-336315

Query Match 85.7%; Score 30; DB 4; Length 223;
Best Local Similarity 85.7%; Pred. No. 2.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSRLY 7
|:|:|:|
Db 188 KISRLH 194

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Job time : 53.0484 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:35:07 ; Search time 2.59677 Seconds
(without alignments)
20.187 Million cell updates/sec

Title: US-10-735-916A-4

Perfect score: 35

Sequence: 1 KVSNNRLY 7

Scoring table: BLOSUM62

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Searched: 57103 seqs, 7488799 residues

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications_AA_New.*
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 - 2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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 - 6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
 - 7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	7	US-11-012-353-4	Sequence 4, Appli
2	35	100.0	112	US-11-012-353-54	Sequence 54, Appl
3	35	100.0	112	US-11-012-353-61	Sequence 61, Appl
4	35	100.0	112	US-11-012-353-65	Sequence 65, Appl
5	35	100.0	122	US-11-012-353-49	Sequence 49, Appl
6	35	100.0	131	US-11-012-353-63	Sequence 63, Appl
7	35	100.0	131	US-11-012-353-67	Sequence 67, Appl
8	30	85.7	488	US-10-821-234-1000	Sequence 1000, Ap
9	28	80.0	232	US-10-467-657-4338	Sequence 4338, Ap
10	27	77.1	168	US-11-108-172-631	Sequence 631, App
11	27	77.1	483	US-11-113-775A-1	Sequence 1, Appli
12	27	77.1	483	US-11-113-775A-2	Sequence 2, Appli
13	27	77.1	483	US-11-113-799-1	Sequence 1, Appli
14	27	77.1	483	US-11-113-799-2	Sequence 2, Appli
15	27	77.1	485	US-10-630-203-12	Sequence 12, Appl
16	27	77.1	485	US-11-113-775A-3	Sequence 3, Appli
17	27	77.1	485	US-11-113-799-3	Sequence 3, Appli
18	27	77.1	1032	US-11-014-367-3	Sequence 3, Appli
19	26	74.3	99	US-10-467-657-4402	Sequence 4402, Ap
20	26	74.3	425	US-11-096-276-2	Sequence 2, Appli
21	26	74.3	439	US-11-082-389-80	Sequence 80, Appl
22	26	74.3	495	US-10-510-386-188	Sequence 188, App
23	26	74.3	496	US-10-793-626-1030	Sequence 1030, Ap
24	26	74.3	513	US-10-878-556A-112	Sequence 112, App
25	26	74.3	564	US-11-082-389-78	Sequence 78, Appl

26	74.3	724	6	US-10-793-626-968	Sequence 968, App
27	71.4	45	6	US-10-957-887B-238	Sequence 238, App
28	71.4	45	6	US-10-957-887B-242	Sequence 242, App
29	71.4	211	6	US-10-467-657-2142	Sequence 2142, Ap
30	71.4	311	6	US-10-793-626-1248	Sequence 1248, Ap
31	68.6	7	6	US-10-932-334-5	Sequence 5, Appli
32	68.6	7	7	US-11-125-837-2	Sequence 2, Appli
33	68.6	7	7	US-11-125-837-14	Sequence 14, Appl
34	68.6	7	7	US-11-105-708-18	Sequence 18, Appl
35	68.6	43	6	US-10-957-887B-67	Sequence 67, Appl
36	68.6	100	6	US-10-932-334-56	Sequence 56, Appl
37	68.6	100	7	US-11-054-669-75	Sequence 75, Appl
38	68.6	100	7	US-11-084-554-107	Sequence 107, App
39	68.6	100	7	US-11-084-554-118	Sequence 118, App
40	68.6	112	6	US-10-502-145-15	Sequence 15, Appl
41	68.6	112	6	US-10-502-145-19	Sequence 19, Appl
42	68.6	112	6	US-10-502-145-23	Sequence 23, Appl
43	68.6	112	6	US-10-507-662-39	Sequence 39, Appl
44	68.6	112	7	US-11-012-353-55	Sequence 55, Appl
45	68.6	112	7	US-11-012-353-56	Sequence 56, Appl

ALIGNMENTS

RESULT 1
US-11-012-353-4
; Sequence 4, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID RECEPTORS ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 4
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-012-353-4

Query Match 100.0%; Score 35; DB 7; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.3e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNNRLY 7
| | | | |
Db 1 KVSNNRLY 7

RESULT 2
US-11-012-353-54
; Sequence 54, Application US/11012353

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; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; PRIOR FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 54
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-012-353-54

Query Match      100.0%; Score 35; DB 7; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNNRLY 7
Db 55 KVSNNRLY 61

RESULT 3
US-11-012-353-61
; Sequence 61, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; PRIOR FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 61
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-012-353-65

Query Match      100.0%; Score 35; DB 7; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNNRLY 7
Db 55 KVSNNRLY 61

RESULT 4
US-11-012-353-65
; Sequence 65, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 65
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-012-353-65

Query Match      100.0%; Score 35; DB 7; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNNRLY 7
Db 55 KVSNNRLY 61

RESULT 5
US-11-012-353-49
; Sequence 49, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; FILE REFERENCE: 017753-198
; SEQ ID NO 61
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; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-012-353-61

Query Match      100.0%; Score 35; DB 7; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNNRLY 7
Db 55 KVSNNRLY 61

RESULT 4
US-11-012-353-65
; Sequence 65, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 65
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-012-353-65

Query Match      100.0%; Score 35; DB 7; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNNRLY 7
Db 55 KVSNNRLY 61

RESULT 5
US-11-012-353-49
; Sequence 49, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; FILE REFERENCE: 017753-198
; SEQ ID NO 61
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;; CURRENT APPLICATION NUMBER: US/11/012,353
;; CURRENT FILING DATE: 2004-12-16
;; PRIOR APPLICATION NUMBER: 10/735,916
;; PRIOR FILING DATE: 2003-12-16
;; PRIOR APPLICATION NUMBER: FR 0308538
;; PRIOR FILING DATE: 2003-07-11
;; PRIOR APPLICATION NUMBER: PCT/FR03/00178
;; PRIOR FILING DATE: 2003-01-20
;; PRIOR APPLICATION NUMBER: FR 0205753
;; PRIOR FILING DATE: 2002-05-07
;; PRIOR APPLICATION NUMBER: FR 0200653
;; PRIOR FILING DATE: 2002-01-18
;; PRIOR APPLICATION NUMBER: FR 0200654
;; PRIOR FILING DATE: 2002-01-18
;; NUMBER OF SEQ ID NOS: 162
;; SOFTWARE: PatentIn Ver. 3.3
;; SEQ ID NO 49
;; LENGTH: 122
;; TYPE: PRT
;; ORGANISM: Mus musculus
US-11-012-353-49

Query Match 100.0%; Score 35; DB 7; Length 122;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSNNLY 7
|||||||
DB 65 KVSNNLY 71

RESULT 6
US-11-012-353-63
;; Sequence 63, Application US/11012353
;; Publication No. US20050249730A1
;; GENERAL INFORMATION:
;; APPLICANT: GOETTSCH, LILIANE
;; APPLICANT: CORVAIA, NATHALIE
;; APPLICANT: DUFLOS, ALAIN
;; APPLICANT: HABUW, JEAN-FRANCOIS
;; APPLICANT: LEGER, OLIVIER
;; APPLICANT: BECK, ALAIN
;; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-1 HYBRID
;; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF

;; FILE REFERENCE: 017753-198
;; CURRENT APPLICATION NUMBER: US/11/012,353
;; CURRENT FILING DATE: 2004-12-16
;; PRIOR APPLICATION NUMBER: 10/735,916
;; PRIOR FILING DATE: 2003-12-16
;; PRIOR APPLICATION NUMBER: FR 0308538
;; PRIOR FILING DATE: 2003-07-11
;; PRIOR APPLICATION NUMBER: PCT/FR03/00178
;; PRIOR FILING DATE: 2003-01-20
;; PRIOR APPLICATION NUMBER: FR 0205753
;; PRIOR FILING DATE: 2002-05-07
;; PRIOR APPLICATION NUMBER: FR 0200653
;; PRIOR FILING DATE: 2002-01-18
;; PRIOR APPLICATION NUMBER: FR 0200654
;; PRIOR FILING DATE: 2002-01-18
;; NUMBER OF SEQ ID NOS: 162
;; SOFTWARE: PatentIn Ver. 3.3
;; SEQ ID NO 63
;; LENGTH: 131
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-012-353-63

Query Match 100.0%; Score 35; DB 7; Length 131;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSNNLY 7
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DB 74 KVSNNLY 80

RESULT 7
US-11-012-353-67
;; Sequence 67, Application US/11012353
;; Publication No. US20050249730A1
;; GENERAL INFORMATION:
;; APPLICANT: GOETTSCH, LILIANE
;; APPLICANT: CORVAIA, NATHALIE
;; APPLICANT: DUFLOS, ALAIN
;; APPLICANT: HABUW, JEAN-FRANCOIS
;; APPLICANT: LEGER, OLIVIER
;; APPLICANT: BECK, ALAIN
;; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-1 HYBRID
;; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
;; FILE REFERENCE: 017753-198
;; CURRENT APPLICATION NUMBER: US/11/012,353
;; CURRENT FILING DATE: 2004-12-16
;; PRIOR APPLICATION NUMBER: 10/735,916
;; PRIOR FILING DATE: 2003-12-16
;; PRIOR APPLICATION NUMBER: FR 0308538
;; PRIOR FILING DATE: 2003-07-11
;; PRIOR APPLICATION NUMBER: PCT/FR03/00178
;; PRIOR FILING DATE: 2003-01-20
;; PRIOR APPLICATION NUMBER: FR 0205753
;; PRIOR FILING DATE: 2002-05-07
;; PRIOR APPLICATION NUMBER: FR 0200653
;; PRIOR FILING DATE: 2002-01-18
;; PRIOR APPLICATION NUMBER: FR 0200654
;; PRIOR FILING DATE: 2002-01-18
;; NUMBER OF SEQ ID NOS: 162
;; SOFTWARE: PatentIn Ver. 3.3
;; SEQ ID NO 67
;; LENGTH: 131
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-012-353-67

Query Match 100.0%; Score 35; DB 7; Length 131;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSNNLY 7
|||||||
DB 74 KVSNNLY 80

RESULT 8
US-10-821-234-1000
;; Sequence 1000, Application US/10821234
;; Publication No. US20050255114A1
;; GENERAL INFORMATION:
;; APPLICANT: Labat, Ivan
;; APPLICANT: Andarmani, Susan
;; APPLICANT: Stache-Crain, Birgit
;; APPLICANT: Tang, Y. Tom
;; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
;; FILE REFERENCE: 821A
;; CURRENT APPLICATION NUMBER: US/10/821,234
;; CURRENT FILING DATE: 2004-04-07
;; PRIOR APPLICATION NUMBER: US 60/462,047
;; PRIOR FILING DATE: 2003-04-07
;; NUMBER OF SEQ ID NOS: 1704
;; SOFTWARE: pt_seq_genes Version 1.0
;; SEQ ID NO 1000
;; LENGTH: 488
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-821-234-1000

Query Match 85.7%; Score 30; DB 6; Length 488;
Best Local Similarity 85.7%; Pred. No. 13;

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Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVSNNLY 7
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Db 187 KYSNNLY 193

RESULT 9
US-10-467-657-4338
; Sequence 4338, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4338
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4338

Query Match 80.0%; Score 28; DB 6; Length 232;
Best Local Similarity 71.4%; Pred. No. 16;
Matches 5; Conservative 1; Mismatches 0; Gaps 0;

Qy 1 KVSNNLY 7
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Db 211 RVNNLY 217

RESULT 10
US-11-108-172-631
; Sequence 631, Application US/11108172
; Publication No. US20050260177A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yuhui
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedwick Thomas S.
; APPLICANT: Carter, Darick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C15
; CURRENT APPLICATION NUMBER: US/11/108,172
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 10/025,380
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US 09/922,217
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 09/833,263
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US 09/649,811

; PRIOR FILING DATE: 2000-08-28
; PRIOR APPLICATION NUMBER: US 09/609,448
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/575,251
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/519,444
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: US 09/504,629
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: US 09/480,321
; PRIOR FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: US 09/476,296
; PRIOR FILING DATE: 1999-12-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1130
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 631
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-108-172-631

Query Match 77.1%; Score 27; DB 7; Length 168;
Best Local Similarity 71.4%; Pred. No. 19;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVSNNLY 7
   :|||
Db 137 RYSNNLY 143

RESULT 11
US-11-113-775A-1
; Sequence 1, Application US/11113775A
; Publication No. US20050261158A1
; GENERAL INFORMATION:
; APPLICANT: Kottwitz, Beatriz
; APPLICANT: Pegelow, Ulrich
; TITLE OF INVENTION: DETERGENT WITH RINSE SURFACTANT AND A SPECIAL ALPHA-AMYLASE
; FILE REFERENCE: HENK-0124
; CURRENT APPLICATION NUMBER: US/11/113,775A
; CURRENT FILING DATE: 2005-04-25
; PRIOR APPLICATION NUMBER: DE 102004020430.6
; PRIOR FILING DATE: 2004-04-27
; PRIOR APPLICATION NUMBER: DE 102004048591.7
; PRIOR FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-11-113-775A-1

Query Match 77.1%; Score 27; DB 7; Length 483;
Best Local Similarity 57.1%; Pred. No. 59;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNNLY 7
   ||:|
Db 172 KLNNNLY 178

RESULT 12
US-11-113-775A-2
; Sequence 2, Application US/11113775A
; Publication No. US20050261158A1
; GENERAL INFORMATION:
; APPLICANT: Kottwitz, Beatriz
; APPLICANT: Pegelow, Ulrich
; TITLE OF INVENTION: DETERGENT WITH RINSE SURFACTANT AND A SPECIAL ALPHA-AMYLASE
; FILE REFERENCE: HENK-0124
; CURRENT APPLICATION NUMBER: US/11/113,775A
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; CURRENT FILING DATE: 2005-04-25
; PRIOR APPLICATION NUMBER: DE 102004020430.6
; PRIOR FILING DATE: 2004-04-27
; PRIOR APPLICATION NUMBER: DE 102004048591.7
; PRIOR FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-11-113-775A-2

Query Match 77.1%; Score 27; DB 7; Length 483;
Best Local Similarity 57.1%; Pred. No. 59;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSNRLY 7
|::||:|
Db 172 KLNRIY 178

RESULT 13
US-11-113-799-1
; Sequence 1, Application US/11113799
; Publication No. US20050261156A1
; GENERAL INFORMATION:
; APPLICANT: Kottwitz, Beatriz
; APPLICANT: Pegelow, Ulrich
; TITLE OF INVENTION: DETERGENT WITH SULFO-POLYMER RINSE AID AND A SPECIAL
; FILE REFERENCE: HENK-0123 / H 06113
; CURRENT APPLICATION NUMBER: US/11/113,799
; CURRENT FILING DATE: 2005-04-25
; PRIOR APPLICATION NUMBER: DE 102004020431.4
; PRIOR FILING DATE: 2004-04-27
; PRIOR APPLICATION NUMBER: DE 102004048590.9
; PRIOR FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Variant of Seq. ID No. 3
US-11-113-799-1

Query Match 77.1%; Score 27; DB 7; Length 483;
Best Local Similarity 57.1%; Pred. No. 59;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSNRLY 7
|::||:|
Db 172 KLNRIY 178

RESULT 14
US-11-113-799-2
; Sequence 2, Application US/11113799
; Publication No. US20050261156A1
; GENERAL INFORMATION:
; APPLICANT: Kottwitz, Beatriz
; APPLICANT: Pegelow, Ulrich
; TITLE OF INVENTION: DETERGENT WITH SULFO-POLYMER RINSE AID AND A SPECIAL
; FILE REFERENCE: HENK-0123 / H 06113
; CURRENT APPLICATION NUMBER: US/11/113,799
; CURRENT FILING DATE: 2005-04-25
; PRIOR APPLICATION NUMBER: DE 102004020431.4
; PRIOR FILING DATE: 2004-04-27
; PRIOR APPLICATION NUMBER: DE 102004048590.9
; PRIOR FILING DATE: 2004-10-04

; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Variant of Seq. ID No. 3
US-11-113-799-2

Query Match 77.1%; Score 27; DB 7; Length 483;
Best Local Similarity 57.1%; Pred. No. 59;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSNRLY 7
|::||:|
Db 172 KLNRIY 178

RESULT 15
US-10-630-203-12
; Sequence 12, Application US/10630203
; Publication No. US20050250663A1
; GENERAL INFORMATION:
; APPLICANT: Novozymes A/S
; APPLICANT: Thisted, Thomas
; APPLICANT: Kjaerulff, Soren
; APPLICANT: Andersen, Carsten
; APPLICANT: Fugleang, Claus Crone
; TITLE OF INVENTION: Alpha-amylase mutants with altered properties
; FILE REFERENCE: 10062.200-US
; CURRENT APPLICATION NUMBER: US/10/630,203
; CURRENT FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: US/09/918,543
; PRIOR FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-10-630-203-12

Query Match 77.1%; Score 27; DB 6; Length 485;
Best Local Similarity 57.1%; Pred. No. 60;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSNRLY 7
|::||:|
Db 172 KLNRIY 178

Search completed: December 30, 2005, 14:15:20
Job time : 2.59677 secs

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OM protein - protein search, using sw model

Run on: December 30, 2005, 14:26:51 ; Search time 183 Seconds
(without alignments)

16.807 Million cell updates/sec

Title: US-10-735-916A-4

Perfect score: 35

Sequence: 1 KVSNNLY 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 49830

Minimum DB seq length: 7

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_21.*

1: Geneseq1980s.*

2: Geneseq1990s.*

3: Geneseq2000s.*

4: Geneseq2001s.*

5: Geneseq2002s.*

6: Geneseq2003as.*

7: Geneseq2003bs.*

8: Geneseq2004s.*

9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	7	7	ADJ76838 CDR seque
2	35	100.0	7	9	ADZ67008 Murine in
3	27	77.1	7	7	ADD94240 Mouse HUI
4	26	74.3	7	6	ABP72121 Mouse FGF
5	26	74.3	7	7	ADD28189 Mouse lec
6	26	74.3	7	7	ADD94239 Mouse HUI
7	26	74.3	7	7	ADZ6487 Mouse ant
8	26	74.3	7	7	ADL3323 Murine an
9	26	74.3	7	8	ADR68225 Murine 26
10	24	68.6	7	2	AAR75492 Mouse ant
11	24	68.6	7	2	AAR75492 CDR2 reg
12	24	68.6	7	2	AAR70921 CDR2 of t
13	24	68.6	7	2	AAR70927 CDR2 of t
14	24	68.6	7	2	AAR71895 Anti-huma
15	24	68.6	7	3	AAY80282 Humanised
16	24	68.6	7	3	AAB12906 Anti-huma
17	24	68.6	7	3	AAB21365 Mouse ant
18	24	68.6	7	4	AAR70735 Human lig
19	24	68.6	7	4	AAG67671 Complemen
20	24	68.6	7	4	AAB97199 Murine an
21	24	68.6	7	5	ABP62375 Human imm
22	24	68.6	7	5	AAR70350 Mouse Kap
23	24	68.6	7	6	ABP58277 Murine mo
24	24	68.6	7	6	ABR40266 Murine pe

25	24	68.6	7	6	ABR39455 Anti-Abet
26	24	68.6	7	6	ABU08302 Mouse ant
27	24	68.6	7	6	ABR39783 Anti-Abet
28	24	68.6	7	6	ABG79999 Humanised
29	24	68.6	7	7	ADC03152 Colon spe
30	24	68.6	7	7	ADE27681 Mouse ant
31	24	68.6	7	7	ADD94149 Mouse HUI
32	24	68.6	7	7	ADZ94056 Anti-Abet
33	24	68.6	7	7	ADH61993 Mouse ant
34	24	68.6	7	8	ADH17765 Murine an
35	24	68.6	7	8	ADL93322 Human CD4
36	24	68.6	7	8	ADN61704 Humanised
37	24	68.6	7	8	ADM78082 Human SJB
38	24	68.6	7	8	ADM78106 Human SJB
39	24	68.6	7	8	ADM78124 Human SJB
40	24	68.6	7	8	ADM78130 Human SJB
41	24	68.6	7	8	ADP84868 Complemen
42	24	68.6	7	8	ADR19272 Glycosyla
43	24	68.6	7	8	ADS87340 Humanised
44	24	68.6	7	8	ADR68224 Murine 26
45	24	68.6	7	8	ADR68226 Murine 26

ALIGNMENTS

RESULT 1
ADJ76838
ID ADJ76838 standard; peptide; 7 AA.
XX
AC ADJ76838;
XX
DT 06-MAY-2004 (first entry)
XX
DE CDR sequence for anti-IGF-1R antibody.
XX
KW cytostatic; antipsoriatic; antibody;
KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;
KW or epidermal growth factor receptor; EGFR; signal transduction pathway;
KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;
KW CDR.
XX
OS Mus musculus.
XX
PN WO2003059951-A2.
XX
PD 24-JUL-2003.
XX
PF 20-JAN-2003; 2003WO-FR000178.
XX
PR 18-JAN-2002; 2002FR-00000653.
PR 18-JAN-2002; 2002FR-00000654.
PR 07-MAY-2002; 2002FR-00005753.
XX
PA (FABR) FABRE MEDICAMENT SA PIERRE.
XX
PI Goetsch L, Corvaia N, Leger O;
XX
DR WPI; 2003-569653/53.
DR N-PSDB; ADJ76837.
XX
PT New antibodies that bind to human insulin-like growth factor receptor,
XX useful for treatment, prevention and diagnosis of cancers.
XX
PS Claim 1; SEQ ID NO 4; 164pp; French.
XX
CC The invention relates to an isolated antibody (Ab), and its functional
CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-
CC 1R) and optionally: (i) inhibit natural binding of insulin-like growth
CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine
CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or
CC treat diseases associated with overexpression and/or abnormal activity of
CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with

CC hyperactivity of signal transduction pathways mediated by interaction of
 CC these receptors with their ligands. Especially they inhibit
 CC transformation of normal cells to tumor cells, inhibit growth and/or
 CC proliferation of tumor cells, so are useful against cancers of the
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents an
 CC CDR sequence used to generate the Ab of the invention.

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 35; DB 7; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNNRLY 7
 |||||
 Db 1 KVSNNRLY 7

RESULT 2
 ADZ67008

ID ADZ67008 standard; peptide; 7 AA.

AC ADZ67008;

XX 30-JUN-2005 (first entry)

DE Murine insulin-like growth factor T receptor IGF-1R CDR SEQ ID NO:4.

KW Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
 KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;
 KW musculoskeletal disease; respiratory disease; lung tumor;
 KW endocrine disease; gynecology and obstetrics; breast tumor;
 KW endometrial carcinoma; gastrointestinal disease; colon tumor;
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder.

XX Mus musculus.

OS US2005084906-A1.

XX 21-APR-2005.

XX 16-DEC-2003; 2003US-00735916.

XX 18-JAN-2002; 2002FR-00000653.

XX 18-JAN-2002; 2002FR-00000654.

XX 07-MAY-2002; 2002FR-00005753.

XX 20-JAN-2003; 2003WO-FR000178.

XX 11-JUL-2003; 2003FR-00008538.

XX (GOET/) GOETSCH L.

XX (CORV/) CORVAIA N.

XX (LGE/) LGER O.

XX (DUF/) DUFLOS A.

XX (HAEU/) HAEUW J.

XX (BECK/) BECK A.

PI Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;

XX WPI; 2005-321968/33.

DR N-PSDB; ADZ67007.

XX Novel isolated anti-insulin-like growth factor I receptor (IGF-1R)

PT antibody or its functional fragment, being capable of binding human IGF-1R

PT IR and specifically inhibiting tyrosine kinase activity of receptor,

CC specifically inhibiting tyrosine kinase activity of the receptor,
 CC comprising a light or heavy chain having at least one complementary
 CC determining region (CDR) consisting of one of two fully defined 16 amino
 CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in
 CC the preparation of a medicament intended for the prevention or treatment
 CC of an illness connected with an overexpression and/or an abnormal
 CC activation of the IGF-1R and/or EGFR, and/or connected with a
 CC hyperactivation of the transduction pathway of the signal mediated by the
 CC interaction of IGF1 or IGF2 with IGF-1R and/or of EGF with EGFR, where
 CC the administration of the medicament does not induce or only slightly
 CC induces secondary effects connected with inhibition of the insulin
 CC receptor. The antibody is useful for preparation of a medicament intended
 CC to inhibit the transformation of normal cells into cells with tumoral
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is
 CC useful for preparation of a medicament intended to inhibit the growth
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a
 CC medicament intended for prevention or for the treatment of cancer, where
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the
 CC preparation of a medicament intended for the prevention or for the
 CC treatment of psoriasis. (I) is useful in preparation of a medicament
 CC intended for the specific targeting of a biologically active compound to
 CC cells expressing or overexpressing the IGF-1R and/or EGFR receptor. (I)
 CC is useful for in vitro diagnosis of illnesses induced by an
 CC overexpression or an underexpression of the IGF-1R and/or EGFR receptor
 CC starting from a biological sample in which the abnormal presence, of IGF-
 CC IR and/or EGFR receptor is suspected, which involves contacting the
 CC biological sample with (I), which is optionally labeled. The present
 CC sequence is used in the exemplification of the invention.

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 35; DB 9; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNNRLY 7
 |||||
 Db 1 KVSNNRLY 7

RESULT 3

ADD94240

ID ADD94240 standard; peptide; 7 AA.

AC ADD94240;

XX 29-JAN-2004 (first entry)

XX Mouse HUI77 mutant light chain CDR amino acid sequence SeqID125.

DE grafted antibody; complementarity determining region; CDR; light CDR;
 XX heavy CDR; cryptic collagen epitope; solid tumour;
 KW new blood vessel growth; angiogenesis; tumour growth; cytostatic;
 KW collagen agonist; collagen antagonist; cancer metastasis;
 KW anti-cryptic collagen; HUI77; variable region light chain; murine;
 KW mutant; mutein.

XX Synthetic.

OS Mus musculus.

XX WO2003046204-A2.

XX 05-JUN-2003.

XX 26-NOV-2002; 2002WO-US038147.

XX 26-NOV-2001; 2001US-00995529.

XX 06-DEC-2001; 2001US-00011250.

PA (CELL-) CELL MATRIX INC.
 XX Watking JD, Huse WD, Tang Y, Broek D, Brooks PC;
 XX WPI; 2003-513649/48.
 XX
 XX New cryptic collagen antibody with one or more complementarity
 PT determining regions, useful for diagnosing and treating disorders
 PT associated with angiogenesis, tumor growth and/or cancer metastasis.
 XX
 XX Claim 24; SEQ ID NO 125; 232pp; English.
 XX
 XX This invention relates to a novel grafted antibody or its functional
 CC fragment comprising one or more complementarity determining regions
 CC (CDRs) of a defined light CDR and a heavy CDR with at least one amino
 CC acid (aa) substitution where the antibody has specific binding activity
 CC for a cryptic collagen epitope. The growth of all solid tumours requires
 CC new blood vessel growth, angiogenesis, inhibition of which is an approach
 CC to limiting tumour growth. The invention may allow development of
 CC therapeutics with a cytostatic activity as a collagen agonist or
 CC antagonist. The invention is useful for diagnosing and treating disorders
 CC associated with angiogenesis, tumour growth and/or cancer metastasis. The
 CC present sequence is the amino acid sequence of a mutant mouse anti-
 CC cryptic collagen site antibody HUI77 variable region light chain CDR
 CC which may be used during the creation of an antibody of the invention.
 XX
 XX Sequence 7 AA;
 SQ
 Query Match 77.1%; Score 27; DB 7; Length 7;
 Best Local Similarity 71.4%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KVSNNRLY 7
 Db 1 KVSNNRPF 7
 RESULT 4
 ID ABP72121 standard; peptide; 7 AA.
 XX
 AC ABP72121;
 XX
 XX 03-JUN-2003 (first entry)
 DT Mouse FGF-8 related protein CDR2 SEQ ID 9.
 XX
 DE Mouse; humanised; antibody; fibroblast growth factor 8; FGF8; cytostatic;
 KW cancer; prostate; breast; ovarian; testicular; CDR2.
 XX
 XX Mus musculus.
 OS
 XX WO2003002608-A1.
 PN
 XX 09-JAN-2003.
 PD
 XX 28-JUN-2002; 2002WO-JP006591.
 PF
 XX 28-JUN-2001; 2001JP-00196176.
 PR
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 PA
 XX Shitara K, Nakamura K, Hirota M, Shimada N;
 PI WPI; 2003-239169/23.
 XX
 XX Humanised antibodies and antibody fragments reacting with fibroblast
 PT growth factor 8 useful for the treatment and diagnosis of cancer.
 XX
 XX Claim 3; Page 69; 86pp; Japanese.
 PS
 XX The invention relates to novel humanised antibodies and antibody
 CC fragments which react with fibroblast growth factor 8 (FGF8) and inhibit

CC its biological functions. The polypeptides of the invention have
 CC cytostatic activity. The antibody is useful for the treatment of cancer,
 CC including prostate, breast, ovarian and testicular cancer. The present
 CC sequence is used in the exemplification of the invention
 XX
 XX Sequence 7 AA;
 SQ
 Query Match 74.3%; Score 26; DB 6; Length 7;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVSNNRL 6
 Db 1 KVSNNRI 6
 RESULT 5
 ID ADD28189 standard; peptide; 7 AA.
 XX
 AC ADD28189;
 XX
 XX 15-JAN-2004 (first entry)
 DT Mouse lectin tolerance related peptide SEQ ID NO:22.
 XX
 DE Mouse; antibody; lectin; sugar; N-acetylglucosamine;
 KW Fc gamma receptor IIa; cytostatic; antiallergic; immunomodulator;
 KW cardiant; virucide; antibacterial; tumour; allergy; inflammation;
 KW autoimmune disease; circulatory system; viral infection;
 KW bacterial infection.
 XX
 OS Mus musculus.
 XX
 XX WO2003084570-A1.
 PN
 XX 16-OCT-2003.
 PD
 XX 09-APR-2003; 2003WO-JP004505.
 PF
 XX 09-APR-2002; 2002JP-00106951.
 PR
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 PA
 XX Nakamura K, Shitara K, Hatanaka S, Niwa R, Okazaki A;
 PI WPI; 2003-812677/76.
 XX
 XX Drugs containing antibody compositions produced by cells tolerant to
 PT lectin recognizing specific sugar-chain structure, appropriate for
 PT patients suffering from Fc gammaRIIa polymorphism e.g. in treating
 PT tumors.
 XX
 XX Example 3; SEQ ID NO 22; 214pp; Japanese.
 XX
 XX The invention relates to a novel drug containing as the active ingredient
 CC an antibody composition produced by cells tolerant to a lectin
 CC recognising a sugar-chain structure in which an alpha-bond is formed
 CC between the 6-position of N-acetylglucosamine at the reducing end of an N
 CC -glycoside bond-type complex sugar chain and the 1-position of fucose,
 CC which has affinity to human Fc gamma receptor IIa. A drug of the
 CC invention has cytostatic, antiallergic, immunomodulator, cardiant,
 CC virucide, and antibacterial activity. The drugs are useful in screening
 CC and treating patients not suitable for drugs not derived from these
 CC cells, particularly as diagnostics, preventives or remedies for diseases
 CC accompanying tumour, allergy or inflammation, autoimmune diseases,
 CC diseases of the circulatory system, and viral or bacterial infections.
 CC The present sequence is used in the exemplification of the invention.
 XX
 XX Sequence 7 AA;
 SQ
 Query Match 74.3%; Score 26; DB 7; Length 7;
 Best Local Similarity 83.3%; Pred. No. 2e+06;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSNNL 6
 DB 1 KVSNNI 6

RESULT 6
 ADD94239
 ID ADD94239 standard; peptide; 7 AA.
 XX
 AC ADD94239;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Mouse HUI77 mutant light chain CDR amino acid sequence SeqID124.
 XX
 KW grafted antibody; complementarity determining region; CDR; light CDR;
 KW heavy CDR; cryptic collagen epitope; solid tumour;
 KW new blood vessel growth; angiogenesis; tumour growth; cytostatic;
 KW collagen agonist; collagen antagonist; cancer metastasis;
 KW anti-cryptic collagen; HUI77; variable region light chain; mouse; murine;
 KW mutant; mutein.
 XX
 OS Synthetic.
 OS Mus musculus.
 XX
 PN WO2003046204-A2.
 XX
 PD 05-JUN-2003.
 XX
 PF 26-NOV-2002; 2002WO-US038147.
 XX
 PR 26-NOV-2001; 2001US-0095529.
 PR 06-DEC-2001; 2001US-00011250.
 XX
 PA (CELL-) CELL MATRIX INC.
 XX
 PI Watking JD, Huse WD, Tang Y, Broek D, Brooks PC;
 XX
 DR WPI; 2003-513649/48.
 XX
 PT New cryptic collagen antibody with one or more complementarity
 PT determining regions, useful for diagnosing and treating disorders
 PT associated with angiogenesis, tumor growth and/or cancer metastasis.
 XX
 PS Claim 24; SEQ ID NO 124; 232pp; English.
 XX
 CC This invention relates to a novel grafted antibody or its functional
 CC fragment comprising one or more complementarity determining regions
 CC (CDRs) of a defined light CDR and a heavy CDR with at least one amino
 CC acid (aa) substitution where the antibody has specific binding activity
 CC for a cryptic collagen epitope. The growth of all solid tumours requires
 CC new blood vessel growth, angiogenesis, inhibition of which is an approach
 CC to limiting tumour growth. The invention may allow development of
 CC therapeutics with a cytostatic activity as a collagen agonist or
 CC antagonist. The invention is useful for diagnosing and treating disorders
 CC associated with angiogenesis, tumour growth and/or cancer metastasis. The
 CC present sequence is the amino acid sequence of a mutant mouse anti-
 CC cryptic collagen site antibody HUI77 variable region light chain CDR
 CC which may be used during the creation of an antibody of the invention.
 XX
 SQ Sequence 7 AA;

Query Match 74.3%; Score 26; DB 7; Length 7;
 Best Local Similarity 71.4%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSNNLY 7
 DB 1 KVSNNRFW 7

RESULT 7
 ADE36487
 ID ADE36487 standard; peptide; 7 AA.
 XX
 AC ADE36487;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Mouse anti-FGF-8 antibody-related peptide #5.
 XX
 KW arthritis; anti-FGF-8; sic fibroblast growth factor;
 KW cartilage protection agent; joint destruction inhibitor;
 KW synovial proliferation inhibitor; mouse; murine.
 XX
 OS Mus musculus.
 OS WO2003057251-A1.
 PN 17-JUL-2003.
 PD 26-DEC-2002; 2002WO-JP013650.
 XX
 PF 28-DEC-2001; 2001JP-00400677.
 PR
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 PA Tamura T, Uchii M, Suda T, Miki I, Tanaka A;
 XX
 PI WPI; 2003-587078/55.
 DR
 XX Treatment and prevention of arthritis comprising the use of anti-FGF-8
 PT (sic fibroblast growth factor) antibody.
 PT
 XX Claim 11; SEQ ID NO 11; 193pp; Japanese.
 XX
 CC The invention comprises a method for treating and preventing arthritis,
 CC the method involves the use of anti-FGF-8 (sic fibroblast growth factor)
 CC antibody. The antibody and method of the invention is useful for: the
 CC detection, treatment and prevention of arthritis; as a cartilage
 CC protection agent; as a joint destruction inhibitor; and as a synovial
 CC proliferation inhibitor. The present amino acid sequence represents a
 CC mouse peptide that was used in an example of the invention.
 XX
 SQ Sequence 7 AA;

Query Match 74.3%; Score 26; DB 7; Length 7;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSNNL 6
 DB 1 KVSNNI 6

RESULT 8
 ADL35323
 ID ADL35323 standard; peptide; 7 AA.
 XX
 AC ADL35323;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Murine anti-Fc-gamma receptor IIIa antibody-related peptide - SEQ 80.
 XX
 KW antibody binding; Fc-gamma receptor IIIa; Fc region sugar chain;
 KW cytostatic; anti-allergic; anti-inflammatory; immunosuppressive;
 KW vasotropic; virucide; cancer; allergy; inflammatory; autoimmune;
 KW circulatory; viral infection; murine; mouse.
 XX
 OS Mus musculus.
 OS WO2003085119-A1.
 PN

PD 16-OCT-2003.
XX
PF 09-APR-2003; 2003WO-JP004504.
XX
PR 09-APR-2002; 2002JP-00106950.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Nakamura K, Shitara K;
XX
DR WPI; 2003-812729/76.
XX
XX Method of enhancing the binding activity of antibody to Fc-gamma receptor
PT IIIa for production of antibodies with high cytotoxicity as cancer,
PT allergic, viral and other disease therapeutic agents.
XX
XX Example 14; SEQ ID NO 80; 296pp; Japanese.
XX
CC The invention relates to a novel method for enhancing the binding
CC activity of an antibody to the Fc-gamma receptor IIIa by increasing the
CC proportion of N-glycoside bond type complex sugar chains attached to the
CC Fc region of the antibody which do not have the 1-position of fucose
CC bound to the 6-position of N-acetylglucosamine at the reducing end of the
CC sugar chain. The method of the invention has cytostatic, antiallergic,
CC antiinflammatory, immunosuppressive, vasotropic and virucide applications
CC and may be useful for generating antibodies to be used in the treatment,
CC prevention and diagnosis of diseases including cancer, allergies,
CC inflammatory disorders, autoimmune diseases, circulatory disorders and
CC viral infections. The current sequence is that of an anti-Fc-gamma
CC receptor IIIa antibody-related peptide of the invention.
XX
SQ Sequence 7 AA;
Query Match 74.3%; Score 26; DB 7; Length 7;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVSNNRL 6
Db 1 KVSNNRI 6
RESULT 9
ID ADR68225 standard; peptide; 7 AA.
XX
AC ADR68225;
XX
DT 18-NOV-2004 (first entry)
XX
DE Murine 266 antibody light chain CDR2 variant #2.
XX
KW antibody; neuroprotective; nootropic; antibody therapy; antigen-binding;
KW light chain; heavy chain; human; amyloid-beta peptide;
KW complementarity determining region; Alzheimer's disease; murine;
KW humanised antibody.
XX
OS Mus sp.
XX
PN WO2004071408-A2.
XX
PD 26-AUG-2004.
XX
PF 06-FEB-2004; 2004WO-US002004.
XX
PR 10-FEB-2003; 2003US-0446380P.
XX
PA (MOLE-) APPLIED MOLECULAR EVOLUTION INC.
XX
PI Davies J, Tang Y, Watkins JD;
XX
DR WPI; 2004-625759/60.
XX

PT New humanized antibody or its antigen-binding portion that specifically
PT binds human amyloid-beta peptide, useful in the manufacture of a
PT medicament for treating Alzheimer's disease.
XX
XX Claim 1; SEQ ID NO 24; 58pp; English.
XX
XX The invention relates to an antibody, or its antigen-binding portion,
CC comprising a light chain and a heavy chain that specifically binds human
CC amyloid-beta (Abeta) peptide. The new antibody or its antigen-binding
CC portion that specifically binds human Abeta comprises a light chain and a
CC heavy chain. The light chain comprises a light chain: complementarity
CC determining region 1 (CDR1) comprising amino acid sequences ADR68208-
CC ADR68223; CDR2 comprising amino acid sequences ADR68224-ADR68228; and
CC CDR3 comprising amino acid sequences ADR68229-ADR68237. The heavy chain
CC comprises a heavy chain: CDR1 comprising amino acid sequences ADR68238-
CC ADR68239; CDR2 comprising amino acid sequences ADR68240-ADR68269; and
CC CDR3 comprising amino acid sequences ADR68270-ADR68277; provided that the
CC antibody does not comprise: a light chain CDR1 comprising the sequence
CC ADR68208; a light chain CDR2 comprising the sequence ADR68224; a light
CC chain CDR3 comprising the sequence ADR68229; a heavy CDR1 comprising the
CC sequence ADR68238; a heavy CDR2 comprising the sequence ADR68240; or a
CC heavy CDR3 comprising the sequence ADR68270. The antibody is useful in
CC the manufacture of a medicament for treating Alzheimer's disease. This
CC sequence corresponds to an example of the CDR2 from the murine 266
CC antibody light chain used to generate the humanised antibody of the
CC invention.
XX
SQ Sequence 7 AA;
Query Match 74.3%; Score 26; DB 8; Length 7;
Best Local Similarity 71.4%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 KVSNNRL 7
Db 1 KVSNNRF 7
RESULT 10
ID AAR75492 standard; peptide; 7 AA.
XX
AC AAR75492;
XX
DT 07-FEB-1996 (first entry)
XX
DE Mouse antibody variable region CDR2 peptide #5.
XX
KW Primer; amplification; PCR; mouse; kappa chain; heavy chain; Fab;
KW antibody; immunotolerance; animal; variegated display library; CDR;
KW variable region; antigen; immunorecessive; cell surface marker; foetal;
KW cancer; stem cell; variant; therapy; Alzheimer's disease; hybridoma;
KW familial hypercholesterolaemia; binding affinity;
KW complementarity determining region.
XX
OS Synthetic.
XX
PN WO9515982-A2.
XX
PD 15-JUN-1995.
XX
PF 08-DEC-1994; 94WO-US014106.
XX
PR 08-DEC-1993; 93US-00164022.
PR 06-DEC-1994; 94US-00350400.
XX
PA (GENZ) GENZYME CORP.
XX
PI Barsomian G, Copeland DP, Hillhouse D, Johnson T;
XX
DR WPI; 1995-224291/29.
XX
PT Generating new antibodies specific for immunorecessive epitopes - by

PT selection from variegated V gene library cloned from immunotolerance
PT derived antibody repertoire, useful in diagnosis, purificn. and therapy,
PT e.g. of cancer.
XX
PS Claim 75; Page 96; 109pp; English.
XX
CC Peptides AAR75462-92 are examples of complementarity determining regions
CC (CDRs) used to generate antibodies against immunorecessive antigens. The
CC CDRs are derived from the heavy and light chain variable regions of the
CC antibodies FB3-2 (AAQ92500-1), F4-7 (AAQ92502-3) and H3-3 (AAQ92504-5).
CC The peptides AAR75488-92 represent CDR2 from the variable regions of the
CC above antibodies, used to generate a single variable region. The CDR
CC sequences were isolated from a variegated display library (VDL) of
CC variable regions derived from a repertoire of antibodies from an
CC immunocolerised animal. The VDL is generated by PCR amplifying the
CC variable regions from the antibody coding sequences using the primers
CC AAQ74153-74. The constructed antibodies are generated against an
CC immunorecessive antigen e.g. a cell surface marker on a foetal, cancer or
CC stem cell, which can differentiate between variant or related forms of
CC the antigen. The antibodies generated can be used in the diagnosis, e.g.
CC detection of the immunorecessive antigen, or in therapy e.g. of cancer,
CC Alzheimer's disease or familial hypercholesterolaemia. The method of
CC production of the antibody allows rapid and sensitive isolation of
CC antibodies that would be difficult to isolate by standard methods. The
CC antibodies produced have greater binding affinity than those produced by
CC combinatorial/hybridoma methods
XX
SQ Sequence 7 AA;

Query Match 68.6%; Score 24; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNR 5
Db 1 KVSNR 5

RESULT 11
AAW31748
ID AAW31748 standard; peptide; 7 AA.
AC AAW31748;
XX
DT 15-APR-1998 (first entry)
XX
DE CDR2 region of L chain subunit of Fas specific antibody.
XX
XX Fas; antibody; human; immunoglobulin; variable region; rheumatism;
KW autoimmune disease; rheumatoid arthritis; therapy; CDR; light chain;
KW complementarity determining region.
XX
XX Synthetic.
OS
XX EP799891-A1.
PN
XX 08-OCT-1997.
PD
XX 27-MAR-1997; 97EP-00302415.
PF
XX 01-APR-1996; 96JP-00078570.
PR
XX (SANY) SANKYO CO LTD.
PA
XX Serizawa N, Ichikawa K, Nakahara K, Yonehara S;
PI WPI; 1997-482673/45.
XX
XX Anti-Fas recombinant antibodies - useful for treating auto-immune
PT diseases, especially rheumatoid arthritis.
PT
XX Claim 10; Page 28; 72pp; English.
XX

CC This sequence represents a fragment of the protein of the invention. The
CC protein of the invention is a recombinant protein (A), that comprises at
CC least one region corresponding to an immunoglobulin (Ig) variable region
CC which enables the protein to recognise and specifically bind to an
CC antigen, preferably human Fas, and has substantially no more
CC immunogenicity in a human patient than a human antibody. The proteins are
CC useful for treating autoimmune diseases, especially rheumatism
CC (rheumatoid arthritis). (A) is based on a murine monoclonal antibody. As
CC the protein lacks the constant region, it has substantially no more
CC immunogenicity in the human patient than a human antibody
XX
SQ Sequence 7 AA;

Query Match 68.6%; Score 24; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNR 5
Db 1 KVSNR 5

RESULT 12
AAW70921
ID AAW70921 standard; peptide; 7 AA.
XX
AC AAW70921;
XX
DT 14-OCT-1998 (first entry)
XX
DE CDR2 of the light chain of monoclonal antibody RV-138.
XX
XX Pathogenic virus; tropism; mucosa; CDR region; monoclonal antibody;
KW respiratory syncytial virus; RSV; VP6 protein; rota virus; RV;
KW viral infection; inhibit; fusion; protection; transcription;
KW antiviral agent; prophylaxis; diagnosis; infection; contamination.
XX
XX Synthetic.
OS
XX Mus sp.
XX
XX FR2758331-A1.
PN
XX 17-JUL-1998.
PD
XX 14-JAN-1997; 97FR-00000300.
PF
XX 14-JAN-1997; 97FR-00000300.
PR
XX (UYBO-) UNIV BOURGOGNE.
PA
XX WPI; 1998-390320/34.
DR
XX New peptide(s) recognising viral epitope with tropism to mucosa - useful
PT for, e.g. diagnosing, preventing and treating viral infection(s).
PT
XX Claim 12; Page 29; 51pp; French.
PS
XX AAW70905-46 represent peptide sequences that can recognise, by antigen-
CC antibody type reactions, at least 1 epitope of a pathogenic virus having
CC tropism for the mucosa. AAW70905-16 and AAW70929-46 are analogous to CDR
CC regions of monoclonal antibodies specific for respiratory syncytial virus
CC (RSV). AAW70917-28 are analogous to CDR regions of monoclonal antibodies
CC specific for site III or IV of the VP6 protein of rota virus (RV). The
CC peptides can neutralise viral infections and may also inhibit fusion
CC between infected and uninfected cells or cells and viruses. They provide
CC passive or active protection and/or inhibit transcription of the virus,
CC so are useful as antiviral agents or for prophylaxis, in human or
CC veterinary medicine. The peptides can be labelled and used to diagnose
CC infection or contamination by the virus. The peptides are particularly
CC directed against RSV or RS but may also be used against papilloma, adeno,
CC entero, polio, influenza or immune deficiency viruses
XX
XX Sequence 7 AA;

```

Query Match      68.6%; Score 24; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVSNR 5
      |||||
DB      1 KVSNR 5

RESULT 13
AAW70927
ID AAW70927 standard; peptide; 7 AA.
XX
AC AAW70927;
XX
XX
DT 14-OCT-1998 (first entry)
XX
DE CDR2 of the light chain of monoclonal antibody RV-133.
XX
KW Pathogenic virus; tropism; mucosa; CDR region; monoclonal antibody;
KW respiratory syncytial virus; RSV; VP6 protein; monoclonal antibody;
KW viral infection; inhibit; fusion; protection; transcription;
KW antiviral agent; prophylaxis; diagnosis; infection; contamination.
XX
OS Synthetic.
OS Mus sp.
XX
XX FR2758331-A1.
XX
PN 17-JUL-1998.
PD
XX
XX 14-JAN-1997; 97FR-00000300.
XX
XX 14-JAN-1997; 97FR-00000300.
XX
XX (UYBO-) UNIV BOURGOGNE.
XX
XX WPI; 1998-390320/34.
XX
XX
XX New peptide(s) recognising viral epitope with tropism to mucosa - useful
XX for, e.g. diagnosing, preventing and treating viral infection(s).
XX
XX Claim 12; Page 31; 5lpp; French.
XX
CC AAW70905-46 represent peptide sequences that can recognise, by antigen-
CC antibody type reactions, at least 1 epitope of a pathogenic virus having
CC tropism for the mucosa. AAW70905-16 and AAW70929-46 are analogous to CDR
CC regions of monoclonal antibodies specific for respiratory syncytial virus
CC (RSV). AAW70917-28 are analogous to CDR regions of monoclonal antibodies
CC specific for site III or IV of the VP6 protein of rota virus (RV). The
CC peptides can neutralise viral infections and may also inhibit fusion
CC between infected and uninfected cells or cells and viruses. They provide
CC passive or active protection and/or inhibit transcription of the virus,
CC so are useful as antiviral agents or for prophylaxis, in human or
CC veterinary medicine. The peptides can be labelled and used to diagnose
CC infection or contamination by the virus. The peptides are particularly
CC directed against RSV or RS but may also be used against papilloma, adeno,
CC entero, polio, influenza or immune deficiency viruses
XX
SQ Sequence 7 AA;
Query Match      68.6%; Score 24; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVSNR 5
      |||||
DB      1 KVSNR 5

RESULT 14
AAW71895
ID AAW71895 standard; peptide; 7 AA.
XX
AC AAW71895;
XX
DT 18-JAN-1999 (first entry)
XX
DE Anti-human Fas monoclonal antibody CH11 light chain CDR2.
XX
KW Humanised antibody; Fas; CH11; monoclonal antibody; Mab; apoptosis;
KW autoimmune disease; rheumatoid arthritis; therapy; human; mouse;
KW antibody engineering; complementarity determining region; CDR.
XX
OS Mus musculus.
XX
XX EP866131-A2.
XX
PN 23-SEP-1998.
PD
XX
XX 20-MAR-1998; 98EP-00302113.
XX
XX 21-MAR-1997; 97JP-00067938.
XX
XX (SANY ) SANKYO CO LTD.
XX
XX Serizawa N, Haruyama H, Takahashi T, Nakahara K, Yonehara S;
XX WPI; 1998-482965/42.
XX
XX Production of anti-Fas protein humanised antibodies - for use in inducing
XX apoptosis on Fas expressing cells in the treatment of autoimmune
XX diseases, especially rheumatoid arthritis.
XX
XX Example 4; Page 53; 187pp; English.
XX
CC This peptide comprises complementarity determining region 2 (CDR2) of the
CC light chain variable region (see AAW71889) of the mouse anti-human Fas
CC monoclonal antibody CH11. CDR1 (see AAW71894) and CDR3 (see AAW71896)
CC have also been identified. The invention relates to novel humanised
CC antibodies comprising humanised light and heavy chains (see AAW71876-81)
CC of CH11. These humanised anti-human Fas antibodies are capable of
CC inducing apoptosis in cells expressing Fas (e.g. synovialocytes) and are
CC useful in the treatment of autoimmune disease and chronic rheumatoid
CC arthritis
XX
SQ Sequence 7 AA;
Query Match      68.6%; Score 24; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVSNR 5
      |||||
DB      1 KVSNR 5

RESULT 15
AAW80282
ID AAW80282 standard; peptide; 7 AA.
XX
AC AAW80282;
XX
DT 30-MAY-2000 (first entry)
XX
DE Humanised anti-Fas antibody light chain CDR2 peptide SEQ ID NO:6.
XX
KW Humanised; anti-Fas antibody; mouse hybridoma; autoimmune disease;
KW diagnosis; CDR; complementarity determining region; apoptosis;
KW immunosuppressive.
XX
XX Homo sapiens.
XX
OS Mus sp.
XX
XX JP2000014383-A.

```

XX 18-JAN-2000.
PD
XX
XX 03-JUL-1998; 98JP-00204318.
PF
XX
XX 03-JUL-1998; 98JP-00204318.
PR
XX
XX (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.
PA
XX
XX WPI; 2000-199626/18.
DR
XX
XX Novel recombinant antibody used for treating and diagnosing autoimmune
PT diseases - is humanized anti-Fas antibody which controls and induces
PT apoptosis in cells expressing fas antigen.
XX
XX PS Claim 5; Page 12; 25pp; Japanese.
XX
XX The present invention describes a recombinant antibody (A) which binds to
CC fas antigen, and controls and induces apoptosis in cells which expressed
CC fas antigen. The complementarity determining regions (CDR) of (A) contain
CC amino acid sequences obtained from a mammal other than human, other
CC regions contain amino acid sequences from human and they partly contain
CC modified amino acids. (A) has immunosuppressive activity. (A) is used for
CC treating and/or diagnosing autoimmune diseases. The present sequence
CC represents a specifically claimed light chain CDR2 of (A)
XX
SQ Sequence 7 AA;
Query Match 68.6%; Score 24; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;
OY 1 KVSNR 5
Db 1 KVSNR 5
|||||

Search completed: December 30, 2005, 14:47:21
Job time : 186 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2005, 14:40:17 ; Search time 36 Seconds
(without alignments)
18.709 Million cell updates/sec

Title: US-10-735-916A-4

Perfect score: 35

Sequence: 1 KVSNNRLY 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 141

Minimum DB seq length: 7

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80:**

1: Pir1:**

2: Pir2:**

3: Pir3:**

4: Pir4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	37.1	7	2 A38081	amine oxidase (cop
2	11	31.4	7	2 S42620	aggreccan - bovine
3	11	31.4	7	2 A11483	aspartate transami
4	10	28.6	7	2 S17976	glucose isomerase
5	9	25.7	7	1 NYPG7	hypothalamic hepta
6	9	25.7	7	2 S19630	ribosomal protein
7	9	25.7	7	2 P00663	membrane protein -
8	9	25.7	7	2 A28709	phosphonoacetaldeh
9	9	25.7	7	2 PNO150	omega-gliadine 1'
10	9	25.7	7	2 S78024	ribosomal protein
11	9	25.7	7	2 PH0932	T-cell receptor be
12	9	25.7	7	2 A28340	myomodulin - Calif
13	9	25.7	7	2 ECMUCR	catch-relaxing pep
14	8	22.9	7	2 A60139	fatty-acid synthas
15	8	22.9	7	2 B39127	phosphotransferase
16	8	22.9	7	2 I40504	hypothetical prote
17	8	22.9	7	2 P70520	T-cell receptor be
18	8	22.9	7	2 P70521	T-cell receptor be
19	8	22.9	7	2 S45311	microcin C7 - Esch
20	7	20.0	7	1 A61324	dermorphin - Rohde
21	7	20.0	7	2 S71870	glutathione transf
22	7	20.0	7	2 S71867	glutathione transf
23	7	20.0	7	2 A60224	Met-enkephalin-Arg
24	7	20.0	7	2 S36662	dermorphin (Iys-7)
25	7	20.0	7	2 S21230	dermorphin (Trp-4)
26	7	20.0	7	2 PH1602	Ig H chain V-D-J r
27	7	20.0	7	2 B33932	Ig mu chain D regi
28	7	20.0	7	2 P70663	T-cell receptor be
29	7	20.0	7	2 P70567	T-cell receptor be

30 7 20.0 7 2 P70671 T-cell receptor be
31 7 20.0 7 2 A58718 carnosin U149 - Ca
32 7 20.0 7 2 PC2370 probable H+-transp
33 7 20.0 7 2 PC2132 FMRamide-related
34 7 20.0 7 2 I56695 hypothetical L2 pr
35 6 17.1 7 1 XEYDGD galactose oxidase
36 6 17.1 7 2 JN0859 peptidyl-dipeptida
37 6 17.1 7 2 PH1408 Ig heavy chain V r
38 6 17.1 7 2 S16364 opacity protein P.
39 6 17.1 7 2 S16365 opacity protein P.
40 6 17.1 7 2 S38516 mabinlin II chain
41 6 17.1 7 2 A34818 vicilin 72K chain
42 6 17.1 7 2 H33098 180K exoantigen -
43 6 17.1 7 2 A34026 acetylcholinestera
44 6 17.1 7 2 I50210 gene C-rel protein
45 6 17.1 7 2 C56793 platelet glycoprot

ALIGNMENTS

RESULT 1

A38081
amine oxidase (copper-containing) (EC 1.4.3.6) - yeast (*Pichia angusta*) (fragment)
C;Species: *Pichia angusta*
C;Date: 31-Dec-1993 #sequence_revision 03-Feb-1994 #text_change 20-Apr-2000
C;Accession: A38081
R;Ma, D.; Janes, S.M.; Smith, A.J.; Brown, D.E.; Dooley, D.M.; Klinman, J.P.
J. Biol. Chem. 267, 7979-7982, 1992
A;Title: Tyrosine codon corresponds to topa quinone at the active site of copper amine
A;Reference number: A38081; MUID:92235001; PMID:1569055
A;Accession: A38081
A;Molecule type: protein
A;Residues: 1-7 <MUA>
A;Cross-references: UNIPARC:UPI000017CA48
C;Keywords: copper; oxidoreductase; quinoprotein; topaquinone
F;4/Modified site: topaquinone (Tyr) #status experimental

Query Match 37.1%; Score 13; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 VSNRLY 7
| : |
DB 1 VANYEY 6

RESULT 2

S42620
aggreccan - bovine (fragment)
C;Species: *Bos primigenius taurus* (cattle)
C;Date: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 24-Jul-1998
C;Accession: S42620
R;Vogel, K.G.; Sandy, J.D.; Pogany, G.; Robbins, J.R.
Matrix Biol. 14, 171-179, 1994
A;Title: Aggreccan in bovine tendon.
A;Reference number: S42620; MUID:94340214; PMID:7520336
A;Accession: S42620
A;Molecule type: protein
A;Residues: 1-7 <VOG>
A;Cross-references: UNIPARC:UPI000017C497
A;Experimental source: flexor tendon
C;Keywords: cartilage

Query Match 31.4%; Score 11; DB 2; Length 7;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSNR 5
| : |
DB 4 VSPP 7

RESULT 3
A11483
aspartate transaminase (EC 2.6.1.1), mitochondrial - sheep (fragment)
N:Alternate names: aspartate aminotransferase, mitochondrial
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 20-Aug-1999
C:Accession: A11483
R:Campob-Cavieres, M.; Milstein, C.P.
Biochem. J. 147, 275-281, 1975
A:Title: The sequences of the coenzyme-binding peptide in the cytoplasmic and the mitochondrial
A:Reference number: A11483; MUID:76039441; PMID:1180894
A:Accession: A11483
A:Molecule type: protein
A:Residues: 1-7 <CAM>
A:Cross-references: UNIPARC:UPI000017C59C
A:Experimental source: liver
C:Keywords: aminotransferase, mitochondrion; phosphoprotein; pyridoxal phosphate
F:2/Binding site: pyridoxal phosphate (lys) (covalent) #status experimental

Query Match 31.4%; Score 11; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LY 7
||
DB 6 LY 7

RESULT 4
S17976
glucose isomerase - Thermoanaerobacterium saccharolyticum (fragment)
C:Species: Thermoanaerobacterium saccharolyticum
C:Date: 12-Feb-1998 #sequence_revision 12-Feb-1998 #text_change 09-Jul-2004
C:Accession: S17976
R:Lee, C.; Zeikus, J.G.
Biochem. J. 273, 565-571, 1991
A:Title: Purification and characterization of thermostable glucose isomerase from Clostridium
A:Reference number: S15119; MUID:91144536; PMID:1996956
A:Accession: S17976
A>Status: Preliminary
A:Molecule type: protein
A:Residues: 1-7 <LBE>
A:Cross-references: UNIPROT:P30435; UNIPARC:UPI0000173053
A:Note: the sequence from page 568 is inconsistent with that from page 565 in having 6-G
A:Note: the source is designated as Thermoanaerobacter strain B6A

Query Match 28.6%; Score 10; DB 2; Length 7;
Best Local Similarity 25.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 NRLY 7
||
DB 2 NKIF 5

RESULT 5
NYPG7
hypothalamic heptapeptide - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004
C:Accession: A01417
R:Chang, R.C.C.; Huang, W.Y.; Arimura, A.; Redding, T.W.; Coy, D.H.; Saffran, M.; Kong, Horm. Metab. Res. 13, 228-232, 1981
A:Title: Isolation, structure and synthesis of a heptapeptide with in vitro ACTH-releasing
A:Reference number: A01417; MUID:81213980; PMID:6263778
A:Accession: A01417
A:Molecule type: protein
A:Residues: 1-7 <CHA>
A:Cross-references: UNIPROT:P01153; UNIPARC:UPI000012CFC6
C:Superfamily: hypothalamic heptapeptide
C:Keywords: hypothalamus

Query Match 25.7%; Score 9; DB 1; Length 7;

Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 LY 7
||
DB 2 IY 3

RESULT 6
S19630
ribosomal protein L30 - Streptomyces griseus (fragment)
C:Species: Streptomyces griseus
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 05-Oct-2004
C:Accession: S19630
R:Ochi, K.
Int. J. Syst. Bacteriol. 42, 144-150, 1992
A:Title: Electrophoretic heterogeneity of ribosomal protein At-L30 among actinomycete genera
A:Reference number: S19630; MUID:92144363; PMID:1736962
A:Accession: S19630
A:Molecule type: protein
A:Residues: 1-7 <OCH>
A:Cross-references: UNIPARC:UPI0000177352
A:Experimental source: strain IFO 13189
C:Superfamily: Ribosomal protein L30p
C:Keywords: protein biosynthesis; ribosome

Query Match 25.7%; Score 9; DB 2; Length 7;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVS 3
||
DB 4 KIT 6

RESULT 7
PQ0663
membrane protein - porcine epidemic diarrhea virus (isolate Belgian CV777) (fragment)
C:Species: porcine epidemic diarrhea virus
C:Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 08-Oct-1999
C:Accession: PQ0663
R:Bridgen, A.; Duarte, M.; Tobler, K.; Laude, H.; Ackermann, M.
J. Gen. Virol. 74, 1795-1804, 1993
A:Title: Sequence determination of the nucleocapsid protein gene of the porcine epidemic
A:Title: Sequence determination of the nucleocapsid protein gene of the porcine epidemic
A:Title: Sequence determination of the nucleocapsid protein gene of the porcine epidemic
A:Reference number: JQ2191; MUID:93389433; PMID:8397280
A:Accession: PQ0663
A:Molecule type: mRNA
A:Residues: 1-7 <BRI>
A:Cross-references: UNIPARC:UPI0000170FAC; GB:Z14976; NID:g311650; PIDN:CAA78699.1; PID: C:Comment: This virus is coronavirus related to human coronavirus 229E.
C:Keywords: membrane protein

Query Match 25.7%; Score 9; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KV 2
||
DB 2 KV 3

RESULT 8
A28709
phosphonoacetaldehyde hydrolase - Bacillus cereus (fragment)
C:Species: Bacillus cereus
C:Date: 22-Aug-1988 #sequence_revision 22-Aug-1988 #text_change 30-Sep-1993
C:Accession: A28709
R:Olson, D.B.; Hepburn, T.W.; Moos, M.; Mariano, P.S.; Dunaway-Mariano, D.
Biochemistry 27, 2229-2234, 1988
A:Title: Investigation of the Bacillus cereus phosphonoacetaldehyde hydrolase. Evidence
A:Reference number: A28709; MUID:88241058; PMID:3132206

A;Accession: A28709

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-7 <OLS>

A;Cross-references: UNIPARC:UPI000017AC9C

Query Match 25.7%; Score 9; DB 2; Length 7;
Best Local Similarity 25.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVSN 4
| :
Db 2 KIDH 5

RESULT 9

PN0150
omega-gliadine 1' - Aegilops longissima (fragment)

C;Species: Aegilops longissima

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C;Accession: PN0150

R;Odintsova, T.I.; Egorov, T.A.

Biokhimiia 55, 509-516, 1990

A;Title: N-Terminal sequences of omega-gliadins of Aegilops longissima: On the origin of

A;Reference number: PN0146; MUID:90283493; PMID:2354218

A;Accession: PN0150

A;Molecule type: protein

A;Residues: 1-7 <ODI>

A;Cross-references: UNIPARC:UPI000017B0D2

A;Experimental source: strain K-907

Query Match 25.7%; Score 9; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 SNRL 6
| :
Db 1 SRQL 4

RESULT 10

S78024
ribosomal protein Yml21, mitochondrial - yeast (Saccharomyces cerevisiae) (fragment)

C;Species: Saccharomyces cerevisiae

C;Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 14-Nov-1997

C;Accession: S78024

R;Kitakawa, M.; Graack, H.R.; Grohmann, L.; Goldschmidt-Reisin, S.; Herfurth, E.; Wittma

Eur. J. Biochem. 245, 449-456, 1997

A;Title: Identification and characterization of the genes for mitochondrial ribosomal pr

A;Reference number: S78018; MUID:97296414; PMID:9151978

A;Accession: S78024

A;Molecule type: protein

A;Residues: 1-7 <KIT>

A;Cross-references: UNIPARC:UPI000017B33C

C;Genetics:

A;Genome: nuclear

C;Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 25.7%; Score 9; DB 2; Length 7;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 VSNRL 6
| :
Db 2 LXNLL 6

RESULT 11

PH0932

T-cell receptor beta chain V-D-J region (clone 3) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C;Accession: PH0932

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergy

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0932

A;Molecule type: mRNA

A;Residues: 1-7 <GOL>

A;Cross-references: UNIPARC:UPI000017C9E4

A;Experimental source: complete Freund's adjuvant-immunized lymph node

C;Keywords: T-cell receptor

Query Match 25.7%; Score 9; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RL 6
| :
Db 6 RL 7

RESULT 12

A28340
myomodulin - California sea hare

C;Species: Aplysia californica (California sea hare)

C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004

C;Accession: A28340

R;Cropper, E.C.; Tenenbaum, R.; Kolks, M.A.G.; Kupfermann, I.; Weiss, K.R.

Proc. Natl. Acad. Sci. U.S.A. 84, 5483-5486, 1987

A;Title: Myomodulin: A bioactive neuropeptide present in an identified cholinergic bucc

A;Reference number: A28340; MUID:87261010; PMID:3474664

A;Accession: A28340

A;Molecule type: protein

A;Residues: 1-7 <CRO>

A;Cross-references: UNIPROT:PI5513; UNIPARC:UPI000017BD99

Query Match 25.7%; Score 9; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RL 6
| :
Db 6 RL 7

RESULT 13

ECMOCR

catch-relaxing peptide - blue mussel

N;Alternate names: CARP

C;Species: Mytilus edulis (blue mussel)

C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 16-Aug-2004

C;Accession: A29342

R;Hirata, T.; Kubota, I.; Takabatake, I.; Kawahara, A.; Shimamoto, N.; Muneoka, Y.

Brain Res. 422, 374-376, 1987

A;Title: Catch-relaxing peptide isolated from Mytilus pedal ganglia.

A;Reference number: A29342; MUID:88052022; PMID:3676797

A;Accession: A29342

A;Molecule type: protein

A;Residues: 1-7 <HIR>

A;Cross-references: UNIPROT:PI0420; UNIPARC:UPI0000126FB4

C;Comment: This peptide exhibits both potentiating (contraction) and inhibitory (relaxa

C;Keywords: amidated carboxyl end; hormone; retractor muscle

F;7/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 25.7%; Score 9; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RL 6
| :
Db 6 RL 7

RESULT 14

A60139
 fatty-acid synthase (EC 2.3.1.85) - rabbit (fragment)
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 26-May-2000
 C:Accession: A60139
 R:Hardie, D.G.; Dewart, K.B.; Aitken, A.; McCarthy, A.D.
 Biochim. Biophys. Acta 828, 380-382, 1985
 A:Title: Amino acid sequence around the reactive serine residue of the thioesterase domain
 A:Reference number: A60139; MUID:85175165; PMID:3921056
 A:Accession: A60139
 A:Molecule type: protein
 A:Residues: 1-7 <HAR>

A:Cross-references: UNIPARC:UPI00001753A5
 C:Superfamily: rat fatty-acid synthase; 3-oxoacyl-[acyl-carrier-protein] synthase I homologue
 C:Keywords: acyltransferase; carrier protein; coenzyme A; homodimer; multifunctional enzyme
 P:5/Active site: Ser (of oleoyl-[acyl-carrier-protein] hydrolase) #status experimental

Query Match 22.9%; Score 8; DB 2; Length 7;
 Best Local Similarity 33.3%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 VSNRLY 7
 |:
 Db 1 VAGYSY 6

RESULT 15

B39127
 phosphotransferase system enzyme II (EC 2.7.1.69) - Escherichia coli (fragment)
 C:Species: Escherichia coli
 C:Date: 27-Nov-1991 #sequence_revision 27-Nov-1991 #text_change 08-Oct-1999
 C:Accession: B39127
 R:Hardesty, C.; Ferran, C.; DiRienzo, J.M.
 J. Bacteriol. 173, 449-456, 1991
 A:Title: Plasmid-mediated sucrose metabolism in Escherichia coli: characterization of sc

rin.
 A:Reference number: A39127; MUID:91100329; PMID:1846143
 A:Accession: B39127
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-7 <HAR>
 A:Cross-references: UNIPARC:UPI0000170D6E; GB:M38416; NID:9155142; PIDN:AAA98418.1; PID:
 C:Keywords: phosphotransferase

Query Match 22.9%; Score 8; DB 2; Length 7;
 Best Local Similarity 33.3%; Pred. No. 2.8e+05;
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVS 3
 ::
 Db 5 QIS 7

Search completed: December 30, 2005, 14:52:02
 Job time : 43 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2005, 14:27:11 ; Search time 227 Seconds
(without alignments)
21.756 Million cell updates/sec

Title: US-10-735-916A-4

Perfect score: 35

Sequence: 1 KVSNNLY 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 107

Minimum DB seq length: 7

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Uniprot_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	15	42.9	7	2	O50556 ACTAC
2	12	34.3	7	2	Q65578 9ALPH
3	11	31.4	7	1	ALL7 CVPO
4	11	31.4	7	1	FAR1 PROCL
5	11	31.4	7	1	UN06 PINPS
6	11	31.4	7	2	Q9YI09 ADE04
7	11	31.4	7	2	Q9YI00 ADE07
8	11	31.4	7	2	Q9YVE3 ADE07
9	11	31.4	7	2	Q9YQ10 SCORO
10	11	31.4	7	2	O99182 9SMEG
11	10	28.6	7	2	F83492 BIOOC
12	10	28.6	7	2	Q95945 YEAST
13	9	25.7	7	1	CARP MYTED
14	9	25.7	7	1	E105 LITRU
15	9	25.7	7	1	HY7 FIG
16	9	25.7	7	2	P92210 AGRCR
17	9	25.7	7	2	P92214 9POAL
18	9	25.7	7	2	P92218 9POAL
19	9	25.7	7	2	P92221 BROIN
20	9	25.7	7	2	P92226 CRIDE
21	9	25.7	7	2	P92372 9FOAL
22	9	25.7	7	2	P92381 9FOAL
23	9	25.7	7	2	P92385 HORWA
24	9	25.7	7	2	P92387 9POAL
25	9	25.7	7	2	P92390 HETPI
26	9	25.7	7	2	P92393 HORVU
27	9	25.7	7	2	P92403 LOPEL
28	9	25.7	7	2	P92421 PSAFR
29	9	25.7	7	2	P92425 PSEPI
30	9	25.7	7	2	P92427 PERIDCTYON
31	9	25.7	7	2	P92430 AEGTYP

32 9 25.7 7 2 P92440 THIBE
33 9 25.7 7 2 P92442 TARCM
34 9 25.7 7 2 Q47029 ENTCL
35 9 25.7 7 2 Q8GL04 BORBU
36 9 25.7 7 2 Q8GL12 BORBU
37 9 25.7 7 2 P70804 AZOVI
38 8 22.9 7 1 IPYR CANAL
39 8 22.9 7 1 UF04 MOUSE
40 8 22.9 7 2 Q15903 HUMAN
41 8 22.9 7 2 Q47505 ECOLI
42 8 22.9 7 2 O55184 RAT
43 8 22.9 7 2 Q63480 RAT
44 7 20.0 7 1 ALL2 CARMA
45 7 20.0 7 1 ALL3 CARMA

P92440 thinopyrum
P92442 taeniatheru
Q47029 enterobacte
Q8GL04 borrelia bu
Q8GL12 borrelia bu
P70804 azotobacter
P83777 candida alb
P83642 mus musculu
Q15903 homo sapien
Q47505 escherichia
O55184 rattus norv
Q63480 rattus norv
P81805 carcinus ma
P81806 carcinus ma

ALIGNMENTS

RESULT 1
O50556 ACTAC
ID O50556 ACTAC PRELIMINARY; PRT; 7 AA.
AC O50556;
DT 01-JUN-1998 (T-EMBLrel. 06, Created)
DT 01-JUN-1998 (T-EMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)
DE GlyA (Fragment).
GN Name=glyA;
OS Actinobacillus actinomycetemcomitans (Haemophilus actinomycetemcomitans).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Actinobacillus.
OX NCBI_TaxID=714;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 33384;
RX MEDLINE=96355846; PubMed=8751884;
RA Kolodrubetz D., Spitznagel J. Jr., Wang B., Phillips L.H., Jacobs C., Kraig E.;
RT "cis Elements and trans factors are both important in strain-specific regulation of the leukotoxin gene in Actinobacillus actinomycetemcomitans";
RT actinomycetemcomitans";
RL Infect. Immun. 64:3451-3460(1996).
DR ENBL; US1862; AAB88721.1; -; Genomic_DNA.
FT NON TER 1
SQ SEQUENCE 7 AA; 832 MW; 6DCB42D767340420 CRC64;

Query Match 42.9%; Score 15; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NRL 6
DB 1 NRL 3

RESULT 2
Q65578 9ALPH
ID Q65578 9ALPH PRELIMINARY; PRT; 7 AA.
AC Q65578;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Hypothetical protein (fragment).
OS Bovine herpesvirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=10320;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Cooper;
RX MEDLINE=95313343; PubMed=7793062;
RA Vicek C., Benes V., Lu Z., Kutish G.F., Paces V., Rock D.,

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RA Letchworth G.J., Schwyz M.;
RT "Nucleotide sequence analysis of a 30-kb region of the bovine
RT herpesvirus 1 genome which exhibits a colinear gene arrangement with
RT the UL21 to UL4 genes of herpes simplex virus.";
RL Virolgy 210:100-108(1995).
DR EMBL; 248053; CAA88130.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 7 AA; 758 MW; 6DD33455B1F1B1C0 CRC64;

Query Match 34.3%; Score 12; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.2e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SNR 5
DB 4 SNK 6

RESULT 3
ALL7_CYDPO STANDARD; PRT; 7 AA.
ID ALL7_CYDPO
AC P82158;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Cydiaastatin-7.
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=82600;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829; DOI=10.1016/S0196-9781(97)00188-5;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309(1997).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the allatostatin family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 873 MW; 672879CAB8569350 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 7;
Best Local Similarity 33.3%; Pred. No. 2.2e+06;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 RLY 7
DB 1 KMY 3

RESULT 4
FAR1_PROCL STANDARD; PRT; 7 AA.
ID FAR1_PROCL
AC P38459;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cardioexcitatory FMRFamide homolog NFI.
OS Procamburus clarkii (Red swamp crayfish).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;

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OC Astacoidea; Cambaridae; Procamburus.
OX NCBI_TaxID=6728;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Pericardial organs;
RX MEDLINE=93248032; PubMed=8387183; DOI=10.1016/0196-9781(93)90021-8;
RA Mercier A.J., Orchard I., Tebrugge V., Skerrett M.;
RT "Isolation of two FMRFamide-related peptides from crayfish pericardial
RT organs.";
RL Peptides 14:137-143(1993).
CC -1- FUNCTION: Increases the rate and amplitude of spontaneous
CC contractions of semi-isolated hearts. Increases the amplitude of
CC excitatory postsynaptic potentials in abdominal extensor muscle.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 966 MW; 69D40729C4540420 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NR 5
DB 1 NR 2

RESULT 5
UN06_PINPS STANDARD; PRT; 7 AA.
ID UN06_PINPS
AC P81675;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Unknown protein from 2D-PAGE of needles (N141) (Fragment).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RX DOI=10.1002/(SICI)1522-2683(19990101)20:4<1098::AID-ELPS1098>3.3.CO;2-Q;
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Flomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 6.6, its MW is: 25 kDa.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
KW Direct protein sequencing.
FT NON_TER 1
FT NON_TER 7
SQ SEQUENCE 7 AA; 823 MW; 69D76724486B5740 CRC64;

Query Match 31.4%; Score 11; DB 1; Length 7;

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Best Local Similarity 100.0%; Pred. No. 2.2e+06; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 6 LY 7
| |
Db 1 LY 2

RESULT 6
Q9YIQ9_ADE04
ID Q9YIQ9_ADE04 PRELIMINARY; PRT; 7 AA.
AC Q9YIQ9;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE PVI core protein (Fragment).
GN Name=pVI;
OS Human adenovirus 4 (HAdV-4).
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=28280;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2-G T95-873;
RX MEDLINE=99175282; PubMed=10074533;
RA Crawford-Miksz L.K.; Nang R.N.; Schnurr D.P.;
RT "Strain variation in adenovirus serotypes 4 and 7a causing acute
respiratory disease."
RL J. Clin. Microbiol. 37:1107-1112(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2-G T95-873;
RA Crawford-Miksz L.K.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF065064; AAD03659.1; -; Genomic_DNA.
FT NON_TER 1 1
SQ SEQUENCE 7 AA; 980 MW; 7B5EA414140322A0 CRC64;

Query Match 31.4%; Score 11; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 RLY 7
| |
Db 5 RCY 7

RESULT 7
Q9YIRO_ADE07
ID Q9YIRO_ADE07 PRELIMINARY; PRT; 7 AA.
AC Q9YIRO;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE PVI core protein (Fragment).
GN Name=pVI;
OS Human adenovirus type 7a.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=85755;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Kn T96-0620;
RX MEDLINE=99175282; PubMed=10074533;
RA Crawford-Miksz L.K.; Nang R.N.; Schnurr D.P.;
RT "Strain variation in adenovirus serotypes 4 and 7a causing acute
respiratory disease."
RL J. Clin. Microbiol. 37:1107-1112(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Kn T96-0620;
RA Crawford-Miksz L.K.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF065068; AAD03668.1; -; Genomic_DNA.
FT NON_TER 1 1

SQ SEQUENCE 7 AA; 980 MW; 7B5EA414140322A0 CRC64;

Query Match 31.4%; Score 11; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 RLY 7
| |
Db 5 RCY 7

RESULT 8
Q9YVE3_ADE07
ID Q9YVE3_ADE07 PRELIMINARY; PRT; 7 AA.
AC Q9YVE3;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PVI core protein (Fragment).
GN Name=pVI;
OS Human adenovirus 7 (HAdV-7).
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=10519;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Gomen;
RX MEDLINE=99175282; PubMed=10074533;
RA Crawford-Miksz L.K.; Nang R.N.; Schnurr D.P.;
RT "Strain variation in adenovirus serotypes 4 and 7a causing acute
respiratory disease."
RL J. Clin. Microbiol. 37:1107-1112(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Gomen;
RA Crawford-Miksz L.K.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF065065; AAD03662.1; -; Genomic_DNA.
FT NON_TER 1 1
SQ SEQUENCE 7 AA; 980 MW; 7B5EA414140322A0 CRC64;

Query Match 31.4%; Score 11; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 RLY 7
| |
Db 5 RCY 7

RESULT 9
Q9YQ10_9COCO
ID Q9YQ10_9COCO PRELIMINARY; PRT; 7 AA.
AC Q9YQ10;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical fusion protein.
OS Transmissible gastroenteritis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus; Group 1 species.
OX NCBI_TaxID=11149;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=88078100; PubMed=2825819; DOI=10.1016/0300-9084(87)90178-7;
RA Raeschaert D., Gelfi J., Laude H.;
RT "Enteric coronavirus TGSV: partial sequence of the genomic RNA, its
organization and expression."
RL Biochimie 69:591-600(1987).
RN [2]
RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=95159435; PubMed=7856095;
RA Eleouet J., Raeschaert D., Lambert P., Levy L., Vende P., Laude H.;
RT "Complete sequence (20 kilobases) of the polyprotein-encoding gene 1

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RT of transmissible gastroenteritis virus.";
RL Virology 206:817-822(1995).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99099045; PubMed=9882359;
RA Izeta A., Smerdou C., Alonso S., Penzes Z., Mendez A., Piana-Duran J.,
RA Enjuanes L.;
RT "Replication and packaging of transmissible gastroenteritis
RT coronavirus-derived synthetic minigenomes.";
RL J. Virol. 73:1535-1545(1999).
DR EMBL; AJ011482; CAA09625.1; -; Genomic_RNA.
KW Hypothetical protein.
SQ SEQUENCE 7 AA; 927 MW; 69D6D7273B5726F0 CRC64;

Query Match 31.4%; Score 11; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LY 7
DB 2 LY 3

RESULT 10
O99182_9SMEG
ID O99182_9SMEG PRELIMINARY; PRT; 7 AA.
AC O99182;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Cytochrome oxidase I (Fragment).
GN Name=COI;
OS Gnatholebias zonatus.
OG Mitochondrion.
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Cyprinodontiformes; Aplocheilidae; Rivulinae; Gnatholebias.
OX NCBI_TaxID=135316;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20072928; PubMed=10603257; DOI=10.1006/mpev.1999.0656;
RA Murphy W.J., Thomerson J.E., Collier G.E.;
RT "Phylogeny of the Neotropical killifish family Rivulidae
RT (Cyprinodontiformes, Aplocheiloidei) inferred from mitochondrial DNA
RT sequences.";
RL Mol. Phylogenet. Evol. 13:289-301(1999).
DR EMBL; AF002591; AAD01074.1; -; Genomic DNA.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 1 1
SQ SEQUENCE 7 AA; 899 MW; 672721F6CB572030 CRC64;

Query Match 31.4%; Score 11; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LY 7
DB 2 LY 3

RESULT 11
P83492_BIOOC
ID P83492_BIOOC PRELIMINARY; PRT; 7 AA.
AC P83492;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Alkaline protease Gr3 (EC 3.4.21.-) (Fragment).
OS Bionectria ochroleuca (Glocladium roseum).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Bionectriaceae; Bionectria.

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OX NCBI_TaxID=29856;
RN [1]
RP PROTEIN SEQUENCE, FUNCTION, AND SUBCELLULAR LOCATION.
RC STRAIN=Gr87;
RA Zhao M., Zhang K.;
RL Submitted (DEC-2002) to Swiss-Prot.
CC -!- FUNCTION: Acts as a serine protease.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0004252; F:serine-type endopeptidase activity; NAS.
DR InterPro; IPR000209; Pept_S8_S53.
DR PROSITE; PS00136; SUBTILASE_ASF; PARTIAL.
DR PROSITE; PS00137; SUBTILASE_HIS; PARTIAL.
DR PROSITE; PS00138; SUBTILASE_SER; PARTIAL.
KW Hydrolase; Serine protease.
FT NON TER 7 7
SQ SEQUENCE 7 AA; 688 MW; 776DD455A6C1ADB0 CRC64;

Query Match 28.6%; Score 10; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SN 4
DB 4 SN 5

RESULT 12
Q95945_YEAST
ID Q95945_YEAST PRELIMINARY; PRT; 7 AA.
AC Q95945;
DT 01-FEB-1997 (TReMBLrel. 02, Created)
DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Inside intron 5 (Fragment).
OS Saccharomyces cerevisiae (Baker's yeast).
OG Mitochondrion.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=D273-10B;
RX MEDLINE=81069885; PubMed=6254986;
RA Bonitz S.G., Coruzzi G., Thalenfeld B.E., Tzagoloff A., Macino G.;
RT "Assembly of the mitochondrial membrane system. Structure and
RT nucleotide sequence of the gene coding for subunit 1 of yeast
RT cytochrome oxidase.";
RL J. Biol. Chem. 255:11927-11941(1980).
DR EMBL; V00694; CAA24066.1; -; Genomic DNA.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 1 1
SQ SEQUENCE 7 AA; 859 MW; 75B7232362CDC460 CRC64;

Query Match 28.6%; Score 10; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.2e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVS 3
DB 5 KLS 7

RESULT 13
CARP_MYTED
ID CARP_MYTED STANDARD; PRT; 7 AA.
AC P10420;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Catch-relaxing peptide (CARP).

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OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OC Mytiloidea; Mytilidae; Mytilinae; Mytilus.
RN NCBI_TaxID=6550;
[1]
RN PROTEIN SEQUENCE.
RX MEDLINE=88052022; PubMed=3676797;
RA Hirata T., Kubota I., Takabatake I., Kawahara A., Shimamoto N.,
RA Muneoka Y.;
RT "catch-relaxing peptide isolated from Mytilus pedal ganglia.";
RL Brain Res. 422:374-376(1987).
CC -|- FUNCTION: This peptide exhibits both potentiating (contraction)
CC and inhibitory (relaxation) effects on the anterior bysuss
CC retractor muscle.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC PIR; A29342; ECMUCR.
DR Amidation; Direct protein sequencing; Hormone.
KW Leucine amide.
FT MOD RES 7
SQ SEQUENCE 7 AA; 831 MW; 6734072687669DB0 CRC64;

Query Match 25.7%; Score 9; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RL 6
Db 6 RL 7

RESULT 14
EI05 LITRU STANDARD; PRT; 7 AA.
ID P82101;
AC P82101;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Electrin-5.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylinae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RN PROTEIN SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Expressed by the skin glands.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC Amidation; Amphibian defense peptide; Direct protein sequencing.
KW MOD RES 7
FT Alanine amide.
SQ SEQUENCE 7 AA; 834 MW; 6DD058076B0B5030 CRC64;

Query Match 25.7%; Score 9; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.2e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 LY 7
Db 1 IY 2

RESULT 15
HY7 PIG STANDARD; PRT; 7 AA.
ID HY7 PIG
AC P01153;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hypothalamic heptapeptide.
DE Hypothalamic heptapeptide.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RN PROTEIN SEQUENCE, AND SYNTHESIS.
RX MEDLINE=81213980; PubMed=6263778;
RA Chang R.C.C., Huang W.-Y., Arimura A., Redding T.W., Coy D.H.,
RA Saffran M., Kong A., Hamilton J.W., Coun D.V., Schally A.V.;
RT "Isolation, structure and synthesis of a heptapeptide with in vitro
RT ACTH-releasing activity from porcine hypothalamus.";
RL Horm. Metab. Res. 13:228-232(1981).
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC PIR; A01417; NYPG7.
DR Direct protein sequencing.
KW SEQUENCE 7 AA; 957 MW; 632B45B1FB5059A0 CRC64;

Query Match 25.7%; Score 9; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.2e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 LY 7
Db 2 IY 3

Search completed: December 30, 2005, 14:51:14
Job time : 229 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2005, 14:44:07 ; Search time 45 Seconds
(without alignments)
12.861 Million cell updates/sec

Title: US-10-735-916A-4

Perfect score: 35

Sequence: 1 KVSNNLY 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 17689

Minimum DB seq length: 7

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5 COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/6 COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/H COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/PTUS COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/RE COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	68.6	7	1	US-08-053-171-28
2	24	68.6	7	1	US-08-560-558B-30
3	24	68.6	7	2	US-09-217-268B-30
4	24	68.6	7	2	US-09-563-222C-30
5	24	68.6	7	2	US-09-914-695-22
6	24	68.6	7	2	US-09-518-737-9
7	21	60.0	7	1	US-08-244-626-6
8	20	57.1	7	2	US-10-226-795-29
9	19	54.3	7	2	US-09-563-222C-9
10	19	54.3	7	2	US-09-254-180C-5
11	19	54.3	7	2	US-09-724-409-4
12	19	54.3	7	2	US-09-724-530-4
13	19	54.3	7	2	US-09-623-548A-654
14	19	54.3	7	2	US-09-657-276-654
15	19	54.3	7	2	US-09-328-296-4
16	18	51.4	7	2	US-09-128-572-47
17	18	51.4	7	2	US-09-782-385A-47
18	17	48.6	7	1	US-08-672-610A-23
19	17	48.6	7	1	US-08-790-912-8
20	17	48.6	7	2	US-09-187-859-2663
21	17	48.6	7	2	US-09-187-859-2693
22	17	48.6	7	2	US-09-187-859-3177
23	17	48.6	7	2	US-09-187-859-3267
24	17	48.6	7	2	US-09-839-542B-2663
25	17	48.6	7	2	US-09-839-542B-2693
26	17	48.6	7	2	US-09-839-542B-3177
27	17	48.6	7	2	US-09-839-542B-3267

28	17	48.6	7	2	US-09-535-852-521	Sequence 521, App
29	17	48.6	7	2	US-09-535-852-611	Sequence 611, App
30	17	48.6	7	2	US-09-206-786A-23	Sequence 23, Appl
31	17	48.6	7	2	US-09-936-588-129	Sequence 129, App
32	17	48.6	7	2	US-10-006-869-2693	Sequence 2663, Ap
33	17	48.6	7	2	US-10-006-869-3177	Sequence 3177, Ap
34	17	48.6	7	2	US-10-006-869-3267	Sequence 3267, Ap
35	17	48.6	7	1	US-08-153-799-11	Sequence 11, Appl
36	16	45.7	7	1	US-08-793-490-7	Sequence 7, Appl
37	16	45.7	7	2	US-09-128-572-45	Sequence 45, Appl
38	16	45.7	7	2	US-09-326-718-5	Sequence 5, Appl
39	16	45.7	7	2	US-09-336-093-11	Sequence 11, Appl
40	16	45.7	7	2	US-08-952-445-8	Sequence 8, Appl
41	16	45.7	7	2	US-09-461-325-321	Sequence 321, App
42	16	45.7	7	2	US-08-135-319A-21	Sequence 21, Appl
43	16	45.7	7	2	US-09-557-465D-11	Sequence 11, Appl
44	16	45.7	7	2	US-10-012-542-321	Sequence 321, App
45	16	45.7	7	2		

ALIGNMENTS

RESULT 1
US-08-053-171-28
; Sequence 28, Application US/08053171
; Patent No. 5562903
; GENERAL INFORMATION:
; APPLICANT: Co, Loibner
; TITLE OF INVENTION: Antibody Derivatives
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,171
; FILING DATE: 22-APR-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-54-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..7
; OTHER INFORMATION: /note= "Second
; OTHER INFORMATION: complementarity-determining region (CDR2) of
; OTHER INFORMATION: BR55-2 antibody light chain"
US-08-053-171-28

Query Match 68.6%; Score 24; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 KVSNR 5
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Db      1 KVSNR 5

RESULT 2
US-08-560-558E-30
; Sequence 30, Application US/08560558E
; Patent No. 5891996
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Humanized and chimeric monoclonal
; TITLE OF INVENTION: antibodies that recognize epidermal growth factor receptor
; TITLE OF INVENTION: EGF-R; diagnostic and therapeutic use.
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allen C. Turner, TRASK, BRITT & ROSSA
; STREET: P.O. Box 2250
; CITY: Salt Lake City
; STATE: Utah
; COUNTRY: United States of America
; ZIP: 84110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: WINDOWS95
; SOFTWARE: WordPerfect 5.1/5.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/560,558E
; FILING DATE: No. 5891996ember 17, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Turner, Allen C.
; REGISTRATION NUMBER: 33,041
; REFERENCE/DOCKET NUMBER: 2720US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (801) 532-1922
; TELEFAX: (801) 531-9168
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-560-558E-30

Query Match      68.6%; Score 24; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVSNR 5
      |||||
Db      1 KVSNR 5

RESULT 3
US-09-217-268B-30
; Sequence 30, Application US/09217268B
; Patent No. 6506883
; GENERAL INFORMATION:
; APPLICANT: Mateo de Acosta del Rio, Christina M
; APPLICANT: Rodriguez, Rolando P
; APPLICANT: Frias, Ernesto M
; TITLE OF INVENTION: Humanized and Chimeric Monoclonal Antibodies That Recognize Epide
; TITLE OF INVENTION: Growth Factor Receptor (EGF-R); Diagnostic and Therapeutic Use
; FILE REFERENCE: 2720.IUS
; CURRENT APPLICATION NUMBER: US/09/217,268B
; CURRENT FILING DATE: 1998-12-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 7
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; TYPE: PRT
; ORGANISM: Murine
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: CDR of murine R3 antibody
US-09-217-268B-30

Query Match      68.6%; Score 24; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVSNR 5
      |||||
Db      1 KVSNR 5

RESULT 4
US-09-563-222C-30
; Sequence 30, Application US/09563222C
; Patent No. 6696620
; GENERAL INFORMATION:
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICH B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT APPLICATION NUMBER: US/09/563,222C
; CURRENT FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-563-222C-30

Query Match      68.6%; Score 24; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVSNR 5
      |||||
Db      1 KVSNR 5

RESULT 5
US-09-914-695-22
; Sequence 22, Application US/09914695
; Patent No. 6706487
; GENERAL INFORMATION:
; APPLICANT: Abdel-Meguid, Sherin
; APPLICANT: Ho, Yen Sen
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Taylor, Alexander H.
; TITLE OF INVENTION: Recombinant IL-18 Antagonists Useful in
; FILE REFERENCE: P50897
; CURRENT APPLICATION NUMBER: US/09/914,695
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: PCT/US00/07349
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/125,299
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
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US-09-914-695-22

Query Match 68.6%; Score 24; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSNR 5
Db 1 KVSNR 5

RESULT 6

US-09-518-737-9

; Sequence 9, Application US/09518737
; Patent No. 6709833
; GENERAL INFORMATION:
; APPLICANT: FUKUI, YASUHIRO
; APPLICANT: NAGATA, SATOSHI
; APPLICANT: SHIRAI, RYUICHI
; APPLICANT: SAITO, NAOKI
; TITLE OF INVENTION: MONOCLONAL ANTIBODY RECOGNIZING
; FILE REFERENCE: 1965/49618
; CURRENT APPLICATION NUMBER: US/09/518,737
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: JP 1999-250209
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-518-737-9

Query Match 68.6%; Score 24; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSNR 5
Db 1 KVSNR 5

RESULT 7

US-08-244-626-6

; Sequence 6, Application US/08244626
; Patent No. 5502167
; GENERAL INFORMATION:
; APPLICANT: Waldmann, Herman
; APPLICANT: Walsh, Louise
; APPLICANT: Crowe, James Scott
; APPLICANT: Lewis, Alan Peter
; TITLE OF INVENTION: CDR GRAFTED HUMANISED CHIMERIC T-CELL
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, p.c.
; STREET: 555 Thirteenth Street, N. W.
; CITY: Washington
; STATE: D. C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/244,626
; FILING DATE: July 15, 1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/GB92/02251
; FILING DATE: December 4, 1992
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Ernst, Barbara G.
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1808-153A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-244-626-6

Query Match 60.0%; Score 21; DB 1; Length 7;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSNR 5
Db 1 KVSNR 5

RESULT 8

US-10-226-795-29

; Sequence 29, Application US/10226795
; Patent No. 6875433
; GENERAL INFORMATION:
; APPLICANT: HART, MARY KATE
; APPLICANT: WILSON, JULIE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND COMPLEMENTARITY-DETERMINING
; FILE REFERENCE: ARMY 166
; CURRENT APPLICATION NUMBER: US/10/226,795
; CURRENT FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic light
; OTHER INFORMATION: chain of Mab EGP6D8-1-2 amino acid sequence
US-10-226-795-29

Query Match 57.1%; Score 20; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVSNR 5
Db 1 KASNR 5

RESULT 9

US-09-563-222C-9

; Sequence 9, Application US/09563222C
; Patent No. 6696620
; GENERAL INFORMATION:
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICH B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT APPLICATION NUMBER: US/09/563,222C
; CURRENT FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-563-222C-9

Query Match 54.3%; Score 19; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSNR 5
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Db 2 VSNR 5

RESULT 10
US-09-254-180C-5
; Sequence 5, Application US/09254180C
; Patent No. 677540
; GENERAL INFORMATION:
; APPLICANT: OKUMURA, Ko
; APPLICANT: EDA, Yasuyuki
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: USHIO, Yoshitaka
; APPLICANT: HIGUCHI, Hirofumi
; APPLICANT: NAKATA, Motomi
; TITLE OF INVENTION: Humanized Immunoglobulins Specifically Reactive to Fas Ligand or
; TITLE OF INVENTION: Fragments Thereof, and Apoptosis-Induced Site From Fas Ligand
; FILE REFERENCE: 050006-0055
; CURRENT APPLICATION NUMBER: US/09/254,180C
; CURRENT FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: PCT/JP97/02983
; PRIOR FILING DATE: 1997-08-27
; PRIOR APPLICATION NUMBER: 271546/1996
; PRIOR FILING DATE: 1996-09-20
; PRIOR APPLICATION NUMBER: 231472/1996
; PRIOR FILING DATE: 1996-09-02
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mouse
US-09-254-180C-5

Query Match 54.3%; Score 19; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSNR 5
|||
Db 2 VSNR 5

RESULT 11
US-09-724-409-4
; Sequence 4, Application US/09724409
; Patent No. 6838261
; GENERAL INFORMATION:
; APPLICANT: Siegall, Clay
; APPLICANT: Wahl, Alan
; APPLICANT: Francisco, Joseph
; APPLICANT: Fell, H. Perry
; TITLE OF INVENTION: RECOMBINANT ANTI-CD40 ANTIBODY AND USES THEREOF
; FILE REFERENCE: 9632-005
; CURRENT APPLICATION NUMBER: US/09/724,409
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/328,296
; PRIOR FILING DATE: 1999-06-08

; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-724-409-4

Query Match 54.3%; Score 19; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSNR 5
|||
Db 2 VSNR 5

RESULT 12
US-09-724-530-4
; Sequence 4, Application US/09724530
; Patent No. 6843989
; GENERAL INFORMATION:
; APPLICANT: Siegall, Clay
; APPLICANT: Wahl, Alan
; APPLICANT: Francisco, Joseph
; APPLICANT: Fell, H. Perry
; TITLE OF INVENTION: RECOMBINANT ANTI-CD40 ANTIBODY AND USES THEREOF
; FILE REFERENCE: 9632-005
; CURRENT APPLICATION NUMBER: US/09/724,530
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/328,296
; PRIOR FILING DATE: CURRENT FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-724-530-4

Query Match 54.3%; Score 19; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSNR 5
|||
Db 2 VSNR 5

RESULT 13
US-09-623-548A-654
; Sequence 654, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 654
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-623-548A-654

Query Match 54.3%; Score 19; DB 2; Length 7;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NRLY 7
||:|
Db 1 NRVY 4

RESULT 14

US-09-657-276-654
; Sequence 654, Application US/09657276
; Patent No. 6887470
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 654
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-654

Query Match 54.3%; Score 19; DB 2; Length 7;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NRLY 7
||:|
Db 1 NRVY 4

RESULT 15

US-09-328-296-4
; Sequence 4, Application US/09328296
; Patent No. 6946129
; GENERAL INFORMATION:
; APPLICANT: Siegall, Clay
; APPLICANT: Wahl, Alan
; APPLICANT: Francisco, Joseph
; APPLICANT: Fell, H. Perry
; TITLE OF INVENTION: RECOMBINANT ANTI-CD40 ANTIBODY AND USES THEREOF
; FILE REFERENCE: 9632-005

; CURRENT APPLICATION NUMBER: US/09/328,296
; CURRENT FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-328-296-4

Query Match 54.3%; Score 19; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSNR 5
||||
Db 2 VSNR 5

Search completed: December 30, 2005, 14:52:47
Job time : 46 secs

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OM protein - protein search, using sw model

Run on: December 30, 2005, 14:51:25 ; Search time 159 Seconds
(without alignments)
18.395 Million cell updates/sec

Title: US-10-735-916A-4

Perfect score: 35

Sequence: 1 KVSNNRLY 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 28819

Minimum DB seq length: 7

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main.*

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4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	7	5	US-10-735-916A-4
2	27	77.1	7	3	US-09-995-529-125
3	27	77.1	7	3	US-09-995-529-125
4	26	74.3	7	3	US-09-995-529-124
5	26	74.3	7	3	US-09-995-529-124
6	26	74.3	7	4	US-10-434-469-11
7	26	74.3	7	5	US-10-482-105-9
8	26	74.3	7	5	US-10-409-611-80
9	26	74.3	7	5	US-10-409-608A-22
10	26	74.3	7	5	US-10-500-207A-11
11	24	68.6	7	3	US-09-217-268B-30
12	24	68.6	7	3	US-09-796-744-9
13	24	68.6	7	3	US-09-518-737-9
14	24	68.6	7	3	US-09-563-222-30
15	24	68.6	7	3	US-09-995-529-34
16	24	68.6	7	3	US-09-995-529-34
17	24	68.6	7	4	US-10-231-452-6
18	24	68.6	7	4	US-10-226-435A-2
19	24	68.6	7	4	US-10-663-244-17
20	24	68.6	7	4	US-10-762-629-22
21	24	68.6	7	4	US-10-487-322-2
22	24	68.6	7	4	US-10-783-950-30
23	24	68.6	7	5	US-10-487-326-2
24	24	68.6	7	5	US-10-486-908-2
25	24	68.6	7	5	US-10-729-441-5
26	24	68.6	7	5	US-10-723-748-9
27	24	68.6	7	5	US-10-687-035-7

28 24 68.6 7 5 US-10-505-980-6 Sequence 6, Appli
29 24 68.6 7 5 US-10-512-527-2 Sequence 2, Appli
30 24 68.6 7 5 US-10-810-881A-57 Sequence 57, Appli
31 24 68.6 7 5 US-10-497-475-2 Sequence 2, Appli
32 24 68.6 7 5 US-10-897-406-5 Sequence 5, Appli
33 24 68.6 7 6 US-11-009-443-5 Sequence 5, Appli
34 24 68.6 7 6 US-11-009-443-17 Sequence 17, Appli
35 24 68.6 7 6 US-11-070-697-2 Sequence 2, Appli
36 24 68.6 7 6 US-11-094-718-9 Sequence 9, Appli
37 23 65.7 7 3 US-09-972-656-16 Sequence 16, Appli
38 23 65.7 7 5 US-10-877-773-116 Sequence 116, App
39 23 65.7 7 5 US-10-877-774-116 Sequence 116, App
40 23 65.7 7 5 US-10-946-647-271 Sequence 271, App
41 20 57.1 7 3 US-09-995-529-121 Sequence 121, App
42 20 57.1 7 3 US-09-995-529-121 Sequence 121, App
43 20 57.1 7 4 US-10-022-066-40 Sequence 40, Appli
44 20 57.1 7 4 US-10-022-066-141 Sequence 141, App
45 20 57.1 7 4 US-10-022-066-443 Sequence 443, App

ALIGNMENTS

RESULT 1
US-10-735-916A-4
; Sequence 4, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BUCK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-735-916A-4

Query Match 100.0%; Score 35; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNNRLY 7
Db 1 KVSNNRLY 7

RESULT 2
US-09-995-529-125
; Sequence 125, Application US/09995529
; Publication No. US20030099655A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying

```
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; TITLE OF INVENTION: Related Methods
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody mutation
US-09-995-529-125
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Query Match 77.1%; Score 27; DB 3; Length 7;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```
QY 1 KVSNNRLY 7
Db 1 KVSNNRFF 7
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RESULT 3

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US-09-995-529-125
; Sequence 125, Application US/09995529
; Publication No. US20040091482A9
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; TITLE OF INVENTION: Related Methods
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody mutation
US-09-995-529-125
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```
Query Match 77.1%; Score 27; DB 3; Length 7;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```
QY 1 KVSNNRLY 7
Db 1 KVSNNRFF 7
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RESULT 4

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US-09-995-529-124
; Sequence 124, Application US/09995529
; Publication No. US20030099655A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; TITLE OF INVENTION: Related Methods
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124
; LENGTH: 7
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```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody mutation
US-09-995-529-124
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Query Match 74.3%; Score 26; DB 3; Length 7;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```
QY 1 KVSNNRLY 7
Db 1 KVSNNRFF 7
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RESULT 5

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US-09-995-529-124
; Sequence 124, Application US/09995529
; Publication No. US20040091482A9
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; TITLE OF INVENTION: Related Methods
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody mutation
US-09-995-529-124
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Query Match 74.3%; Score 26; DB 3; Length 7;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY 1 KVSNNRLY 7
Db 1 KVSNNRFF 7
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RESULT 6

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US-10-434-469-11
; Sequence 11, Application US/10434469
; Publication No. US20040091480A1
; GENERAL INFORMATION:
; APPLICANT: Nobuo HANAI
; APPLICANT: Motoo YAMASAKI
; APPLICANT: Akira FURUYA
; APPLICANT: Akira TANAKA
; APPLICANT: Kenya SHITARA
; APPLICANT: Naoki SHIWADA
; TITLE OF INVENTION: Anti-fibroblast growth factor-8 monoclonal antibod
; FILE REFERENCE: 249-310
; CURRENT APPLICATION NUMBER: US/10/434,469
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: JP 08-081754
; PRIOR FILING DATE: 1996-04-03
; PRIOR APPLICATION NUMBER: US 08/832,236
; PRIOR FILING DATE: 1997-04-03
; PRIOR APPLICATION NUMBER: US 09/326,590
; PRIOR FILING DATE: 1999-06-07
; PRIOR APPLICATION NUMBER: US 09/876,040
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
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; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-434-469-11

Query Match      74.3%; Score 26; DB 4; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSURL 6
   |||||:
Db 1 KVSURI 6

RESULT 7
US-10-482-105-9
; Sequence 9, Application US/10482105
; Publication No. US20040253234A1
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD
; TITLE OF INVENTION: Humanized anti-FGF-8 antibody and the antibody fragment thereof
; FILE REFERENCE: 11399W01
; CURRENT APPLICATION NUMBER: US/10/482,105
; CURRENT FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: JP2001-196176
; PRIOR FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-482-105-9

Query Match      74.3%; Score 26; DB 5; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSURL 6
   |||||:
Db 1 KVSURI 6

RESULT 8
US-10-409-611-80
; Sequence 80, Application US/10409611
; Publication No. US20040259150A1
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
; TITLE OF INVENTION: Method of enhancing of binding activity of antibody composition b
; FILE REFERENCE: 249-303
; CURRENT APPLICATION NUMBER: US/10/409,611
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: P2002-106950
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-409-611-80

Query Match      74.3%; Score 26; DB 5; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSURL 6
   |||||:
Db 1 KVSURI 6
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RESULT 9
US-10-409-608A-22
; Sequence 22, Application US/10409608A
; Publication No. US20050031613A1
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
; TITLE OF INVENTION: Therapeutic agent for patients having human FcγRIIIa
; FILE REFERENCE: 249-304
; CURRENT APPLICATION NUMBER: US/10/409,608A
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: 2002-106951
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-409-608A-22

Query Match      74.3%; Score 26; DB 5; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSURL 6
   |||||:
Db 1 KVSURI 6

RESULT 10
US-10-500-207A-11
; Sequence 11, Application US/10500207A
; Publication No. US20050175608A1
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD
; TITLE OF INVENTION: AGENT FOR TREATING ARTHRITIS
; FILE REFERENCE: 1442
; CURRENT APPLICATION NUMBER: US/10/500,207A
; CURRENT FILING DATE: 2004-06-28
; PRIOR APPLICATION NUMBER: JP2001-400677
; PRIOR FILING DATE: 2001-12-28
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-500-207A-11

Query Match      74.3%; Score 26; DB 5; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSURL 6
   |||||:
Db 1 KVSURI 6

RESULT 11
US-09-217-268B-30
; Sequence 30, Application US/09217268B
; Patent No. US20020065398A1
; GENERAL INFORMATION:
; APPLICANT: Mateo de Acosta del Rio, Christina M
; APPLICANT: Rodriguez, Rolando P
; APPLICANT: Frias, Ernesto M
; TITLE OF INVENTION: Humanized and Chimeric Monoclonal Antibodies That Recognize Epid
; FILE REFERENCE: 2720.1US
; CURRENT APPLICATION NUMBER: US/09/217,268B
; CURRENT FILING DATE: 1998-12-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 30
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Murine
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: CDR of murine R3 antibody
US-09-217-268B-30

Query Match      68.6%; Score 24; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNR 5
Db 1 KVSNR 5

RESULT 12
US-09-796-744-9
; Sequence 9, Application US/09796744
; Patent No. US20020098527A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: SHOJI, EMI
; APPLICANT: SAKURADA, MIKKIKO
; APPLICANT: FURUYA, AKIKO
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: NIWA, RINPEI
; APPLICANT: SHIBATA, KENJI
; APPLICANT: YAMASAKI, MOTOO
; TITLE OF INVENTION: GENE RECOMBINANT ANTIBODY AND ANTIBODY FRAGMENT THEREOF
; FILE REFERENCE: 249-170
; CURRENT APPLICATION NUMBER: US/09/796,744
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: JP 2000-59508
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: JP 2000-401563
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-796-744-9

Query Match      68.6%; Score 24; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNR 5
Db 1 KVSNR 5

RESULT 13
US-09-518-737-9
; Sequence 9, Application US/09518737
; Publication No. US20030008321A1
; GENERAL INFORMATION:
; APPLICANT: FUKUI, YASUHIISA
; APPLICANT: NAGATA, SATOSHI
; APPLICANT: SHIRAI, RYUICHI
; APPLICANT: SAITO, NAOAKI
; TITLE OF INVENTION: MONOCLONAL ANTIBODY RECOGNIZING
; FILE REFERENCE: 1965/49618
; CURRENT APPLICATION NUMBER: US/09/518,737
; CURRENT FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: JP 1999-250209
; PRIOR FILING DATE: 1999-09-03

; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-518-737-9

Query Match      68.6%; Score 24; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNR 5
Db 1 KVSNR 5

RESULT 14
US-09-563-222-30
; Sequence 30, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: HIATT, Andrew
; APPLICANT: HEIN, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; FILE REFERENCE: 310098.406
; CURRENT APPLICATION NUMBER: US/09/563,222
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-563-222-30

Query Match      68.6%; Score 24; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNR 5
Db 1 KVSNR 5

RESULT 15
US-09-995-529-34
; Sequence 34, Application US/09995529
; Publication No. US20030099655A1
; GENERAL INFORMATION:
; APPLICANT: WATKINS, Jeffrey D.
; APPLICANT: HUSE, William D.
; APPLICANT: TANG, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-995-529-34

Query Match      68.6%; Score 24; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNR 5
Db 1 KVSNR 5
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Db 1 KYSNR 5

Search completed: December 30, 2005, 15:05:14
Job time : 160 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model
Run on: December 30, 2005, 14:52:09 ; Search time 12 Seconds
(without alignments)
4.368 Million cell updates/sec

Title: US-10-735-916A-4
Perfect score: 35
Sequence: 1 KVSNNLY 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 1076

Minimum DB seq length: 7
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_New.*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	35	100.0	7	7 US-11-012-353-4	Sequence 4, Appli
2	24	68.6	7	6 US-10-932-334-5	Sequence 5, Appli
3	24	68.6	7	7 US-11-125-837-2	Sequence 2, Appli
4	24	68.6	7	7 US-11-125-837-14	Sequence 14, Appli
5	24	68.6	7	7 US-11-105-708-18	Sequence 18, Appli
6	21	60.0	7	7 US-11-009-939-19	Sequence 19, Appli
7	19	54.3	7	7 US-11-102-743-4	Sequence 4, Appli
8	17	48.6	7	6 US-10-485-788A-334	Sequence 334, App
9	17	48.6	7	7 US-11-096-706-36	Sequence 56, Appli
10	17	48.6	7	7 US-11-096-706-62	Sequence 62, Appli
11	17	48.6	7	7 US-11-096-706-168	Sequence 168, App
12	17	48.6	7	7 US-11-096-706-191	Sequence 191, App
13	17	48.6	7	7 US-11-096-706-194	Sequence 194, App
14	17	48.6	7	7 US-11-096-706-200	Sequence 200, App
15	17	48.6	7	7 US-11-062-186-27	Sequence 27, Appli
16	16	45.7	7	7 US-10-467-657-9189	Sequence 9189, App
17	15	42.9	7	7 US-11-096-706-29	Sequence 29, Appli
18	15	42.9	7	7 US-11-096-706-76	Sequence 76, Appli
19	15	42.9	7	7 US-11-096-706-193	Sequence 193, App
20	15	42.9	7	7 US-11-096-706-202	Sequence 202, App
21	15	42.9	7	7 US-11-096-706-204	Sequence 204, App
22	15	42.9	7	7 US-11-093-274-13	Sequence 13, Appli
23	15	42.9	7	7 US-11-093-274-14	Sequence 14, Appli
24	15	42.9	7	7 US-11-093-274-15	Sequence 15, Appli
25	15	42.9	7	7 US-11-093-274-15	Sequence 15, Appli

26	14	40.0	7	6 US-10-997-066-34	Sequence 34, Appli
27	14	40.0	7	6 US-10-842-877A-4	Sequence 4, Appli
28	14	40.0	7	6 US-10-485-788A-284	Sequence 284, App
29	14	40.0	7	7 US-11-096-706-40	Sequence 40, Appli
30	14	40.0	7	7 US-11-096-706-46	Sequence 46, Appli
31	14	40.0	7	7 US-11-096-706-150	Sequence 150, App
32	14	40.0	7	7 US-11-069-834-12	Sequence 12, Appli
33	13	37.1	7	6 US-10-726-554-10	Sequence 10, Appli
34	13	37.1	7	6 US-10-999-866-56	Sequence 56, Appli
35	13	37.1	7	6 US-10-842-877A-2	Sequence 2, Appli
36	13	37.1	7	6 US-10-842-877A-13	Sequence 13, Appli
37	13	37.1	7	6 US-10-842-877A-17	Sequence 17, Appli
38	13	37.1	7	6 US-10-842-877A-18	Sequence 18, Appli
39	13	37.1	7	6 US-10-485-788A-164	Sequence 164, App
40	13	37.1	7	6 US-10-485-788A-274	Sequence 274, App
41	13	37.1	7	7 US-11-096-706-58	Sequence 58, Appli
42	13	37.1	7	7 US-11-096-706-175	Sequence 175, App
43	12	34.3	7	6 US-10-516-768-37	Sequence 37, Appli
44	12	34.3	7	6 US-10-997-759-11	Sequence 11, Appli
45	12	34.3	7	6 US-10-467-657-9107	Sequence 9107, Ap

ALIGNMENTS

RESULT 1
US-11-012-353-4
; Sequence 4, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETTSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; PRIOR FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn ver. 3.3
; SEQ ID NO 4
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-012-353-4

Query Match 100.0%; Score 35; DB 7; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.3e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNNLY 7
| | | | |
Db 1 KVSNNLY 7

RESULT 2
US-10-932-334-5
; Sequence 5, Application US/10932334

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; Publication No. US20050249728A1
; GENERAL INFORMATION:
; APPLICANT: ImmunoGen, Inc.
; TITLE OF INVENTION: ANTI-IGF-1 RECEPTOR ANTIBODY
; FILE REFERENCE: A8689
; CURRENT APPLICATION NUMBER: US/10/932,334
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US/10/729,441
; PRIOR FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: 10/170,390
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antibody light chain complementarity determining region
US-10-932-334-5

Query Match      68.6%; Score 24; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.3e+04;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNR 5
Db 1 KVSNR 5

RESULT 3
US-11-125-837-2
; Sequence 2, Application US/11125837
; Publication No. US20050266003A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Rong-Hwa
; APPLICANT: Chang, Chung Nan
; APPLICANT: Chen, Pei-Jiun
; APPLICANT: Huang, Chiu-Chen
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 13062-011001
; CURRENT APPLICATION NUMBER: US/11/125,837
; CURRENT FILING DATE: 2005-05-10
; PRIOR APPLICATION NUMBER: US 60/569,892
; PRIOR FILING DATE: 2004-05-10
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-125-837-2

Query Match      68.6%; Score 24; DB 7; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.3e+04;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNR 5
Db 1 KVSNR 5

RESULT 4
US-11-125-837-14
; Sequence 14, Application US/11125837
; Publication No. US20050266003A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Rong-Hwa
; APPLICANT: Chang, Chung Nan
; APPLICANT: Chen, Pei-Jiun
; APPLICANT: Huang, Chiu-Chen
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 13062-011001
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; CURRENT APPLICATION NUMBER: US/11/125,837
; CURRENT FILING DATE: 2005-05-10
; PRIOR APPLICATION NUMBER: US 60/569,892
; PRIOR FILING DATE: 2004-05-10
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-125-837-14

Query Match      68.6%; Score 24; DB 7; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.3e+04;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNR 5
Db 1 KVSNR 5

RESULT 5
US-11-105-708-18
; Sequence 18, Application US/11105708
; Publication No. US20050281821A1
; GENERAL INFORMATION:
; APPLICANT: Pernasetti, Flavia
; APPLICANT: Freimark, Bruce
; APPLICANT: Van Eggs, Dennis
; APPLICANT: Brooke, Peter C
; TITLE OF INVENTION: Method and Composition for Angiogenesis Inhibition
; FILE REFERENCE: 30797-704.501
; CURRENT APPLICATION NUMBER: US/11/105,708
; CURRENT FILING DATE: 2005-04-13
; PRIOR APPLICATION NUMBER: 09/478,977
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: 60/152,496
; PRIOR FILING DATE: 1999-09-02
; PRIOR APPLICATION NUMBER: 60/143,534
; PRIOR FILING DATE: 1999-09-02
; PRIOR APPLICATION NUMBER: 60/114,878
; PRIOR FILING DATE: 1999-01-06
; PRIOR APPLICATION NUMBER: 60/114,877
; PRIOR FILING DATE: 1999-01-06
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-105-708-18

Query Match      68.6%; Score 24; DB 7; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.3e+04;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVSNR 5
Db 1 KVSNR 5

RESULT 6
US-11-009-939-19
; Sequence 19, Application US/11009939
; Publication No. US2005026598A1
; GENERAL INFORMATION:
; APPLICANT: Elson, Greg Christopher Andrew
; TITLE OF INVENTION: Neutralizing Antibodies and Methods of Use Thereof
; FILE REFERENCE: 23135-402
; CURRENT APPLICATION NUMBER: US/11/009,939
; CURRENT FILING DATE: 2005-12-10
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; PRIOR APPLICATION NUMBER: 60/528,811
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 60/528,812
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 60/528,962
; PRIOR FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-009-939-19

Query Match 60.0%; Score 21; DB 7; Length 7;
Best Local Similarity 80.0%; Pred. No. 4.3e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVSNR 5
DB 1 RVSNR 5

RESULT 7
US-11-102-743-4
; Sequence 4, Application US/11102743
; Publication No. US20050266002A1
; GENERAL INFORMATION:
; APPLICANT: Siegal, Clay
; APPLICANT: Wahli, Alan
; APPLICANT: Francisco, Joseph
; APPLICANT: Fell, H. Perry
; TITLE OF INVENTION: RECOMBINANT ANTI-CD40 ANTIBODY AND USES THEREOF
; FILE REFERENCE: 9632-005
; CURRENT APPLICATION NUMBER: US/11/102,743
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US/09/328,296
; PRIOR FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-102-743-4

Query Match 54.3%; Score 19; DB 7; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.3e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSNR 5
DB 2 VSNR 5

RESULT 8
US-10-485-788A-334
; Sequence 334, Application US/10485788A
; Publication No. US20050282743A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Rabinowitz, Joshua D.
; APPLICANT: Schweizer, Johannes
; APPLICANT: Carlick, Deanna Marie
; APPLICANT: Arbor Vita Corporation
; TITLE OF INVENTION: Molecular Interactions in Cells
; FILE REFERENCE: 20054-003320US
; CURRENT APPLICATION NUMBER: US/10/485,788A
; CURRENT FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: US 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/360,061
; PRIOR FILING DATE: 2002-02-25

; PRIOR APPLICATION NUMBER: WO PCT/US02/24655
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 334
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-485-788A-334

Query Match 48.6%; Score 17; DB 6; Length 7;
Best Local Similarity 60.0%; Pred. No. 4.3e+04;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 SNRLY 7
DB 2 SHQLY 6

RESULT 9
US-11-096-706-34
; Sequence 34, Application US/11096706
; Publication No. US20050245476A1
; GENERAL INFORMATION:
; APPLICANT: Sangamo Biosciences, Inc.
; APPLICANT: Collingwood, Trevor
; TITLE OF INVENTION: Treatment of Neuropathic Pain with Zinc Finger Proteins
; FILE REFERENCE: 019496-008220US
; CURRENT APPLICATION NUMBER: US/11/096,706
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 60/560,535
; PRIOR FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 60/576,757
; PRIOR FILING DATE: 2004-06-02
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Chemically synthesized peptide (zinc finger protein recognition
; OTHER INFORMATION: region)
US-11-096-706-34

Query Match 48.6%; Score 17; DB 7; Length 7;
Best Local Similarity 75.0%; Pred. No. 4.3e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SNRL 6
DB 3 SNRI 6

RESULT 10
US-11-096-706-56
; Sequence 56, Application US/11096706
; Publication No. US20050245476A1
; GENERAL INFORMATION:
; APPLICANT: Sangamo Biosciences, Inc.
; APPLICANT: Collingwood, Trevor
; TITLE OF INVENTION: Treatment of Neuropathic Pain with Zinc Finger Proteins
; FILE REFERENCE: 019496-008220US
; CURRENT APPLICATION NUMBER: US/11/096,706
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 60/560,535
; PRIOR FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 60/576,757
; PRIOR FILING DATE: 2004-06-02
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 56
; LENGTH: 7

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; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Chemically synthesized peptide (zinc finger protein recognition
; OTHER INFORMATION: region)
US-11-096-706-56

Query Match      48.6%; Score 17; DB 7; Length 7;
Best Local Similarity 75.0%; Pred. No. 4.3e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 SNRL 6
Db      3 SNRI 6

RESULT 11
US-11-096-706-62
; Sequence 62, Application US/11096706
; Publication No. US20050245476A1
; GENERAL INFORMATION:
; APPLICANT: Sangamo Biosciences, Inc.
; APPLICANT: Collingwood, Trevor
; TITLE OF INVENTION: Treatment of Neuropathic Pain with Zinc Finger Proteins
; FILE REFERENCE: 019496-008220US
; CURRENT APPLICATION NUMBER: US/11/096,706
; CURRENT FILING DATE: 2005-04-01
; PRIOR FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 60/560,535
; PRIOR FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 60/576,757
; PRIOR FILING DATE: 2004-06-02
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 62
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Chemically synthesized peptide (zinc finger protein recognition
; OTHER INFORMATION: region)
US-11-096-706-62

Query Match      48.6%; Score 17; DB 7; Length 7;
Best Local Similarity 75.0%; Pred. No. 4.3e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 SNRL 6
Db      3 SNRI 6

RESULT 12
US-11-096-706-168
; Sequence 168, Application US/11096706
; Publication No. US20050245476A1
; GENERAL INFORMATION:
; APPLICANT: Sangamo Biosciences, Inc.
; APPLICANT: Collingwood, Trevor
; TITLE OF INVENTION: Treatment of Neuropathic Pain with Zinc Finger Proteins
; FILE REFERENCE: 019496-008220US
; CURRENT APPLICATION NUMBER: US/11/096,706
; CURRENT FILING DATE: 2005-04-01
; PRIOR FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 60/560,535
; PRIOR FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 60/576,757
; PRIOR FILING DATE: 2004-06-02
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 168
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Chemically synthesized peptide (zinc finger protein binding
; OTHER INFORMATION: domain)
US-11-096-706-168

Query Match      48.6%; Score 17; DB 7; Length 7;
Best Local Similarity 75.0%; Pred. No. 4.3e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 SNRL 6
Db      3 SNRI 6

RESULT 13
US-11-096-706-191
; Sequence 191, Application US/11096706
; Publication No. US20050245476A1
; GENERAL INFORMATION:
; APPLICANT: Sangamo Biosciences, Inc.
; APPLICANT: Collingwood, Trevor
; TITLE OF INVENTION: Treatment of Neuropathic Pain with Zinc Finger Proteins
; FILE REFERENCE: 019496-008220US
; CURRENT APPLICATION NUMBER: US/11/096,706
; CURRENT FILING DATE: 2005-04-01
; PRIOR FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 60/560,535
; PRIOR FILING DATE: 2004-06-02
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 191
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Chemically synthesized peptide (zinc finger protein binding
; OTHER INFORMATION: domain)
US-11-096-706-191

Query Match      48.6%; Score 17; DB 7; Length 7;
Best Local Similarity 75.0%; Pred. No. 4.3e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 SNRL 6
Db      3 SNRI 6

RESULT 14
US-11-096-706-194
; Sequence 194, Application US/11096706
; Publication No. US20050245476A1
; GENERAL INFORMATION:
; APPLICANT: Sangamo Biosciences, Inc.
; APPLICANT: Collingwood, Trevor
; TITLE OF INVENTION: Treatment of Neuropathic Pain with Zinc Finger Proteins
; FILE REFERENCE: 019496-008220US
; CURRENT APPLICATION NUMBER: US/11/096,706
; CURRENT FILING DATE: 2005-04-01
; PRIOR FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 60/560,535
; PRIOR FILING DATE: 2004-06-02
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 194
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Chemically synthesized peptide (zinc finger protein binding
; OTHER INFORMATION: domain)
US-11-096-706-194
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Query Match 48.6%; Score 17; DB 7; Length 7;
Best Local Similarity 75.0%; Pred. No. 4.3e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SNRL 6
|||:
Db 3 SNRI 6

RESULT 15

US-11-096-706-200
; Sequence 200, Application US/11096706
; Publication No. US20050245476A1
; GENERAL INFORMATION:
; APPLICANT: Sangamo Biosciences, Inc.
; APPLICANT: Collingwood, Trevor
; TITLE OF INVENTION: Treatment of Neuropathic Pain with Zinc Finger Proteins
; FILE REFERENCE: 019496-008220US
; CURRENT APPLICATION NUMBER: US/11/096,706
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 60/560,535
; PRIOR FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 60/576,757
; PRIOR FILING DATE: 2004-06-02
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 200
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Chemically synthesized peptide (zinc finger protein binding
; OTHER INFORMATION: domain)
US-11-096-706-200

Query Match 48.6%; Score 17; DB 7; Length 7;
Best Local Similarity 75.0%; Pred. No. 4.3e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SNRL 6
|||:
Db 3 SNRI 6

Search completed: December 30, 2005, 15:05:35
Job time : 16 secs

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QM protein - protein search, using sw model

Run on: December 30, 2005, 13:14:26 ; Search time 20.1774 Seconds
(without alignments)
36.877 Million cell updates/sec

Title: US-10-735-916A-6

Perfect score: 56

Sequence: 1 FQGSHPWT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:*
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 - 2: /cgn2_6/ptodata/1/iaa/6 COMB.pbp:*
 - 3: /cgn2_6/ptodata/1/iaa/H COMB.pbp:*
 - 4: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pbp:*
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 - 6: /cgn2_6/ptodata/1/iaa/backfiles1.pbp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	112	1	US-08-752-844-15
2	56	100.0	112	1	US-08-591-196-15
3	56	100.0	112	2	US-03-293-533-15
4	56	100.0	149	1	US-08-752-844-2
5	56	100.0	149	1	US-08-591-196-2
6	56	100.0	149	2	US-09-192-838B-2
7	56	100.0	149	2	US-03-293-533-2
8	56	100.0	149	2	US-03-324-191-2
9	56	100.0	263	1	US-08-752-844-66
10	56	100.0	263	2	US-03-293-533-66
11	53	94.6	9	1	US-07-977-696C-72
12	53	94.6	9	1	US-08-129-930B-72
13	53	94.6	9	2	US-08-976-288A-72
14	53	94.6	9	2	US-08-947-839B-72
15	53	94.6	131	1	US-07-977-696C-11
16	53	94.6	131	1	US-08-129-930B-11
17	53	94.6	131	2	US-08-976-288A-11
18	53	94.6	131	2	US-09-947-839B-11
19	47	83.9	9	1	US-07-977-696C-34
20	47	83.9	9	1	US-08-129-930B-34
21	47	83.9	9	1	US-08-560-558B-31
22	47	83.9	9	2	US-08-134-346A-21
23	47	83.9	9	2	US-08-976-288A-34
24	47	83.9	9	2	US-09-217-268B-31
25	47	83.9	9	2	US-09-947-839B-34
26	47	83.9	110	2	US-10-114-716A-42
27	47	83.9	113	1	US-08-497-312-18

Sequence 15, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 35, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 35, Appl
Sequence 50, Appl
Sequence 130, Appl
Sequence 12, Appl
Sequence 14, Appl
Sequence 29, Appl
Sequence 15, Appl
Sequence 48, Appl
Sequence 50, Appl
Sequence 3, Appl
Sequence 19, Appl

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US-09-217-268B-35
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US-08-129-930B-95
US-08-134-346A-50
US-08-976-288A-95
US-09-726-219A-190
US-09-196-522-190
US-09-646-028-12
US-09-646-028-14
US-08-053-171-29
US-08-053-171-15
US-08-331-398A-48
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US-08-077-252B-3
US-08-859-649-19

ALIGNMENTS

RESULT 1
US-08-752-844-15
; Sequence 15, Application US/08752844
; Patent No. 5935821
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; APPLICANT: Foon, Kenneth A.
; APPLICANT: Chatterjee, Sunil K.
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
; TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/752,844
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Schiff, J. Michael
; REGISTRATION NUMBER: 40,253
; REFERENCE/DOCKET NUMBER: 30414-20002.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-752-844-15

Query Match 100.0%; Score 56; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.0084;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQGSHPWT 9

|||||||

Db 94 FQSHVPWT 102

RESULT 2

US-08-591-196-15
; Sequence 15, Application US/08591196
; Patent No. 5977316
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; APPLICANT: Foon, Kenneth A.
; APPLICANT: Chatterjee, Sunil K.
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
; TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA

ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,196
; FILING DATE: 16-JAN-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Schiff, J. Michael
; REGISTRATION NUMBER: 40,253
; REFERENCE/DOCKET NUMBER: 30414-20002.20
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-591-196-15

Query Match 100.0%; Score 56; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.0084;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQSHVPWT 9

Db 94 FQSHVPWT 102

RESULT 3

US-09-293-533-15
; Sequence 15, Application US/09293533
; Patent No. 6509016
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; APPLICANT: Foon, Kenneth A.
; APPLICANT: Chatterjee, Sunil K.
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
; TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA

ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/293,533
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/752,844
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Schiff, J. Michael
; REGISTRATION NUMBER: 40,253
; REFERENCE/DOCKET NUMBER: 30414-20002.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-293-533-15

Query Match 100.0%; Score 56; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.0084;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQSHVPWT 9

Db 94 FQSHVPWT 102

RESULT 4

US-08-752-844-2
; Sequence 2, Application US/08752844
; Patent No. 5935821
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; APPLICANT: Foon, Kenneth A.
; APPLICANT: Chatterjee, Sunil K.
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
; TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA

ZIP: 94304-1018

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/752,844
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Schiff, J. Michael
; REGISTRATION NUMBER: 40,253
; REFERENCE/DOCKET NUMBER: 30414-20002.21
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792

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; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 149 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-752-844-2

Query Match 100.0%; Score 56; DB 1; Length 149;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQSHVPWT 9
DB 113 FQSHVPWT 121

RESULT 5
US-08-591-196-2
; Sequence 2, Application US/08591196
; Patent No. 5977316
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; APPLICANT: Foon, Kenneth A.
; APPLICANT: Chatterjee, Sunil K.
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
; TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,196
; FILING DATE: 16-JAN-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Schiff, J. Michael
; REGISTRATION NUMBER: 40,253
; REFERENCE/DOCKET NUMBER: 30414-20002.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 149 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-591-196-2

Query Match 100.0%; Score 56; DB 1; Length 149;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQSHVPWT 9
DB 113 FQSHVPWT 121

RESULT 6
US-09-192-838B-2
; Sequence 2, Application US/09192838B
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; Patent No. 6355244
; GENERAL INFORMATION:
; APPLICANT: FOON, Kenneth A.
; APPLICANT: CHATTERJEE, Malaya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF PSORIASIS
; FILE REFERENCE: 304142000500
; CURRENT APPLICATION NUMBER: US/09/192,838B
; CURRENT FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 60/065,774
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Mus Musculus
US-09-192-838B-2

Query Match 100.0%; Score 56; DB 2; Length 149;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQSHVPWT 9
DB 113 FQSHVPWT 121

RESULT 7
US-09-293-533-2
; Sequence 2, Application US/09293533
; Patent No. 6509016
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; APPLICANT: Foon, Kenneth A.
; APPLICANT: Chatterjee, Sunil K.
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
; TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/293,533
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/752,844
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Schiff, J. Michael
; REGISTRATION NUMBER: 40,253
; REFERENCE/DOCKET NUMBER: 30414-20002.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 149 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-293-533-2
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Query Match 100.0%; Score 56; DB 2; Length 149;
Best Local Similarity 100.0%; Pred. No. 0.011; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQSHVPWT 9
DB 113 FQSHVPWT 121

RESULT 8

US-09-324-191-2
; Sequence 2, Application US/09324191
; Patent No. 6562798
; GENERAL INFORMATION:
; APPLICANT: THE UNIVERSITY OF KENTUCKY RESEARCH FOUNDATION
; APPLICANT: CHATTERJEE, Malaya
; APPLICANT: FOON, Kenneth A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF PSORIASIS
; FILE REFERENCE: 304142000540
; CURRENT APPLICATION NUMBER: US/09/324,191
; CURRENT FILING DATE: 1999-06-02
; EARLIER APPLICATION NUMBER: 60/065,774
; EARLIER FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Mus Musculus
US-09-324-191-2

Query Match 100.0%; Score 56; DB 2; Length 149;
Best Local Similarity 100.0%; Pred. No. 0.011; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQSHVPWT 9
DB 113 FQSHVPWT 121

RESULT 9

US-08-752-844-66
; Sequence 66, Application US/08752844
; Patent No. 5935821
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; APPLICANT: Foon, Kenneth A.
; APPLICANT: Chatterjee, Sunil K.
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
; TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/752,844
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Schiff, J. Michael
; REGISTRATION NUMBER: 40,253
; REFERENCE/DOCKET NUMBER: 30414-20002.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600

TELEFAX: (415) 494-0792
TELEX: 706141
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 263 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-752-844-66

Query Match 100.0%; Score 56; DB 1; Length 263;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQSHVPWT 9
DB 245 FQSHVPWT 253

RESULT 10

US-09-293-533-66
; Sequence 66, Application US/09293533
; Patent No. 6509016
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; APPLICANT: Foon, Kenneth A.
; APPLICANT: Chatterjee, Sunil K.
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
; TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/293,533
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/752,844
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Schiff, J. Michael
; REGISTRATION NUMBER: 40,253
; REFERENCE/DOCKET NUMBER: 30414-20002.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 263 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-293-533-66

Query Match 100.0%; Score 56; DB 2; Length 263;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQSHVPWT 9
DB 245 FQSHVPWT 253

RESULT 11
US-07-977-696C-72
; Sequence 72, Application US/07977696C
; Patent No. 5792852
; GENERAL INFORMATION:
; APPLICANT: do Couto, Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides with Specificity
; TITLE OF INVENTION: for Carcinomas and Kit and Diagnostic Vaccination
; TITLE OF INVENTION: and Therapeutic Methods.
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/977,696C
; FILING DATE: 11-16-92
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel Ph.D., Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P66 38227
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 748-6868
; TELEFAX: (510) 748-6688
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-977-696C-72
Query Match 94.6%; Score 53; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 FQGSHPWT 9
Db 1 FQGTHVPWT 9
RESULT 12
US-08-129-930B-72
; Sequence 72, Application US/08129930B
; Patent No. 5804187
; GENERAL INFORMATION:
; APPLICANT: do Couto Dr., Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides with Broad
; TITLE OF INVENTION: Carcinoma Specificity, and Kit and
; TITLE OF INVENTION: Diagnostic Vaccination and
; TITLE OF INVENTION: Therapeutic Methods
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: V. AMZEL & ASSOC.
; STREET: 2055 No. 5804187th Broadway, Suite 201
; CITY: Walnut Creek

STATE: California
COUNTRY: USA
ZIP: 94596
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/129,930B
FILING DATE: September 30, 1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Amzel Ph.D., Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: CRFCC-008A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 521-1333
TELEFAX: (510) 521-3541
TELEX: n.a.
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-129-930B-72
Query Match 94.6%; Score 53; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 FQGSHPWT 9
Db 1 FQGTHVPWT 9
RESULT 13
US-08-976-288A-72
; Sequence 72, Application US/08976288A
; Patent No. 6315997
; GENERAL INFORMATION:
; APPLICANT: do Couto Dr., Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides With Broad
; TITLE OF INVENTION: Carcinoma Specificity, and Kit and
; TITLE OF INVENTION: Diagnostic Vaccination and
; TITLE OF INVENTION: Therapeutic Methods
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder & Poplawski
; STREET: 444 South Flower St., 19th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976,288A
; FILING DATE: No. 6315997ember 21, 1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/129,930
; FILING DATE: September 30, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/977,696
; FILING DATE: No. 6315997ember 16, 1992

ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel Ph.D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P6639938
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
TELEX: n.a.
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-976-288A-72

Query Match 94.6%; Score 53; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPVPT 9
DB 1 FQGTHVPWT 9

RESULT 14
US-09-947-839B-72
Sequence 72, Application US/09947839B
Patent No. 6936706
GENERAL INFORMATION:
APPLICANT: do Couto, Fernando J.R.
Ceriani Dr., Roberto L.
Peterson Dr., Jerry A.
Padlan Dr., Eduardo A.
TITLE OF INVENTION: Analogue Peptides with Specificity
for Carcinomas and Kit and Diagnostic Vaccination
and Therapeutic Methods.

NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: V. Amzel & Assoc.
STREET: P.O. Box 159
CITY: Gladwyne
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19035
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/09/947,839B
APPLICATION NUMBER: US/09/947,839B
FILING DATE: 06-Sep-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Amzel Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: CRFC-083
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-649-0609
TELEFAX: 240-359-0299
TELEX: n.a.

INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 72:
US-09-947-839B-72

Query Match 94.6%; Score 53; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 FQGSHPVPT 9
DB 1 FQGTHVPWT 9

RESULT 15
US-07-977-696C-11
Sequence 11, Application US/07977696C
Patent No. 5792852
GENERAL INFORMATION:
APPLICANT: do Couto, Fernando J.R.
Ceriani Dr., Roberto L.
Peterson Dr., Jerry A.
Padlan Dr., Eduardo A.
TITLE OF INVENTION: Analogue Peptides with Specificity
for Carcinomas and Kit and Diagnostic Vaccination
and Therapeutic Methods.
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/07/977,696C
APPLICATION NUMBER: US/07/977,696C
FILING DATE: 11-16-92
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Amzel Ph.D., Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38227
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 748-6868
TELEFAX: (510) 748-6868
TELEX: n.a.
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-977-696C-11

Query Match 94.6%; Score 53; DB 1; Length 131;
Best Local Similarity 88.9%; Pred. No. 0.035;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPVPT 9
DB 113 FQGTHVPWT 121

Search completed: December 30, 2005, 13:37:17
Job time : 20.1774 secs

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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:02:01 ; Search time 79.9839 Seconds
(without alignments)
49.440 Million cell updates/sec

Title: US-10-735-916A-6

Perfect score: 56

Sequence: 1 FQGSHPWT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_21.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	9	5	ABP52345 Fv region
2	56	100.0	9	7	ADJ94151 Mouse HUI
3	56	100.0	9	7	ADJ76840 CDR seque
4	56	100.0	9	9	ADZ67010 Murine in
5	56	100.0	109	5	ABP52310 Fv region
6	56	100.0	112	2	RAY49217 Light cha
7	56	100.0	112	2	RAY25397 WO9932630
8	56	100.0	112	5	AAE15711 Mouse mon
9	56	100.0	112	5	AAE15713 Mouse mon
10	56	100.0	112	5	AAE15704 Mouse mon
11	56	100.0	112	5	AAE15712 Mouse mon
12	56	100.0	112	6	ADA14777 Peptide f
13	56	100.0	112	7	ADC35319 Anti-Idio
14	56	100.0	112	7	ADJ94125 Mouse HUI
15	56	100.0	112	7	ADJ76888 Anti-IGF-
16	56	100.0	112	7	ADJ76890 Anti-IGF-
17	56	100.0	112	7	ADJ76899 Anti-IGF-
18	56	100.0	112	7	ADJ76895 Anti-IGF-
19	56	100.0	112	7	ADJ80422 Murine an
20	56	100.0	112	7	ADJ80420 Hybrid hu
21	56	100.0	112	7	ADJ80419 Hybrid hu
22	56	100.0	112	7	ADJ80421 Hybrid hu
23	56	100.0	112	9	ADZ67058 Murine im
24	56	100.0	112	9	ADZ67069 Human ant

25	56	100.0	112	9	ADZ67060	Adz67060 Mouse ant
26	56	100.0	112	9	ADZ67065	Adz67065 Human ant
27	56	100.0	114	8	ADI26490	ADI26490 Human ECL
28	56	100.0	114	8	ADI26498	ADI26498 Human ECL
29	56	100.0	115	1	AAP81364	AAP81364 Light cha
30	56	100.0	115	1	AAP81366	AAP81366 Light cha
31	56	100.0	119	1	AAP81366	AAP81366 Chimeric
32	56	100.0	120	1	AAB62303	AAB62303 Chimeric
33	56	100.0	122	7	ADJ76883	Adj76883 Anti-IGF-
34	56	100.0	122	7	ADZ67053	Adz67053 Murine im
35	56	100.0	131	7	ADJ76901	Adj76901 Anti-IGF-
36	56	100.0	131	7	ADJ76897	Adj76897 Anti-IGF-
37	56	100.0	131	9	ADZ67071	Adz67071 Human ant
38	56	100.0	131	9	ADZ67067	Adz67067 Human ant
39	56	100.0	149	2	AAW03199	AAW03199 Anti-Idio
40	56	100.0	149	2	AAW03199	AAW03199 Mab 1A7 1
41	56	100.0	149	2	AAW03199	AAW03199 Mab 1A7 1
42	56	100.0	149	2	AAW03199	AAW03199 Mab 1A7 1
43	56	100.0	149	6	ADA14768	Ada14768 Mouse ant
44	56	100.0	149	7	ADC35310	Adc35310 Monoclonal
45	56	100.0	249	1	AAP80154	AAP80154 Biosynthe

ALIGNMENTS

RESULT 1
ABP52345
ID ABP52345 standard; peptide; 9 AA.
XX AC ABP52345;
XX AC ABP52345;
DT 17-OCT-2002 (first entry)
XX Fv region SC100 antibody CDR-L3 amino acid sequence.
DE Cytotoxic T lymphocyte; CTL; T helper; MAGE3; cytotoxic T cell response;
KW tumour; immune response; cancer; vaccine; antibody.
XX Mus musculus.
OS Synthetic.
XX WO200258728-A2.
PN 01-AUG-2002.
XX 28-JAN-2002; 2002WO-GB0000354.
XX 26-JAN-2001; 2001GB-00002145.
PR (SCAN-) SCANCEL LTD.
(CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
FI Durrant LG, Parsons T, Robins A;
XX WPI; 2002-608418/65.
XX Use of polypeptides and nucleic acids encoding the polypeptides, in
PT manufacturing medicament for stimulating a cytotoxic T cell response and
PT for preventing or treating cancer, e.g. colorectal, lung, breast or
PT ovarian cancer.
XX Example 11; Page 46; 87pp; English.
XX The present invention describes the use of a polypeptide (I) in the
CC manufacture of a medicament for stimulating a cytotoxic T cell response,
CC where (I) comprises a first portion comprising the part of human FC that
CC binds to CD64 and a second portion comprising one or more heterologous T
CC cell epitopes. Also described is a method of stimulating a cytotoxic T
CC cell response in a patient such as a mammal, preferably human, by
CC administering (I) to the patient. (I) has cytostatic activity and can be
CC used in vaccine production. (I) and the nucleic acid encoding (I) are
CC useful in the manufacture of a medicament for stimulating cytotoxic T

CC	cell response. The medicament is useful for preventing and/or treating cancer, e.g. colorectal, lung, breast, gastric or ovarian cancer. The medicament stimulates cytotoxic and helper T cell responses. The antibodies are useful as vaccines to stimulate helper and cytotoxic T cell responses. The polypeptides and nucleic acids are useful in optimising immunisation schedules for enhancing a protective immune response against cancer. The present sequence represents an Fv region SC100 antibody CDR-L3 amino acid sequence which is used in an example from the present invention
XX	
XX	
SQ	Sequence 9 AA;
	Query Match 100.0%; Score 56; DB 5; Length 9;
	Best Local Similarity 100.0%; Pred. No. 2e+06;
	Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 FQGSHVPEWT 9
DB	1 FQGSHVPEWT 9
RESULT 2	
ADD94151	ID ADD94151 standard; peptide; 9 AA.
XX	AC
XX	ADD94151;
XX	
DT	29-JAN-2004 (first entry)
XX	
DE	Mouse HUI77 light chain CDR3 partial amino acid sequence SeqID36.
XX	
KW	grafted antibody; complementarity determining region; CDR; light CDR; heavy CDR; cryptic collagen epitope; solid tumour;
KW	new blood vessel growth; angiogenesis; tumour growth; cytostatic;
KW	collagen agonist; collagen antagonist; cancer metastasis;
KW	anti-cryptic collagen; antibody; HUI77; variable region light chain;
KW	mouse; murine.
XX	
OS	Mus musculus.
XX	
PN	WO2003046204-A2.
XX	
PD	05-JUN-2003.
XX	
PX	26-NOV-2002; 2002WO-US038147.
PF	
XX	
PR	26-NOV-2001; 2001US-00995529.
PR	06-DEC-2001; 2001US-00011250.
XX	
PA	(CELL-) CELL MATRIX INC.
XX	
PI	Watking JD, Huse WD, Tang Y, Broek D, Brooks PC;
XX	
DR	WPI; 2003-513649/48.
DR	N-PSDE; ADD94150.
XX	
PT	New cryptic collagen antibody with one or more complementarity determining regions, useful for diagnosing and treating disorders associated with angiogenesis, tumor growth and/or cancer metastasis.
PT	
XX	
PS	Claim 25; SEQ ID NO 36; 232pp; English.
XX	
CC	This invention relates to a novel grafted antibody or its functional fragment comprising one or more complementarity determining regions (CDRs) of a defined light CDR and a heavy CDR with at least one amino acid (aa) substitution where the antibody has specific binding activity for a cryptic collagen epitope. The growth of all solid tumours requires new blood vessel growth, angiogenesis, inhibition of which is an approach to limiting tumour growth. The invention may allow development of therapeutics with a cytostatic activity as a collagen agonist or antagonist. The invention is useful for diagnosing and treating disorders associated with angiogenesis, tumour growth and/or cancer metastasis. The present sequence is the partial amino acid sequence of a mouse anti-

CC cryptic collagen site antibody HUI77 variable region light chain CDR
CC which is related to the invention.

XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 56; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. NO. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 1 FQGSHPVPT 9
| | | | | | | | | |
Db 1 FQGSHPVPT 9

RESULT 3

ID ADJ76840

XX ADJ76840 standard; peptide; 9 AA.

AC ADJ76840;

XX

XX

DT 06-MAY-2004 (first entry)

XX

DE CDR sequence for anti-IGF-1R antibody.

XX

XX

KW cytosolic; antipsoriatic; antibody;
KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;
KW or epidermal growth factor receptor; EGFR; signal transduction pathway;
KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;
KW CDR.

XX

OS Mus musculus.

XX

XX WO2003059951-A2.

PN

XX

PD 24-JUL-2003.

XX

XX

PF 20-JAN-2003; 2003WO-FR000178.

XX

XX 18-JAN-2002; 2002FR-00000653.

PR

FR 18-JAN-2002; 2002FR-00000854.

PR

XX 07-MAY-2002; 2002FR-00005753.

XX

PA (FABR) FABRE MEDICAMENT SA PIERRE.

XX

PI Goetsch L, Corvaia N, Leger O;

XX

XX WPI; 2003-569653/53.

DR

XX N-PSDB; ADJ76839.

XX

PT New antibodies that bind to human insulin-like growth factor receptor,
PT useful for treatment, prevention and diagnosis of cancers.

XX

XX Claim 1; SEQ ID NO 6; 164pp; French.

PS

XX The invention relates to an isolated antibody (Ab), and its functional
CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-
CC 1R) and optionally: (i) inhibit natural binding of insulin-like growth
CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine
CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or
CC treat diseases associated with overexpression and/or abnormal activity of
CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with
CC hyperactivity of signal transduction pathways mediated by interaction of
CC these receptors with their ligands. Especially they inhibit
CC transformation of normal cells to tumor cells, inhibit growth and/or
CC proliferation of tumor cells, so are useful against cancers of the
CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
CC also for treating psoriasis. Ab are also used to diagnose diseases caused
CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents an
CC CDR sequence used to generate the Ab of the invention.

XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 56; DB 7; Length 9;

XX

Best Local Similarity 100.0%; Pred. No. 2e+06; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPWPT 9
| | | | |
Db 1 FQGSHPWPT 9

RESULT 4
ADZ67010
ID ADZ67010 standard; peptide; 9 AA.

AC ADZ67010;
XX
XX 30-JUN-2005 (first entry)
DT

XX Murine insulin-like growth factor T receptor IGF-IR CDR SEQ ID NO:6.

XX Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;
KW musculoskeletal disease; respiratory disease; lung tumor;
KW endocrine disease; gynecology and obstetrics; breast tumor;
KW endometrial carcinoma; gastrointestinal disease; colon tumor;
KW antipsoriatic; psoriasis; dermatological disease; immune disorder.

XX Mus musculus.

XX US2005084906-A1.

XX 21-APR-2005.

XX 16-DEC-2003; 2003US-00735916.

XX 18-JAN-2002; 2002FR-00000653.

XX 18-JAN-2002; 2002FR-00000654.

XX 07-MAY-2002; 2002FR-00005753.

XX 20-JAN-2003; 2003WO-FR000178.

XX 11-JUL-2003; 2003FR-00008538.

XX (GOET/) GOETSCH L.

XX (CORV/) CORVAIA N.

XX (LEGE/) LEGER O.

XX (DUFL/) DUFLOS A.

XX (HAEU/) HAEUW J.

XX (BECK/) BECK A.

XX Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;

PI WPI; 2005-321968/33.

XX N-PSDB; ADZ67009.

XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)
XX antibody or its functional fragment, being capable of binding human IGF-
XX IR and specifically inhibiting tyrosine kinase activity of receptor,
XX useful for treating cancer.

XX Claim 1; SEQ ID NO 6; 125pp; English.

XX The invention relates to a novel isolated anti-insulin-like growth factor
XX I receptor (IGF-IR) antibody (I) or its functional fragment, being
XX capable of binding to human IGF-IR and, if necessary, capable of
XX specifically inhibiting tyrosine kinase activity of the receptor,
XX comprising a light or heavy chain having at least one complementary
XX determining region (CDR) consisting of one of two fully defined 16 amino
XX acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in
XX the preparation of a medicament intended for the prevention or treatment
XX of an illness connected with an overexpression and/or an abnormal
XX activation of the IGF-IR and/or EGFR, and/or connected with a
XX hyperactivation of the transduction pathway of the signal mediated by the
XX interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where
XX the administration of the medicament does not induce or only slightly
XX induces secondary effects connected with inhibition of the insulin
XX receptor. The antibody is useful for preparation of a medicament intended

CC to inhibit the transformation of normal cells into cells with tumoral
CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-
CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is
CC useful for preparation of a medicament intended to inhibit the growth
CC and/or the proliferation of tumor cells, preferably IGF-dependent,
CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or
CC HER2/neu-dependent cells. (I) is useful in the preparation of a
CC medicament intended for prevention or for the treatment of cancer, where
CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,
CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the
CC preparation of a medicament intended for the prevention or for the
CC treatment of psoriasis. (I) is useful in preparation of a medicament
CC intended for the specific targeting of a biologically active compound to
CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)
CC is useful for in vitro diagnosis of illnesses induced by an
CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor
CC starting from a biological sample in which the abnormal presence, of IGF-
CC IR and/or EGFR receptor is suspected, which involves contacting the
CC biological sample with (I), which is optionally labeled. The present
CC sequence is used in the exemplification of the invention.

XX Sequence 9 AA;

Query Match 100.0%; Score 56; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPWPT 9
| | | | |
Db 1 FQGSHPWPT 9

RESULT 5
ABP52310
ID ABP52310 standard; peptide; 109 AA.

XX AC ABP52310;

XX 17-OCT-2002 (first entry)
DT

XX Fv region SC100 antibody light chain related amino acid sequence #1.

XX Cytotoxic T lymphocyte; CTL; T helper; MAGE3; cytotoxic T cell response;
XX tumour; immune response; cancer; vaccine; antibody.

XX Mus musculus.

XX Synthetic.

XX WO200258728-A2.

XX 01-AUG-2002.

XX 28-JAN-2002; 2002WO-GB000354.

XX 26-JAN-2001; 2001GB-00002145.

XX (SCAN-) SCANCEL LTD.

XX (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.

XX Durrant LG, Parsons T, Robins A;

XX WPI; 2002-608418/65.

XX Use of polypeptides and nucleic acids encoding the polypeptides, in
XX manufacturing medicament for stimulating a cytotoxic T cell response and
XX for preventing or treating cancer, e.g. colorectal, lung, breast or
XX ovarian cancer.

XX Example 11; Page 38; 87pp; English.

XX The present invention describes the use of a polypeptide (I) in the
XX manufacture of a medicament for stimulating a cytotoxic T cell response,
XX where (I) comprises a first portion comprising the part of human Fc that

CC binds to CD64 and a second portion comprising one or more heterologous T
 CC cell epitopes. Also described is a method of stimulating a cytotoxic T
 CC cell response in a patient such as a mammal, preferably human, by
 CC administering (I) to the patient. (I) has cytostatic activity and can be
 CC used in vaccine production. (I) and the nucleic acid encoding (I) are
 CC useful in the manufacture of a medicament for stimulating cytotoxic T
 CC cell response. The medicament is useful for preventing and/or treating
 CC cancer, e.g. colorectal, lung, breast, gastric or ovarian cancer. The
 CC medicament stimulates cytotoxic and helper T cell responses. The
 CC antibodies are useful as vaccines to stimulate helper and cytotoxic T
 CC cell responses. The polypeptides and nucleic acids are useful in
 CC optimising immunisation schedules for enhancing a protective immune
 CC response against cancer. The present sequence represents an Fv region
 CC SC100 antibody light chain related amino acid sequence which is used in
 CC an example from the present invention

XX
 SQ Sequence 109 AA;

Query Match 100.0%; Score 56; DB 5; Length 109;
 Best Local Similarity 100.0%; Pred. No. 0.064;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPVPT 9
 Db 94 FQGSHPVPT 102
 |||||

RESULT 6
 AAY49217
 ID AAY49217 standard; protein; 112 AA.
 AC AAY49217;
 DT 07-FEB-2000 (first entry)
 XX
 XX Light chain variable region consensus sequence.
 DE
 XX Monoclonal antibody; MAb; 1A7; GD2; immune response; melanoma;
 KW neuroblastoma; glioma; soft tissue carcinoma; small cell carcinoma;
 KW tumor-associated antigen.
 XX
 XX Synthetic.
 OS
 XX US5977316-A.
 PN
 XX 02-NOV-1999.
 PD
 XX 16-JAN-1996; 96US-00591196.
 PF
 XX 17-JAN-1995; 95US-00372676.
 PR
 XX (KENT) UNIV KENTUCKY.
 PA
 XX Foon KA, Chatterjee SK, Chatterjee M;
 PI WPI; 1996-354530/35.
 DR
 XX Monoclonal antibody 1A7 and related polynucleotide(s) and polypeptide(s)
 PT - useful to treat or palliate a GD2-associated disease, e.g. melanoma and
 PT glioma.
 PS
 XX Disclosure; Fig 3C; 74pp; English.

CC The invention provides a monoclonal antibody (MAb) designated 1A7, which
 CC elicits an anti-GD2 (tumor-associated antigen) immunological response in
 CC humans. MAb 1A7 has defined light and heavy chain variable region
 CC sequences. The MAb 1A7 and polypeptides can be used for eliciting an anti
 CC -GD2 immune response. The polypeptides can also be used for detecting or
 CC purifying anti-GD2 antibody. The products can be used for treating GD2 -
 CC associated diseases, e.g. melanoma, neuroblastoma, glioma, soft tissue
 CC carcinoma, and small cell carcinoma. They can be used for palliating the
 CC disease or for reducing the risk of recurrence. The present sequence
 CC represents the light chain variable region consensus sequence

XX
 SQ Sequence 112 AA;

Query Match 100.0%; Score 56; DB 2; Length 112;
 Best Local Similarity 100.0%; Pred. No. 0.066;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPVPT 9
 Db 94 FQGSHPVPT 102
 |||||

RESULT 7
 AAY25397
 ID AAY25397 standard; protein; 112 AA.
 XX
 AC AAY25397;
 DT 07-SEP-1999 (first entry)
 XX
 XX WO9932630 Seq ID 36.
 DE
 KW Paraquat; antibody; light chain; herbicide; resistant; crop plant;
 KW weed control; tolerant; diquat; photosynthesis inhibitor; photosystem I;
 KW free radical; lipid peroxidation; electron transport; photosystem II;
 KW vacuole; cell surface; cytotoxic; sensitive.
 XX
 OS Unidentified.
 XX
 XX WO9932630-A1.
 PN
 XX 01-JUL-1999.
 PD
 XX 15-DEC-1998; 98WO-GB003760.
 PF
 XX 19-DEC-1997; 97GB-00026955.
 PR
 XX (ZENES) ZENECA LTD.
 PA
 XX Holt DC, Jones PG;
 PI WPI; 1999-405173/34.
 DR
 XX Herbicide binding proteins and related polynucleotides.
 PT
 XX Disclosure; Page 44-45; 60pp; English.

CC This invention describes a novel herbicide binding protein which can
 CC confer herbicide resistance activity. Crop plants, such as soybean,
 CC cotton, tobacco, sugarbeet, oilseed rape, canola, flax, sunflower,
 CC potato, tomato, alfalfa, lettuce, maize, wheat, sorghum, rye, bananas,
 CC barley, oat, turf grass, forage grass, sugar cane, pea, field bean, rice,
 CC pine, poplar, apple, grape, citrus or nut plants, transformed with a
 CC herbicide binding protein gene are resistant to the herbicide. Hence,
 CC weeds can be selectively resistant in a field of the transformed crops.
 CC The plants are substantially resistant or tolerant to herbicides, such as
 CC paraquat or diquat, that inhibit photosynthesis by accepting electrons
 CC from photosystem I thus generating free radicals which cause lipid
 CC peroxidation or by blocking electron transport in photosystem II. The
 CC herbicide binding proteins advantageously sequester the herbicide, e.g.
 CC at the cell surface or in the vacuoles of a treated plant. Sequestration
 CC at the cell surface prevents the entry of the herbicide into the cell so
 CC that the herbicide cannot reach its intracellular target and exert any
 CC significant cytotoxic effect. The herbicide binding protein inhibits the
 CC mobility of the herbicide from the application site to the whole plant
 CC preventing the herbicide reaching particularly sensitive organs.
 CC Additionally, tolerant plants can be produced against herbicides that
 CC have more than one target site

XX
 SQ Sequence 112 AA;

Query Match 100.0%; Score 56; DB 2; Length 112;
 Best Local Similarity 100.0%; Pred. No. 0.066;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPWT 9
DB 94 FQGSHPWT 102

RESULT 8
AAE15711
ID AAE15711 standard; protein; 112 AA.
AC AAE15711;
XX 12-MAR-2002 (first entry)
XX Mouse monoclonal antibody alpha 340 Vx region variant, 340VKb.
XX
XX Mouse; humanised form; monoclonal antibody alpha 340; gene therapy;
KW epidermal growth factor receptor; EGF; cancer; colorectal; lung; breast;
KW gastric; ovarian; immune response; cytostatic; cell growth; apoptosis;
KW inhibitor; mutant; mutein; variant.
XX
OS Mus sp.
OS Synthetic.

Key Location/Qualifiers
FT Misc-difference 7 /note= "Wild type Thr substituted with Ser"
FT Misc-difference 14 /note= "Wild type Ser substituted with Thr"
FT Misc-difference 15 /note= "Wild type Leu substituted with Pro"
FT Misc-difference 17 /note= "Wild type Asp substituted with Glu"
FT Misc-difference 18 /note= "Wild type Gln substituted with Pro"
FT Misc-difference 29 /note= "Wild type Ile substituted with Leu"
FT Misc-difference 50 /note= "Wild type Lys substituted with Gln"
FT Misc-difference 88 /note= "Wild type Leu substituted with Thr"
FT Misc-difference 90 /note= "Wild type Ile substituted with Val"
FT Misc-difference 109 /note= "Wild type Leu substituted with Val"
FT Misc-difference 112 /note= "Wild type Asn substituted with Lys"

WO200188138-A1.
22-NOV-2001.
21-MAY-2001; 2001WO-GB002226.
19-MAY-2000; 2000GB-00011981.
24-AUG-2000; 2000GB-00020794.
(SCAN-) SCANCELL LTD.
Ellis JRM, Durrant LG;
WPI; 2002-062384/08.
New humanized form of mouse monoclonal antibody 340 which binds to
epidermal growth factor receptor and inhibits binding of growth factor,
useful for treating colorectal, lung, breast, gastric and ovarian cancer.
Example 2; Fig 7; 53pp; English.
The present invention relates to a humanised form of the antibody 340 (a
mouse monoclonal antibody which binds to epidermal growth factor (EGF)
receptor and inhibits binding of EGF), obtainable from the cell line

CC deposited with the ECACC under accession number 97021428. The humanised
CC form of the antibody 340 is useful in gene therapy, medicine and in the
CC manufacture of a medicament for treatment or prophylaxis of cancer. The
CC invention is useful for treating colorectal, lung, breast, gastric or
CC ovarian cancers or also for preventing the recurrence of cancer after
CC initial treatment or surgery. The invention is also useful for enhancing
CC a protective immune response against cancer by optimised immunisation
CC schedules. The humanised form of the antibody 340 has reduced
CC immunogenicity but shows similar binding to cells expressing EGF
CC receptor, as the original murine antibody and has increased ability to
CC inhibit the growth of EGF receptor expressing cells. The invention is
CC used as cell growth and apoptosis inhibitor. The present sequence is
CC mouse monoclonal antibody alpha 340 deimmunised light chain variable (VK)
CC region variant, 340VKb
XX
XX Sequence 112 AA;
SQ
Query Match 100.0%; Score 56; DB 5; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.066;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FQGSHPWT 9
DB 94 FQGSHPWT 102

RESULT 9
AAE15713
ID AAE15713 standard; protein; 112 AA.
XX
AC AAE15713;
XX 12-MAR-2002 (first entry)
XX Mouse monoclonal antibody alpha 340 Vx region variant, 340VKd.
XX
XX Mouse; humanised form; monoclonal antibody alpha 340; gene therapy;
KW epidermal growth factor receptor; EGF; cancer; colorectal; lung; breast;
KW gastric; ovarian; immune response; cytostatic; cell growth; apoptosis;
KW inhibitor; mutant; mutein; variant.
XX
OS Mus sp.
OS Synthetic.

Key Location/Qualifiers
FT Misc-difference 7 /note= "Wild type Thr substituted with Ser"
FT Misc-difference 14 /note= "Wild type Ser substituted with Thr"
FT Misc-difference 15 /note= "Wild type Leu substituted with Pro"
FT Misc-difference 17 /note= "Wild type Asp substituted with Glu"
FT Misc-difference 18 /note= "Wild type Gln substituted with Pro"
FT Misc-difference 50 /note= "Wild type Lys substituted with Val"
FT Misc-difference 88 /note= "Wild type Leu substituted with Val"
FT Misc-difference 109 /note= "Wild type Leu substituted with Val"
FT Misc-difference 112 /note= "Wild type Asn substituted with Lys"

WO200188138-A1.
22-NOV-2001.
21-MAY-2001; 2001WO-GB002226.
19-MAY-2000; 2000GB-00011981.
24-AUG-2000; 2000GB-00020794.
(SCAN-) SCANCELL LTD.
Ellis JRM, Durrant LG;
WPI; 2002-062384/08.
New humanized form of mouse monoclonal antibody 340 which binds to
epidermal growth factor receptor and inhibits binding of growth factor,
useful for treating colorectal, lung, breast, gastric and ovarian cancer.
Example 2; Fig 7; 53pp; English.
The present invention relates to a humanised form of the antibody 340 (a
mouse monoclonal antibody which binds to epidermal growth factor (EGF)
receptor and inhibits binding of EGF), obtainable from the cell line

FT Misc-difference 18 /note= "Wild type Gln substituted with Pro"
 FT Misc-difference 50 /note= "Wild type Lys substituted with Gln"
 FT Misc-difference 88 /note= "Wild type Leu substituted with Thr"
 FT Misc-difference 90 /note= "Wild type Ile substituted with Val"
 FT Misc-difference 109 /note= "Wild type Leu substituted with Val"
 FT Misc-difference 112 /note= "Wild type Asn substituted with Lys"
 XX WO200188138-A1.
 XX 22-NOV-2001.
 XX 21-MAY-2001; 2001WO-GB002226.
 PR 19-MAY-2000; 2000GB-00011981.
 PR 24-AUG-2000; 2000GB-00020794.
 XX (SCAN-) SCANCELL LTD.
 PA Ellis JRM, Durrant LG;
 XX WPI; 2002-062384/08.
 XX New humanized form of mouse monoclonal antibody 340 which binds to
 PT epidermal growth factor receptor and inhibits binding of growth factor,
 PT useful for treating colorectal, lung, breast, gastric and ovarian cancer.
 XX Example 2; Fig 7; 53pp; English.
 XX The present invention relates to a humanised form of the antibody 340 (a
 CC mouse monoclonal antibody which binds to epidermal growth factor (EGF)
 CC receptor and inhibits binding of EGF), obtainable from the cell line
 CC deposited with the ECACC under accession number 97021428. The humanised
 CC form of the antibody 340 is useful in gene therapy, medicine and in the
 CC manufacture of a medicament for treatment or prophylaxis of cancer. The
 CC invention is useful for treating colorectal, lung, breast, gastric or
 CC ovarian cancers or also for preventing the recurrence of cancer after
 CC initial treatment or surgery. The invention is also useful for enhancing
 CC a protective immune response against cancer by optimised immunisation
 CC schedules. The humanised form of the antibody 340 has reduced
 CC immunogenicity but shows similar binding to cells expressing EGF
 CC receptor, as the original murine antibody and has increased ability to
 CC inhibit the growth of EGF receptor expressing cells. The invention is
 CC used as cell growth and apoptosis inhibitor. The present sequence is
 CC mouse monoclonal antibody alpha 340 deimmunised light chain variable (VK)
 CC region variant, 340VKC
 XX Sequence 112 AA;
 SQ
 Query Match 100.0%; Score 56; DB 5; Length 112;
 Best Local Similarity 100.0%; Pred. No. 0.066;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 FQGSHPVPT 9
 Db 94 FQGSHPVPT 102
 RESULT 12
 ADA14777
 ID ADA14777 standard; peptide; 112 AA.
 XX ADA14777;
 AC ADA14777;
 XX 06-NOV-2003 (first entry)
 DT Peptide from antibody heavy chain resembling 1A7 #6.
 DE
 XX

KW heavy chain variable region; mouse; ganglioside GD2-associated tumour;
 KW melanoma; antibody; anti-idiotypic; monoclonal antibody; 1A7;
 KW neuroblastoma; glioma; sarcoma; small cell lung cancer.
 OS Mus sp.
 XX US6509016-B1.
 XX 21-JAN-2003.
 PD 15-APR-1999; 99US-00293533.
 PF 17-JAN-1995; 95US-00372676.
 PR 16-JAN-1996; 96US-00591196.
 PR 21-NOV-1996; 96US-00752844.
 XX (KENT) UNIV KENTUCKY.
 XX Chatterjee M, Foon KA, Chatterjee SK;
 PI WPI; 2003-401117/38.
 DR Delaying recurrence and/or development of ganglioside GD2-associated
 PT tumor in individual, by administering antibody containing light and heavy
 PT chain variable region sequences contained in sequence of specified amino
 PT acids.
 XX Example 2; Fig 3; 82pp; English.
 PS The invention relates to the recurrence and/or development of a
 CC ganglioside GD2-associated tumour, e.g. melanoma, in an individual which
 CC is delayed by administration of an antibody comprising light and heavy
 CC chain variable region sequences of the anti-idiotypic monoclonal antibody
 CC 1A7. The antibody is used for delaying recurrence and/or development of
 CC GD2-associated tumour, e.g. melanoma, neuroblastoma, glioma, sarcoma, or
 CC small cell lung cancer, in individual, and for treating individual with
 CC GD2-associated tumour. The present sequence is a unique peptide region
 CC from an antibody sequence resembling the anti-idiotypic antibody 1A7 heavy
 CC chain.
 XX Sequence 112 AA;
 SQ
 Query Match 100.0%; Score 56; DB 6; Length 112;
 Best Local Similarity 100.0%; Pred. No. 0.066;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 FQGSHPVPT 9
 Db 94 FQGSHPVPT 102
 RESULT 13
 ADC35319
 ID ADC35319 standard; protein; 112 AA.
 XX ADC35319;
 AC ADC35319;
 XX 18-DEC-2003 (first entry)
 DT Anti-idiotypic antibody VL region consensus sequence.
 XX Mouse; monoclonal antibody; 1A7; anti-idiotypic antibody; ganglioside GD2;
 KW cytostatic; melanoma; neuroblastoma; small cell lung cancer; tumour;
 KW antibody; variable region; VH; VL; glioma; soft tissue sarcoma; vaccine.
 XX Synthetic.
 OS Mus sp.
 XX US2003114398-A1.
 PN 19-JUN-2003.
 XX 21-MAY-2002; 2002US-00153401.
 PF

XX 17-JAN-1995; 95US-00372676.
 PR 16-JAN-1996; 96US-00591196.
 PR 15-APR-1999; 99US-00293533.
 XX (CHAT/) CHATTERJEE M.
 PA (FOON/) FOON K A.
 PA (CHAT/) CHATTERJEE S K.
 XX Chatterjee M, Foon KA, Chatterjee SK;
 PI WPI; 2003-810913/76.
 XX Novel anti-idiotypic monoclonal antibody 1A7, that is capable of
 PT recruiting a tumor-specific response against glycosphingolipid GD2,
 PT useful for treating a GD2-associated disease e.g., melanoma, glioma, soft
 PT tissue sarcoma.
 XX Example 2; SEQ ID NO 15; 84pp; English.
 XX The invention relates to a monoclonal antibody 1A7 (an anti-idiotypic
 CC antibody eliciting an anti-GD2(ganglioside) response). Also included are
 CC an antibody producing cell deposited under ATCC Accession No. HB-11786
 CC (or its progeny), a polynucleotide comprising a sequence encoding a
 CC polypeptide with immunological activity of 1A7 (where the polypeptide
 CC comprises at least 5 consecutive amino acids from a variable region of
 CC 1A7), an isolated polynucleotide comprising a region of at least 20
 CC consecutive nucleotides that is capable of forming a stable duplex with a
 CC polynucleotide encoding the light or heavy chain variable region of 1A7
 CC under conditions where the region does not form a stable hybrid with a
 CC polynucleotide consisting of a variable region encoding sequence
 CC appearing as ABC35321 - ADC35370, a host cell comprising the
 CC polynucleotide, a fusion polypeptide comprising 1A7, a humanised antibody
 CC comprising 5 consecutive amino acids from the 1A7 variable regions and a
 CC vaccine comprising the antibodies. The antibodies are useful for
 CC eliciting an immune response in an individual, and for treating a GD2-
 CC associated disease in an individual. The GD2-associated diseases is
 CC chosen from melanoma, neuroblastoma, glioma, soft tissue sarcoma, and
 CC small cell carcinoma. The individual has a clinically detectable tumour,
 CC and the method is for palliating the GD2-associated disease. 1A7 is
 CC preferably useful for treating a tumour that was previously detected in
 CC the individual and has been treated and is clinically undetectable at the
 CC time of the administering of 1A7, or for reducing the risk of recurrence
 CC of a clinically detectable tumour. 1A7 and the humanised antibody are
 CC useful for detecting the presence of an anti-GD2 antibody bound to a
 CC tumour cell. The present sequence represents a consensus sequence for the
 CC light or heavy chain variable region of monoclonal antibody 1A7.
 XX Sequence 112 AA;
 SQ Query Match 100.0%; Score 56; DB 7; Length 112;
 Best Local Similarity 100.0%; Pred. No. 0.066;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FQGSHPVPT 9
 Db 94 FQGSHPVPT 102
 RESULT 14
 ADD94125
 ID ADD94125 standard; protein; 112 AA.
 AC ADD94125;
 XX 29-JAN-2004 (first entry)
 DT Mouse HUI77 variable region light chain partial amino acid sequence.
 DE grafted antibody; complementarity determining region; CDR; light CDR;
 XX heavy CDR; cryptic collagen epitope; solid tumour;
 KW new blood vessel growth; angiogenesis; tumour growth; cytostatic;
 KW collagen agonist; collagen antagonist; cancer metastasis;

KW anti-cryptic collagen; antibody; HUI77; variable region light chain;
 KW mouse; murine.
 XX Mus musculus.
 XX WO2003046204-A2.
 XX 05-JUN-2003.
 XX 26-NOV-2002; 2002WO-US038147.
 XX 26-NOV-2001; 2001US-00995529.
 PR 06-DEC-2001; 2001US-00011250.
 XX (CELL-) CELL MATRIX INC.
 PA Watking JD, Huse WD, Tang Y, Broek D, Brooks PC;
 PI WPI; 2003-513649/48.
 DR N-PSDB; ADD94124.
 XX New cryptic collagen antibody with one or more complementarity
 PT determining regions, useful for diagnosing and treating disorders
 PT associated with angiogenesis, tumor growth and/or cancer metastasis.
 XX Example 1; SEQ ID NO 10; 232pp; English.
 XX This invention relates to a novel grafted antibody or its functional
 CC fragment comprising one or more complementarity determining regions
 CC (CDRs) of a defined light CDR and a heavy CDR with at least one amino
 CC acid (aa) substitution where the antibody has specific binding activity
 CC for a cryptic collagen epitope. The growth of all solid tumours requires
 CC new blood vessel growth, angiogenesis, inhibition of which is an approach
 CC to limiting tumour growth. The invention may allow development of
 CC therapeutics with a cytostatic activity as a collagen agonist or
 CC antagonist. The invention is useful for diagnosing and treating disorders
 CC associated with angiogenesis, tumour growth and/or cancer metastasis. The
 CC present sequence is the partial amino acid sequence of the mouse anti-
 CC cryptic collagen site antibody HUI77 variable region light chain used
 CC during the creation of the antibody of the invention.
 XX Sequence 112 AA;
 SQ Query Match 100.0%; Score 56; DB 7; Length 112;
 Best Local Similarity 100.0%; Pred. No. 0.066;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FQGSHPVPT 9
 Db 94 FQGSHPVPT 102
 RESULT 15
 ADJ76888
 ID ADJ76888 standard; protein; 112 AA.
 XX ADJ76888;
 XX 06-MAY-2004 (first entry)
 DT Anti-IGF-IR related protein #5.
 DE cytostatic; antipsoriatic; antibody;
 KW insulin-like growth factor-1 receptor; IGF-IR; tyrosine kinase activity;
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;
 KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;
 KW CDR.
 XX Mus musculus.
 OS WO2003059951-A2.
 PN 24-JUL-2003.

XX 20-JAN-2003; 2003WO-FR000178.
PF 18-JAN-2002; 2002FR-0000653.
XX 18-JAN-2002; 2002FR-0000654.
PR 07-MAY-2002; 2002FR-00005753.
XX (FABR) FABRE MEDICAMENT SA PIERRE.
PA Goetsch L, Corvala N, Leger O;
XX WPI; 2003-569653/53.
XX New antibodies that bind to human insulin-like growth factor receptor,
PT useful for treatment, prevention and diagnosis of cancers.
XX Disclosure; SEQ ID NO 54; 164pp; French.
XX The invention relates to an isolated antibody (Ab), and its functional
CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-
CC 1R) and optionally: (i) inhibit natural binding of insulin-like growth
CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine
CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or
CC treat diseases associated with overexpression and/or abnormal activity of
CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with
CC hyperactivity of signal transduction pathways mediated by interaction of
CC these receptors with their ligands. Especially they inhibit
CC transformation of normal cells to tumor cells, inhibit growth and/or
CC proliferation of tumor cells, so are useful against cancers of the
CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
CC also for treating psoriasis. Ab are also used to diagnose diseases caused
CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a
CC protein sequence used to generate the Ab of the invention.
XX SQ Sequence 112 AA;

Query Match 100.0%; Score 56; DB 7; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.066;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPVPT 9
Db 94 FQGSHPVPT 102

Search completed: December 30, 2005, 13:23:58
Job time : 80.9839 secs

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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:11:41 ; Search time 12.7742 Seconds
(without alignments)
67.789 Million cell updates/sec

Title: US-10-735-916A-6
Perfect score: 56
Sequence: 1 FQSHVPWT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	103	2 PH1043	Ig light chain V r
2	53	94.6	121	2 S67944	Ig kappa chain BrE
3	47	83.9	102	2 S14590	Ig kappa chain V r
4	47	83.9	102	2 S14594	Ig kappa chain V r
5	47	83.9	102	2 S14592	Ig kappa chain V r
6	47	83.9	102	2 S14593	Ig kappa chain V r
7	47	83.9	102	2 E28195	Ig kappa chain V r
8	47	83.9	110	2 S26335	Ig kappa chain V r
9	47	83.9	112	2 D28195	Ig kappa chain V r
10	47	83.9	131	2 B39276	Ig light chain pre
11	46	82.1	103	2 PH1042	Ig light chain V r
12	46	82.1	113	2 PL0203	anti-DNA autoantib
13	45	80.4	114	2 A32987	Ig kappa chain V-I
14	44	78.6	103	2 PH1040	Ig light chain V r
15	44	78.6	112	2 A49715	Ig kappa chain V r
16	44	78.6	219	2 S16112	Ig kappa chain V r
17	43	76.8	101	2 S11126	Ig kappa chain V r
18	43	76.8	102	2 S14591	Ig kappa chain V r
19	43	76.8	112	2 S38719	Ig light chain V r
20	43	76.8	112	2 A36259	Ig kappa chain V r
21	42	75.0	93	2 PH1039	Ig light chain V r
22	42	75.0	112	2 PL0273	Ig kappa chain V r
23	42	75.0	112	2 A31807	Ig kappa chain V r
24	42	75.0	219	2 PC4203	Ig kappa chain (mo
25	42	75.0	389	2 H86676	hypothetical prote
26	41	73.2	103	2 PH1030	Ig light chain V r
27	41	73.2	112	2 H28840	Ig kappa chain V r
28	41	73.2	112	2 B31485	Ig kappa chain V r
29	41	73.2	112	2 A27887	Ig kappa chain V r

30 41 73.2 113 2 E30560 Ig kappa chain V r
31 41 73.2 114 2 A34353 anti-peptide Fab,
32 41 73.2 118 2 PT0359 Ig kappa chain V r
33 41 73.2 131 2 B34904 Ig kappa chain pre
34 41 73.2 131 2 S52449 Ig kappa chain V r
35 41 73.2 131 2 C34904 Ig kappa chain pre
36 41 73.2 219 2 S52028 Ig kappa chain - m
37 41 73.2 225 2 JL0029 Ig kappa chain pre
38 40 71.4 96 2 S55366 Ig kappa chain V r
39 40 71.4 102 2 PH1035 Ig light chain V r
40 40 71.4 119 2 A49032 Ig kappa chain V r
41 39 69.6 111 2 S15673 Ig kappa chain V r
42 39 69.6 112 2 C27887 Ig kappa chain V r
43 38 67.9 103 2 PH1034 Ig light chain V r
44 38 67.9 103 2 PH1038 Ig light chain V r
45 38 67.9 103 2 PH1037 Ig light chain V r

ALIGNMENTS

RESULT 1

PH1043
Ig light chain V region (clone 111.68) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: PH1043

R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A;Title: Both IGM and IGG anti-DNA antibodies are the products of clonally selective B

A;Reference number: PH0971; MUID:92381444; PMID:1512540

A;Accession: PH1043

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-103 <TIL>

A;Cross-references: UNIPROT:Q99M37; UNIPARC:UPI0000176AA5

A;Experimental source: B cell, strain [NZB x NZW]F1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: immunoglobulin

F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 56; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQSHVPWT 9
|||
Db 94 FQSHVPWT 102

RESULT 2

S67944
Ig kappa chain BrE-3 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 05-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C;Accession: S67944

R;Couto, J.R.; Blank, E.W.; Peterson, J.A.; Ceriani, R.L.

Hybridoma 12, 15-23, 1993

A;Title: Cloning of cDNAs encoding the variable domains of antibody BrE-3 and construct

A;Reference number: S67944; MUID:93202671; PMID:8454302

A;Accession: S67944

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-121 <COU>

A;Cross-references: UNIPARC:UPI00001149C2; EMBL:Z22547; NID:g296068; PIDN:CAA80268.1; P

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;25-104/Domain: immunoglobulin homology <IMM>

Query Match 94.6%; Score 53; DB 2; Length 121;
Best Local Similarity 88.9%; Pred. No. 0.022;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQSHVPWT 9

```
Db      103 FQGSHPVPT 111
||||:|||||
RESULT 3
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C:Accession: S14590, S14589
R:Chen, Q.; Stenzel-Poore, M.; Rittenberg, M.B.
submitted to the EMBL Data Library, March 1991
A:Description: Natural polyclonal antibodies differ from Ag-induced antibodies in VH
A:Reference number: S14484
A:Accession: S14590
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-102 <CHE>
A:Cross-references: UNIPARC:UPI0000115F40; EMBL:X58662; NID:G52927; PIDN:CAA41519.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match      83.9%; Score 47; DB 2; Length 102;
Best Local Similarity 88.9%; Pred. No. 0.21;
Matches      8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 FQGSHPVPT 9
      |||||:|
Db      94 FQGSHPVPT 102

RESULT 4
S14594
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C:Accession: S14594
R:Chen, Q.; Stenzel-Poore, M.; Rittenberg, M.B.
submitted to the EMBL Data Library, March 1991
A:Description: Natural polyclonal antibodies differ from Ag-induced antibodies in VH
A:Reference number: S14484
A:Accession: S14594
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-102 <CHE>
A:Cross-references: UNIPARC:UPI0000115F44; EMBL:X58666; NID:G52935; PIDN:CAA41523.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match      83.9%; Score 47; DB 2; Length 102;
Best Local Similarity 88.9%; Pred. No. 0.21;
Matches      8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 FQGSHPVPT 9
      |||||:|
Db      94 FQGSHPVPT 102

RESULT 5
S14592
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C:Accession: S14592
R:Chen, Q.; Stenzel-Poore, M.; Rittenberg, M.B.
submitted to the EMBL Data Library, March 1991
A:Description: Natural polyclonal antibodies differ from Ag-induced antibodies in VH
A:Reference number: S14484
A:Accession: S14592
A>Status: preliminary
A:Molecule type: mRNA
```

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A:Residues: 1-102 <CHE>
A:Cross-references: UNIPARC:UPI0000115F42; EMBL:X58664; NID:G52931; PIDN:CAA41521.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match      83.9%; Score 47; DB 2; Length 102;
Best Local Similarity 88.9%; Pred. No. 0.21;
Matches      8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 FQGSHPVPT 9
      |||||:|
Db      94 FQGSHPVPT 102

RESULT 6
S14593
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C:Accession: S14593
R:Chen, Q.; Stenzel-Poore, M.; Rittenberg, M.B.
submitted to the EMBL Data Library, March 1991
A:Description: Natural polyclonal antibodies differ from Ag-induced antibodies in VH
A:Reference number: S14484
A:Accession: S14593
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-102 <CHE>
A:Cross-references: UNIPARC:UPI0000115F43; EMBL:X58665; NID:G52933; PIDN:CAA41522.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match      83.9%; Score 47; DB 2; Length 102;
Best Local Similarity 88.9%; Pred. No. 0.21;
Matches      8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 FQGSHPVPT 9
      |||||:|
Db      94 FQGSHPVPT 102

RESULT 7
E28195
Ig kappa chain V region (anti-haloperidol antibody E) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 01-Dec-1989 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: E28195
R:Sherman, M.A.; Deans, R.J.; Bolger, M.B.
J. Biol. Chem. 263, 4059-4063, 1988
A:Title: Haloperidol binding to monoclonal antibodies. Hypervariable region amino acid
A:Reference number: A28195; MUID:88153717; PMID:3267217
A:Accession: E28195
A:Molecule type: mRNA
A:Residues: 1-102 <SHE>
A:Cross-references: UNIPROT:Q99M37; UNIPARC:UPI0000176B1B; EMBL:M29770
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:6-85/Domain: immunoglobulin homology <IMM>

Query Match      83.9%; Score 47; DB 2; Length 102;
Best Local Similarity 88.9%; Pred. No. 0.21;
Matches      8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 FQGSHPVPT 9
      |||||:|
Db      84 FQGSHPVPT 92

RESULT 8
S26335
Ig kappa chain V region - mouse
```

C;Species: Mus musculus (house mouse)
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
 C;Accession: S26335
 R;Stark, S.E.; Caton, A.J.
 J. Exp. Med. 174, 613-624, 1991
 A;Title: Antibodies that are specific for a single amino acid interchange in a protein e
 A;Reference number: S26309; MUID:91341421; PMID:1908510
 A;Accession: S26335
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-110 <STA>
 A;Cross-references: UNIPARC:UPI0000115F78; EMBL:XS9183; NID:G52314; PIDN:CAA1893.1; PID
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 83.9%; Score 47; DB 2; Length 110;
 Best Local Similarity 88.9%; Pred. No. 0.23;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPVPT 9
 |||||:
 Db. 94 FQGSHPVPT 102

RESULT 9
 D28195
 Ig kappa chain V region (anti-haloperidol antibody D) - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
 C;Accession: D28195
 R;Sherman, M.A.; Deans, R.J.; Bolger, M.B.
 J. Biol. Chem. 263, 4059-4063, 1988
 A;Title: Haloperidol binding to monoclonal antibodies. Hypervariable region amino acid s
 A;Reference number: A28195; MUID:88153717; PMID:3267217
 A;Accession: D28195
 A;Molecule type: mRNA
 A;Residues: 1-112 <SHE>
 A;Cross-references: UNIPROT:Q99M37; UNIPARC:UPI0000176B01; GB:M19769
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 83.9%; Score 47; DB 2; Length 112;
 Best Local Similarity 88.9%; Pred. No. 0.23;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPVPT 9
 |||||:
 Db. 94 FQGSHPVPT 102

RESULT 10
 B39276
 Ig light chain precursor V-D-J region (6-19) - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 21-Jan-2000
 C;Accession: B39276
 R;Reininger, L.; Berney, T.; Shibata, T.; Spertini, F.; Merino, R.; Izui, S.
 Proc. Natl. Acad. Sci. U.S.A. 87, 10038-10042, 1990
 A;Title: Cryoglobulinemia induced by a murine IgG3 rheumatoid factor: skin vasculitis an
 A;Reference number: A39276; MUID:91088540; PMID:2263605
 A;Accession: B39276
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-131 <REI>
 A;Cross-references: UNIPARC:UPI0000115153; GB:M55313; NID:G198095; PIDN:AAA63385.1; PID:
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: immunoglobulin
 F;35-114/Domain: immunoglobulin homology <IMM>

Query Match 83.9%; Score 47; DB 2; Length 131;
 Best Local Similarity 88.9%; Pred. No. 0.28;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPVPT 9
 |||||:
 Db. 113 FQGSHPVPT 121

RESULT 11
 PH1042
 Ig light chain V region (clone 202.s38) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
 C;Accession: PH1042
 R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
 J. Exp. Med. 176, 761-779, 1992
 A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B
 A;Reference number: PH0971; MUID:92381444; PMID:1512540
 A;Accession: PH1042
 A;Status: nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-103 <TIL>
 A;Cross-references: UNIPROT:Q99M37; UNIPARC:UPI0000176AA4
 A;Experimental source: B cell, strain [NZB x NZW]F1
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: immunoglobulin
 F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 82.1%; Score 46; DB 2; Length 103;
 Best Local Similarity 88.9%; Pred. No. 0.33;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPVPT 9
 |||||:
 Db. 94 FQGSHPVPT 102

RESULT 12
 PL0203
 anti-DNA autoantibody BV17-31, kappa chain V region - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
 C;Accession: PL0203
 R;Smith, R.G.; Voss Jr., E.W.
 Mol. Immunol. 27, 463-470, 1990
 A;Title: Variable region primary structures of monoclonal anti-DNA autoantibodies from
 A;Reference number: PL0198; MUID:90309788; PMID:2114528
 A;Accession: PL0203
 A;Molecule type: mRNA
 A;Residues: 1-113 <SMI>
 A;Cross-references: UNIPARC:UPI0000113786; GB:X53643; NID:G50196; PIDN:CAA37694.1; PID:
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 F;16-95/Domain: immunoglobulin homology <IMM>
 F;24-39/Region: complementarity-determining 1
 F;55-61/Region: complementarity-determining 2
 F;94-102/Region: complementarity-determining 3
 F;101-113/Region: D region

Query Match 82.1%; Score 46; DB 2; Length 113;
 Best Local Similarity 88.9%; Pred. No. 0.36;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPVPT 9
 |||||:
 Db. 94 FQGSHPVPT 102

RESULT 13
 A32967
 Ig kappa chain V-II region TE33 - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 21-Jan-2000
 C;Accession: A32967
 R;Levy, R.; Asulin, O.; Scherf, T.; Levitt, M.; Anglister, J.

```

Biochemistry 28, 7168-7175, 1989
A;Title: Probing antibody diversity by 2D NMR: comparison of amino acid sequences, predicted by NMR and by sequence analysis
A;Reference number: A32967; MUID:90057406; PMID:2819059
A;Accession: A32967
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-114 <LEV>
A;Cross-references: UNIPARC:UPI0000114F5D; GB:M30481; NID:g197157; PIDN:AAA38935.1; PID:16-95/Domain: immunoglobulin homology
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match      80.4%; Score 45; DB 2; Length 114;
Best Local Similarity 77.8%; Pred. No. 0.54;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPWT 9
DB 94 FQGHVPWT 102

Search completed: December 30, 2005, 13:34:54
Job time : 13.7742 secs

RESULT 14
PHI040
IG light chain V region (clone 17s.83) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: PH1040
R;Trillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IGM and Igg anti-DNA antibodies are the products of clonally selective B cell gene rearrangement
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1040
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-103 <TIL>
A;Cross-references: UNIPROT:Q99M37; UNIPARC:UPI00000176AA2
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match      78.6%; Score 44; DB 2; Length 103;
Best Local Similarity 77.8%; Pred. No. 0.74;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPWT 9
DB 94 FQGHVPWT 102

RESULT 15
A49715
IG kappa chain V region (anti-glucuronoxylomannan antibody 439) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 21-Jan-2000
C;Accession: A49715
R;Oateson, E.W.; Welch, W.H.; Kozel, T.R.
J. Biol. Chem. 269, 1858-1864, 1994
A;Title: Protein-polysaccharide interactions. A monoclonal antibody specific for the capsular polysaccharide of Streptococcus pneumoniae
A;Reference number: A49715; MUID:94124530; PMID:8294434
A;Accession: A49715
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-112 <OPT>
A;Cross-references: UNIPARC:UPI0000115509; GB:U01240; NID:g402265; PIDN:AAD10617.1; PID:16-95/Domain: immunoglobulin homology
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match      78.6%; Score 44; DB 2; Length 112;
Best Local Similarity 75.0%; Pred. No. 0.8;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:11:26 ; Search time 81 Seconds
(without alignments)

78.392 Million cell updates/sec

Title: US-10-735-916A-6

Perfect score: 56

Sequence: 1 FQGSHPWT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	82.1	248	2	Q65ZQ7 mus sp. b3(
2	42	75.0	375	2	Q91YR3 MOUSE
3	42	75.0	389	2	Q9CIE7 LACTOCOCUS
4	42	75.0	504	2	Q4HV68 GIBZEA
5	41	73.2	112	2	Q53VP8 MOUSE
6	41	73.2	962	2	Q845Y7 9CHRO
7	41	73.2	962	2	Q845Y8 MICAE
8	41	73.2	993	2	Q48915 MICAE
9	41	73.2	2114	2	Q8RTG4 MICAE
10	41	73.2	2126	2	Q93LR1 MICAE
11	41	73.2	2126	2	Q93LR2 MICAE
12	41	73.2	2126	2	Q9S1A8 MICAE
13	40	71.4	201	2	Q5CFU2 CRYHO
14	40	71.4	982	2	Q51ZV2 MAGGR
15	40	71.4	2133	2	Q7WRQ4 9NOST
16	39.5	70.5	436	2	Q82DC5 STROMA
17	39	69.6	53	2	Q5C219 SCHUA
18	39	69.6	101	1	YB7J SCHPO
19	39	69.6	267	2	Q51HW6 MAGGR
20	39	69.6	348	2	Q854X6 9CAUD
21	39	69.6	463	2	Q6D073 ERWCT
22	39	69.6	508	2	Q6Z5V5 ORYSA
23	39	69.6	510	2	Q511B2 MAGGR
24	39	69.6	694	2	Q6NK77 CORDI
25	39	69.6	700	2	Q6Z5V6 ORYSA
26	39	69.6	1356	2	Q4IOD3 GIBZE
27	38.5	68.8	522	2	Q4J838 SULAC
28	38	67.9	173	2	Q53656 STIAU
29	38	67.9	217	2	Q51MF7 MAGGR
30	38	67.9	232	2	Q82WL3 NITEU
31	38	67.9	303	2	Q4Q3K2_LEIMA

32	38	67.9	342	2	Q850Y4 ORYSA
33	38	67.9	348	2	Q6LNP1 PHOPR
34	38	67.9	402	2	Q5MB05 MICROGADUS
35	38	67.9	460	2	Q8ZBA0 YERSINIA PE
36	38	67.9	461	2	Q66F83 YERPE
37	38	67.9	509	2	Q5QIB0 CAMAC
38	38	67.9	543	2	Q83X81 STRRO
39	38	67.9	564	2	Q53PM9 ORYSA
40	38	67.9	622	2	Q5MB06 MICROGADUS
41	38	67.9	655	2	Q8LN69 ORYSA
42	38	67.9	684	2	Q49319 ARATH
43	38	67.9	773	2	Q7YOC0 ORYSA
44	38	67.9	779	2	Q8H8E2 ORYSA
45	38	67.9	794	2	Q7XTH2 ORYSA

Q850Y4	oryza sativ
Q6LNP1	photobacter
Q5MB05	microgadus
Q8ZBA0	yersinia pe
Q66F83	yersinia ps
Q5QIB0	camptotheca
Q83X81	streptomyce
Q53PM9	oryza sativ
Q5MB06	microgadus
Q8LN69	oryza sativ
Q49319	arabidopsis
Q7YOC0	oryza sativ
Q8H8E2	oryza sativ
Q7XTH2	oryza sativ

ALIGNMENTS

RESULT 1

Q65ZQ7_9MURI PRELIMINARY; PRT; 248 AA.

AC Q65ZQ7; 9MURI PRELIMINARY; PRT; 248 AA.
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE B3(Fv)-PE40 (Fragment).
GN Name=B3(Fv)-PE40;

OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92020904; PubMed=1924323;
RA Brinkmann U., Pai L.H., FitzGerald D.J., Willingham M., Pastan I.;
RT "B3(Fv)-PE38KDEL, a single-chain immunotoxin that causes complete regression of a human carcinoma in mice";
RL Proc. Natl. Acad. Sci. U.S.A. 88:8616-8620(1991).
DR EMBL; S57990; AAB19971.2; -; mRNA.
DR SMR; Q65ZQ7; 4-247.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGv; 2.
DR PROSITE; PS50835; IG LIKE; 2.
FT NON TER 248 248
SQ SEQUENCE 248 AA; 26634 MW; 7A3759B43E570950 CRC64;

Query Match 82.1%; Score 46; DB 2; Length 248;

Best Local Similarity 88.9%; Pred. No. 7;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQGSHPWT 9

Db 229 FQGSHPWT 237

RESULT 2

Q91YR3 MOUSE PRELIMINARY; PRT; 375 AA.

AC Q91YR3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Phf1 protein.
GN Name=Phf1;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.

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OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
RX Expression driven by an MMTV-LTR enhancer.;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinska M.I., Skalek U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
RX Expression driven by an MMTV-LTR enhancer.;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015077; AAH15077.1; -; mRNA.
DR Ensembl; ENSMUSG00000024193; Mus musculus.
DR MGI; MGI:98647; Phf1.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002999; Tudor.
DR InterPro; IPR001965; Znf_PHD.
DR Pfam; PF00628; PHD; 2.
DR SMART; SM00249; PHD; 2.
DR SMART; SM00333; TUDOR; 1.
DR PROSITE; PS01359; ZF_PHD_1; UNKNOWN_1.
DR PROSITE; PS00016; ZF_PHD_2; 1.
SQ SEQUENCE 375 AA; 41146 MW; 57D88E19A5BBB729 CRC64;

Query Match 75.0%; Score 42; DB 2; Length 375;
Best Local Similarity 85.7%; Pred. No. 53;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QGSHVPW 8
Db 359 EGSHVFW 365
:|||||

RESULT 3
Q9CIE7 LACIA
ID Q9CIE7 LACIA PRELIMINARY; PRT; 389 AA.
AC Q9CIE7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Cellulose-specific PTS system IIC component (EC 2.7.1.69).
GN Names=ptsC; OrderedLocNames=IL0416;
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=IL1403;

RX MEDLINE=21235186; PubMed=11337471; DOI=10.1101/gr.CR-1697R;
RA Bolotin A., Wincker P., Mauger S., Jaillon O., Matarne K.,
RA Weissenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
RT lactis ssp. lactis IL1403.";
RL Genome Res. 11:731-753 (2001).
DR EMBL; AE006278; AAK04514.1; -; Genomic_DNA.
DR PIR; H86676; H86676.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008982; F:protein-N(P)-phosphohistidine-sugar phospho. .; IEA.
DR GO; GO:0005351; F:sugar porter activity; IEA.
DR GO; GO:0006740; F:transferase activity; IEA.
DR GO; GO:0009401; F:phosphoenolpyruvate-dependent sugar phospho. .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003352; PTrans_EIIC.
DR InterPro; IPR004501; Pts_lac.
DR Pfam; PF02378; PTS_EIIC_1.
DR TIGRfams; TIGR00410; lacB; 1.
KW Complete proteome.
SQ SEQUENCE 389 AA; 41700 MW; F49D2C3095FCF347 CRC64;

Query Match 75.0%; Score 42; DB 2; Length 389;
Best Local Similarity 66.7%; Pred. No. 55;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FQGHVPWT 9
Db 325 FNGAIVPWT 333
|::|||

RESULT 4
Q4HV68 GIBZE
ID Q4HV68 GIBZE PRELIMINARY; PRT; 504 AA.
AC Q4HV68;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=FG1140.1;
OS Gibberella zeae PH-1.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
OX NCBI_TaxID=229533;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PH-1;
RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,
RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepel Y., Collymore A., Cooke A., Cooke P., Corum B., Dearellano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,
RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafer N.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J., Manning J.,
RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Maneus L.,
RA Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rogov P.,
RA Roman J., Schauer S., Schupbach R., Seaman S., Severy P., Smirnov S.,
RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
RA Vassiliou H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.;
RT "Fusarium graminearum genome sequence.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

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CC preliminary data.
 DR EMBL; AACW01000459; EAA74791.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 504 AA; 55160 MW; 26098EA86A332C2F CRC64;
 Query Match 75.0%; Score 42; DB 2; Length 504;
 Best Local Similarity 66.7%; Pred. No. 72;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 FQGSHPVPT 9
 |||||:
 Db 72 FVGSHPVPT 80
 |||||:
 RESULT 5
 Q53VP8 MOUSE
 ID Q53VP8 MOUSE PRELIMINARY; PRT; 112 AA.
 AC Q53VP8;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Kappa chain (Fragment).
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=86136012; PubMed=3937730;
 RA Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
 RT "The idiotypic network and the internal image; possible regulation of
 RT a germ-line network by paucigene encoded Ab2 (anti-idiotypic)
 RT antibodies in the GAT system.";
 RL ENBO J. 4:3681-3688 (1985).
 RN [2]
 RP NUCLEOTIDE SEQUENCE OF 108-109.
 RA Fougereau M.;
 RL Submitted (NOV-1986) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X03386; CAA27113.1; -; mRNA.
 FT NON_TER 1 1
 FT NON_TER 112 112
 SQ SEQUENCE 112 AA; 12266 MW; C844B7881A89C18A CRC64;
 Query Match 73.2%; Score 41; DB 2; Length 112;
 Best Local Similarity 77.8%; Pred. No. 24;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 FQGSHPVPT 9
 |||||:
 Db 94 FQGIHVPY 102
 |||||:
 RESULT 6
 Q845Y7 9CHRO
 ID Q845Y7 9CHRO PRELIMINARY; PRT; 962 AA.
 AC Q845Y7;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Microcystin synthetase (Fragment).
 GN Namecmyb;
 OS Microcystis viridis.
 CC Bacteria; Cyanobacteria; Chroococcales; Microcystis.
 OX NCBI_TaxID=44822;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NIES102;
 RA Yoshida T., Shi R., Chinen H., Yuki Y., Yoshida M., Kondo R.,
 RA Shingo H.;
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme family.

DR EMBL; AB092807; BAC57997.1; -; Genomic_DNA.
 DR HSSP; P14687; 1AMU.
 DR GO; GO:0048037; F:cofactor binding; IEA.
 DR GO; GO:0016874; F:ligase activity; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro; IPR010071; AA_adenyl_dom.
 DR InterPro; IPR009081; ACP_like.
 DR InterPro; IPR000873; AMP_bind.
 DR InterPro; IPR001242; Condensatn.
 DR InterPro; IPR006163; Phspanteth_bind.
 DR Pfam; PF00501; AMP-binding; 1.
 DR Pfam; PF00668; Condensation; 1.
 DR Pfam; PF00550; PP-binding; 1.
 DR PRINTS; PR00154; AMPBINDING.
 DR TIGRFAMs; TIGR01733; AA-adenyl-dom; 1.
 DR PROSITE; PS50075; ACP_DOMAIN; 1.
 DR PROSITE; PS00455; AMP_BINDING; 1.
 FT NON_TER 1 1
 FT NON_TER 962 962
 SQ SEQUENCE 962 AA; 108980 MW; 2510459A5CCD484F CRC64;
 Query Match 73.2%; Score 41; DB 2; Length 962;
 Best Local Similarity 66.7%; Pred. No. 2.1e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 FQGSHPVPT 9
 |||||:
 Db 862 FVGSHPVPT 870
 |||||:
 RESULT 7
 Q845Y8 MICAE
 ID Q845Y8 MICAE PRELIMINARY; PRT; 962 AA.
 AC Q845Y8;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Microcystin synthetase (Fragment).
 GN Namecmyb;
 OS Microcystis aeruginosa.
 CC Bacteria; Cyanobacteria; Chroococcales; Microcystis.
 OX NCBI_TaxID=1126;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NIES298;
 RA Yoshida T., Shi R., Chinen H., Yuki Y., Yoshida M., Kondo R.,
 RA Shingo H.;
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme family.
 CC EMBL; AB092806; BAC57996.1; -; Genomic_DNA.
 DR HSSP; P14687; 1AMU.
 DR GO; GO:0048037; F:cofactor binding; IEA.
 DR GO; GO:0016874; F:ligase activity; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro; IPR010071; AA_adenyl_dom.
 DR InterPro; IPR009081; ACP_like.
 DR InterPro; IPR000873; AMP_bind.
 DR InterPro; IPR001242; Condensatn.
 DR InterPro; IPR001969; Pept_Asp_AS.
 DR InterPro; IPR006163; Phspanteth_bind.
 DR Pfam; PF00501; AMP-binding; 1.
 DR Pfam; PF00668; Condensation; 1.
 DR Pfam; PF00550; PP-binding; 1.
 DR PRINTS; PR00154; AMPBINDING.
 DR TIGRFAMs; TIGR01733; AA-adenyl-dom; 1.
 DR PROSITE; PS50075; ACP_DOMAIN; 1.
 DR PROSITE; PS00455; AMP_BINDING; 1.
 DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.
 FT NON_TER 1 1
 FT NON_TER 962 962
 SQ SEQUENCE 962 AA; 108678 MW; 37F77CFD87F5FCB4 CRC64;

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Query Match          73.2%; Score 41; DB 2; Length 962;
Best Local Similarity 66.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 FOGSHVPWT 9
DB      862 PKGSHLSWT 870

RESULT 8
Q48915 MICAE
ID Q48915 MICAE PRELIMINARY; PRT; 993 AA.
AC Q48915;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Peptide synthetase module (Fragment).
GN Name=peptide synthetase;
OS Microcystis aeruginosa.
OC Bacteria; Cyanobacteria; Chroococcales; Microcystis.
OX NCBI_TaxID=1126;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HUB 5-2-4;
RX MEDLINE=96162875; PubMed=8595871; DOI=10.1016/0378-1097(95)00469-6;
RA Meisner K., Dittmann E., Borner T.;
RT "Toxic and non-toxic strains of the cyanobacterium Microcystis
aeruginosa contain sequences homologous to peptide synthetase genes.";
RL FEMS Microbiol. Lett. 135:295-303(1996).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HUB 5-2-4;
RA Juerchott K.;
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
family.
DR EMBL; Z28338; CAAB2192.1; -; Genomic_DNA.
DR PIR; S49111; S49111.
DR HSSP; Q30409; 1DNY.
DR GO; GO:0048037; F:cofactor binding; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR010071; AA_adenyl_dom.
DR InterPro; IPR009081; ACP_like.
DR InterPro; IPR000873; AMP_bind.
DR InterPro; IPR001242; Condensatn.
DR InterPro; IPR001969; Pept_Asp_AS.
DR InterPro; IPR006163; Phsppanteth_bind.
DR Pfam; PF00501; AMP-binding; 1.
DR Pfam; PF00668; Condensation; 1.
DR Pfam; PF00550; PP-binding; 1.
DR PRINTS; PR00154; AMPBINDING.
DR TIGRFAMs; TIGR01733; AA-adenyl-dom; 1.
DR PROSITE; PS00075; ACP DOMAIN; 1.
DR PROSITE; PS00455; AMP BINDING; 1.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 993
SQ SEQUENCE 993 AA; 112326 MW; 0EC0929E489CBB1E CRC64;

Query Match          73.2%; Score 41; DB 2; Length 993;
Best Local Similarity 66.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 FOGSHVPWT 9
DB      874 PKGSHLSWT 882

RESULT 9
Q8RTG4 MICAE
ID Q8RTG4 MICAE PRELIMINARY; PRT; 2114 AA.
AC Q8RTG4;
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Peptide synthetase module (Fragment).
GN Name=peptide synthetase;
OS Microcystis aeruginosa.
OC Bacteria; Cyanobacteria; Chroococcales; Microcystis.
OX NCBI_TaxID=1126;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=UV 027;
RA Botes E.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY034602; AAK61391.1; -; Genomic_DNA.
DR HSSP; Q30409; 1DNY.
DR GO; GO:0048037; F:cofactor binding; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0031177; P:metabolism; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR010071; AA_adenyl_dom.
DR InterPro; IPR009081; ACP_like.
DR InterPro; IPR000873; AMP_bind.
DR InterPro; IPR001242; Condensatn.

Query Match          73.2%; Score 41; DB 2; Length 2114;
Best Local Similarity 66.7%; Pred. No. 4.6e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 FOGSHVPWT 9
DB      1267 PKGSHLSWT 1275

RESULT 10
Q93LR1 MICAE
ID Q93LR1 MICAE PRELIMINARY; PRT; 2126 AA.
AC Q93LR1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Microcystin synthetase.
GN Name=mcysB;
OS Microcystis aeruginosa.
OC Bacteria; Cyanobacteria; Chroococcales; Microcystis.
OX NCBI_TaxID=1126;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=UV 027;
RA Botes E.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY034602; AAK61391.1; -; Genomic_DNA.
DR HSSP; Q30409; 1DNY.
DR GO; GO:0048037; F:cofactor binding; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0031177; P:metabolism; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR010071; AA_adenyl_dom.
DR InterPro; IPR009081; ACP_like.
DR InterPro; IPR000873; AMP_bind.
DR InterPro; IPR001242; Condensatn.

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DR InterPro; IPR000977; DNA_ligase.
 DR InterPro; IPR006163; Phosphateth_bind.
 DR InterPro; IPR006162; Ppantne S.
 DR Pfam; PF00501; AMP-binding; 2.
 DR Pfam; PF00668; Condensation; 2.
 DR Pfam; PF00550; PP-binding; 2.
 DR PRINTS; PR00154; AMPBINDING.
 DR TIGRFAMs; TIGR01733; AA-adenyl-dom; 1.
 DR PROSITE; PS0075; ACP DOMAIN; 2.
 DR PROSITE; PS00455; AMP BINDING; 1.
 DR PROSITE; PS00697; DNA_LIGASE_A1; UNKNOWN 1.
 DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; 1.
 SQ SEQUENCE 2126 AA; 242439 MW; 6DB575F2A49B1933 CRC64;

Query Match 73.2%; Score 41; DB 2; Length 2126;
 Best Local Similarity 66.7%; Pred. No. 4.6e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FQSHVPWT 9
 |||||:
 Db 1279 FKSHLSWT 1287

RESULT 11

Q3LR2_MICAE
 ID Q3LR2 MICAE PRELIMINARY; PRT; 2126 AA.
 AC Q3LR2;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Microcystin synthetase.
 GN Name=mcys;
 OS Microcystis aeruginosa.
 OC Bacteria; Cyanobacteria; Chroococcales; Microcystis.
 OX NCBI_TaxID=1126;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PCC 7813;
 RA Botes E.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY034601; AAK61390.1; -; Genomic DNA.
 DR HSSP; O30409; IDNY.
 DR GO; GO:0048037; F:cofactor binding; IEA.
 DR GO; GO:0016874; F:ligase activity; IEA.
 DR GO; GO:0031177; F:phosphopantetheine binding; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro; IPR010071; AA-adenyl-dom.
 DR InterPro; IPR009081; ACP like.
 DR InterPro; IPR000873; AMP-bind.
 DR InterPro; IPR001242; Condensatn.
 DR InterPro; IPR000977; DNA_ligase.
 DR InterPro; IPR001969; Pept_Asp_AS.
 DR InterPro; IPR006163; Phosphateth_bind.
 DR InterPro; IPR006162; Ppantne S.
 DR Pfam; PF00501; AMP-binding; 2.
 DR Pfam; PF00668; Condensation; 2.
 DR PRINTS; PR00154; AMPBINDING.
 DR TIGRFAMs; TIGR01733; AA-adenyl-dom; 1.
 DR PROSITE; PS0075; ACP DOMAIN; 2.
 DR PROSITE; PS00455; AMP BINDING; 2.
 DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN 1.
 DR PROSITE; PS00697; DNA_LIGASE_A1; UNKNOWN 1.
 DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; 1.
 SQ SEQUENCE 2126 AA; 242247 MW; 2A8438725198585C CRC64;

Query Match 73.2%; Score 41; DB 2; Length 2126;
 Best Local Similarity 66.7%; Pred. No. 4.6e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FQSHVPWT 9
 |||||:
 Db 1279 FKSHLSWT 1287

RESULT 12

Q9S1A8_MICAE
 ID Q9S1A8 MICAE PRELIMINARY; PRT; 2126 AA.
 AC Q9S1A8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE McyB protein.
 GN Name=mcys;
 OS Microcystis aeruginosa.
 OC Bacteria; Cyanobacteria; Chroococcales; Microcystis.
 OX NCBI_TaxID=1126;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=K-139;
 RX MEDLINE=99398430; PubMed=10467167;
 RA Nishizawa T., Asayama M., Fujii K., Harada K., Shirai M.;
 RT "Genetic analysis of the peptide synthetase genes for a cyclic
 heptapeptide microcystin in Microcystis spp.";
 J. Biochem. 126:520-529 (1999).
 RL J. Biochem. 126:520-529 (1999).
 DR EMBL; AB019578; BAA83993.1; -; Genomic DNA.
 DR HSSP; P14687; IAMU.
 DR GO; GO:0048037; F:cofactor binding; IEA.
 DR GO; GO:0016874; F:ligase activity; IEA.
 DR GO; GO:0031177; F:phosphopantetheine binding; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro; IPR010071; AA-adenyl-dom.
 DR InterPro; IPR009081; ACP like.
 DR InterPro; IPR000873; AMP-bind.
 DR InterPro; IPR001242; Condensatn.
 DR InterPro; IPR000977; DNA_ligase.
 DR InterPro; IPR001969; Pept_Asp_AS.
 DR InterPro; IPR006163; Phosphateth_bind.
 DR InterPro; IPR006162; Ppantne S.
 DR Pfam; PF00501; AMP-binding; 2.
 DR Pfam; PF00668; Condensation; 2.
 DR PRINTS; PR00154; AMPBINDING.
 DR TIGRFAMs; TIGR01733; AA-adenyl-dom; 1.
 DR PROSITE; PS0075; ACP DOMAIN; 2.
 DR PROSITE; PS00455; AMP BINDING; 2.
 DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN 1.
 DR PROSITE; PS00697; DNA_LIGASE_A1; UNKNOWN 1.
 DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; 1.
 SQ SEQUENCE 2126 AA; 242242 MW; D7EFC6C9F6F43AB3 CRC64;

Query Match 73.2%; Score 41; DB 2; Length 2126;
 Best Local Similarity 66.7%; Pred. No. 4.6e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FQSHVPWT 9
 |||||:
 Db 1279 FKSHLSWT 1287

RESULT 13

Q5CFU2_CRYHO
 ID Q5CFU2 CRYHO PRELIMINARY; PRT; 201 AA.
 AC Q5CFU2;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=Chro.70128;
 OS Cryptosporidium hominis.
 OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
 OC Cryptosporidiidae; Cryptosporidium.
 OX NCBI_TaxID=237895;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=TU502;

Query Match 73.2%; Score 41; DB 2; Length 2126;
 Best Local Similarity 66.7%; Pred. No. 4.6e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FQSHVPWT 9
 |||||:
 Db 1279 FKSHLSWT 1287

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RA Xu P., Widmer G., Wang Y., Ozaki L.S., Alves J.M., Serrano M.G.,
RA Puiu D., Manque P., Akiyoshi D., Mackey A.J., Pearson W.R., Dear P.H.,
RA Bankier A.T., Peterson D.L., Abrahamsen M.S., Kapur V., Tzipori S.,
RA Buck G.A.;
RT "The genome of Cryptosporidium hominis.";
RL Nature 431:1107-1112(2004).
DR EMBL; AAE0100406; EAL35474.1; -; Genomic DNA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004518; F:nuclease activity; IEA.
DR InterPro; IPR012337; RNAseH_fold.
KW Hydrolase; Hypothetical protein; Nuclease.
SQ SEQUENCE 201 AA; 23518 MW; FA6A8F84A00E9AA CRC64;

Query Match 71.4%; Score 40; DB 2; Length 201;
Best Local Similarity 85.7%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QGSHVPMW 8
DB 121 QGSHCPW 127

RESULT 14
Q51ZY2 MAGGR
ID Q51ZY2_MAGGR PRELIMINARY; PRT; 982 AA.
AC Q51ZY2;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=MG05904.4;
OS Magnaporthe grisea 70-15.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthae.
OX NCBI_TaxID=242507;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
RA Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
RA Arachi H., Ambruster J., Bachantsang P., Baldwin J., Barry A.,
RA Bayul T., Blitskay B., Bloom T., Blye J., Boguslavskiy L.,
RA Borowsky M., Boukhalter B., Brunache A., Butler J., Calixte N.,
RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
RA Collimore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
RA Dorjee K., Dorris L., Dufey N., Dupes A., Elkins T., Engels R.,
RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,
RA Gnirke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
RA Jaffe D., Jones C., Kamal M., Kamat A., Kamysseilis M., Karlsson E.,
RA Kells C., Kieu A., Kiener P., Kodira C., Kulbokas E., Labutti K.,
RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
RA Lindblad-toh K., Liu X., Lokytang T., Lokytang Y., Lucien O.,
RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
RA Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,
RA McCarthy M., McDonough S., Meghee T., Meldrim J., Meneus L.,
RA Mesirov J., Mihalev A., Mihova T., Mikkelsen T., Mlenga V., Moru K.,
RA Mozes J., Mulrain L., Munson G., Naylor J., News C., Nguyen C.,
RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
RA Norbu N., O'donnell P., Okoawo O., O'leary S., Omotosho B.,
RA O'Neill K., Osman S., Parker S., Perrin D., Phunkhang P., Pigani B.,
RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
RA Rutman M., Schubach R., Seaman C., Settipalli S., Sharpe T.,
RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,
RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
RA Stenson K., Stone C., Stone S., Stubbs M., Talama J., Tchuinga P.,
RA Tenney P., Tesfaye S., Theodore J., Thoultsang Y., Topham K.,
RA Towey S., Teamia T., Tsomo N., Vallee B., Vassiliev H.,
RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,

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RA Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
RA Yang S., Yang X., Yeager S., Yee B., Young G., Zainoun J., Zembeck L.,
RA Zimmer A., Zody M., Lander E.;
RT "The genome sequence of Magnaporthe grisea.";
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Dean R., Mitchell T., Brown D., Pan H., Thon M.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Zhu H., Blackmon B.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACU0100839; EAA52776.1; -; Genomic DNA.
DR InterPro; IPR012351; Cytokine_4_hlx.
DR InterPro; IPR012340; NA-bind_OB_sub.
DR InterPro; IPR009007; Pept_Aspartc_cat.
KW Hypothetical protein.
SQ SEQUENCE 982 AA; 106107 MW; EC7E86B1E6911520 CRC64;

Query Match 71.4%; Score 40; DB 2; Length 982;
Best Local Similarity 71.4%; Pred. No. 3.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 QSHVPMW 9
DB 554 GEHWPMT 560

RESULT 15
Q7WRQ4_9NOST
ID Q7WRQ4_9NOST PRELIMINARY; PRT; 2133 AA.
AC Q7WRQ4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Peptide synthetase.
GN Name=mcys;
OS Anabaena circinalis 90.
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
OX NCBI_TaxID=46234;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX Pubmed=14766543; DOI=10.1128/ASM.70.2.686-692.2004;
RA Rouhiainen L., Vakkilainen T., Siemer B.L., Buikema W., Haselkorn R.,
RA Sivonen K.;
RT "Genes coding for hepatotoxic heptapeptides (microcystins) in the
RT cyanobacterium Anabaena strain 90.";
RL Appl. Environ. Microbiol. 70:686-692 (2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Rouhiainen L., Vakkilainen T., Lumby-Siemer B., Buikema W.,
RA Haselkorn R., Sivonen K.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY212249; AAO62587.1; -; Genomic DNA.
DR EMBL; AJ536156; CAD60102.1; -; Genomic DNA.
DR HSSP; P14687; IAMU.
DR GO; GO:0048037; F:cofactor binding; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0031177; F:phosphopantetheine binding; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR010071; AA_adenyl_dom.
DR InterPro; IPR009081; AMP_bind.
DR InterPro; IPR000873; AMP-like.
DR InterPro; IPR001242; Condensatn.
DR InterPro; IPR000977; DNA_ligase.
DR InterPro; IPR006163; Phosphateth_bind.
DR InterPro; IPR006162; Ppantne_S.

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DR Pfam; PF00501; AMP-binding; 2.
 DR Pfam; PF00668; Condensation; 2.
 DR Pfam; PF00550; PP-binding; 2.
 DR PRINTS; PR00154; AMPBINDING.
 DR TIGRFAMs; TIGR01733; AA-adenyl-dom; 1.
 DR PROSITE; PS00075; ACP_DOMAIN; 2.
 DR PROSITE; PS00455; AMP_BINDING; 2.
 DR PROSITE; PS00697; DNA_LIGASE_A1; UNKNOWN 1.
 DR PROSITE; PS00012; PHOSPHOPANTETHEINE; 2.
 SQ SEQUENCE 2133 AA; 243072 MW; AF806DB0F9372FE7 CRC64;

Query Match 71.4%; Score 40; DB 2; Length 2133;
 Best Local Similarity 66.7%; Pred. No. 7e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FQSHVPWT 9
 Db 1286 FNGSHLSWT 1294

Search completed: December 30, 2005, 13:33:26
 Job time : 84 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:33:42 ; Search time 66.9194 Seconds
(without alignments)
56.194 Million cell updates/sec

Title: US-10-735-916A-6

Perfect score: 56

Sequence: 1 FQSHVPWT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:
1: /cgm2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgm2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgm2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgm2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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6: /cgm2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	9	3	US-09-995-529-36
2	56	100.0	9	3	US-09-995-529-36
3	56	100.0	9	4	US-10-470-045-48
4	56	100.0	9	5	US-10-735-916A-6
5	56	100.0	49	4	US-10-470-045-94
6	56	100.0	112	3	US-09-995-529-10
7	56	100.0	112	3	US-09-995-529-10
8	56	100.0	112	4	US-10-153-401-15
9	56	100.0	112	4	US-10-308-817-172
10	56	100.0	112	4	US-10-308-817-179
11	56	100.0	112	4	US-10-308-817-180
12	56	100.0	112	4	US-10-308-817-181
13	56	100.0	112	4	US-10-308-817-182
14	56	100.0	112	4	US-10-453-698-172
15	56	100.0	112	4	US-10-453-698-179
16	56	100.0	112	4	US-10-453-698-180
17	56	100.0	112	4	US-10-453-698-181
18	56	100.0	112	4	US-10-453-698-182
19	56	100.0	112	4	US-10-258-728-4
20	56	100.0	112	4	US-10-258-728-25
21	56	100.0	112	4	US-10-258-728-26
22	56	100.0	112	4	US-10-258-728-27
23	56	100.0	112	4	US-10-258-728-28
24	56	100.0	112	5	US-10-735-916A-54
25	56	100.0	112	5	US-10-735-916A-56
26	56	100.0	112	5	US-10-735-916A-61
27	56	100.0	112	5	US-10-735-916A-65

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28      56 100.0 122 5 US-10-735-916A-49
29      56 100.0 131 5 US-10-735-916A-63
30      56 100.0 131 5 US-10-735-916A-67
31      56 100.0 149 3 US-09-990-205-2
32      56 100.0 149 4 US-10-153-401-2
33      56 100.0 249 6 US-11-093-103-84
34      56 100.0 263 4 US-10-153-401-66
35      53 94.6 9 3 US-09-947-839-72
36      53 94.6 131 3 US-09-947-839-11
37      52 92.9 9 3 US-09-995-529-128
38      52 92.9 9 3 US-09-995-529-132
39      52 92.9 9 3 US-09-995-529-138
40      52 92.9 9 3 US-09-995-529-138
41      52 92.9 9 3 US-09-995-529-132
42      52 92.9 9 3 US-09-995-529-138
43      51 91.1 9 3 US-09-995-529-139
44      51 91.1 9 3 US-09-995-529-140
45      51 91.1 9 3 US-09-995-529-141

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ALIGNMENTS

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RESULT 1
US-09-995-529-36
; Sequence 36, Application US/09995529
; Publication No. US20030099655A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; TITLE OF INVENTION: Related Methods
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-995-529-36

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Query Match      100.0%; Score 56; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 FQSHVPWT 9
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DB      1 FQSHVPWT 9

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RESULT 2
US-09-995-529-36
; Sequence 36, Application US/09995529
; Publication No. US20040091482A9
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; TITLE OF INVENTION: Related Methods
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-995-529-36

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Query Match 100.0%; Score 56; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQGSHPVPT 9
| | | | |
Db 1 FQGSHPVPT 9

RESULT 3

US-10-470-045-48
; Sequence 48, Application US/10470045
; Publication No. US20040146505A1
; GENERAL INFORMATION:
; APPLICANT: Scancell Limited
; APPLICANT: Durrant, Linda Gillian
; APPLICANT: Parsons, Tina
; TITLE OF INVENTION: Substances
; FILE REFERENCE: P32181WO/NJL
; CURRENT APPLICATION NUMBER: US/10/470,045
; CURRENT FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: GB 0102145.0
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-470-045-48

Query Match 100.0%; Score 56; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQGSHPVPT 9
| | | | |
Db 1 FQGSHPVPT 9

RESULT 4

US-10-735-916A-6
; Sequence 6, Application US/10735916A
; Publication No. US2005084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10/735,916A
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-735-916A-6

Query Match 100.0%; Score 56; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQGSHPVPT 9
| | | | |
Db 1 FQGSHPVPT 9

RESULT 5

US-10-470-045-94
; Sequence 94, Application US/10470045
; Publication No. US20040146505A1
; GENERAL INFORMATION:
; APPLICANT: Scancell Limited
; APPLICANT: Durrant, Linda Gillian
; APPLICANT: Parsons, Tina
; TITLE OF INVENTION: Substances
; FILE REFERENCE: P32181WO/NJL
; CURRENT APPLICATION NUMBER: US/10/470,045
; CURRENT FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: GB 0102145.0
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 94
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-470-045-94

Query Match 100.0%; Score 56; DB 4; Length 49;
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQGSHPVPT 9
| | | | |
Db 34 FQGSHPVPT 42

RESULT 6

US-09-995-529-10
; Sequence 10, Application US/0995529
; Publication No. US20030099655A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; TITLE OF INVENTION: Related Methods
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-995-529-10

Query Match 100.0%; Score 56; DB 3; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQGSHPVPT 9
| | | | |
Db 94 FQGSHPVPT 102

RESULT 7

US-09-995-529-10

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; Sequence 10, Application US/09995529
; Publication No. US20040091482A9
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; TITLE OF INVENTION: Related Methods
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-995-529-10

Query Match      100.0%; Score 56; DB 3; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FQGSHPVPT 9
DB      94 FQGSHPVPT 102

RESULT 8
US-10-153-401-15
; Sequence 15, Application US/10153401
; Publication No. US20030114398A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; APPLICANT: Foon, Kenneth A.
; APPLICANT: Chatterjee, Sunil K.
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
; TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/153,401
; FILING DATE: 27-Aug-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/293,533
; FILING DATE: 1999-04-15
; APPLICATION NUMBER: US 08/372,676
; FILING DATE: 1995-01-17
; APPLICATION NUMBER: US 08/591,196
; FILING DATE: 1996-01-16
; ATTORNEY/AGENT INFORMATION:
; NAME: Catherine M. Polizzi
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 304142000202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids

; Sequence 10, Application US/09995529
; Publication No. US20040091482A9
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; TITLE OF INVENTION: Related Methods
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-995-529-10

Query Match      100.0%; Score 56; DB 3; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FQGSHPVPT 9
DB      94 FQGSHPVPT 102

RESULT 9
US-10-308-817-172
; Sequence 172, Application US/10308817
; Publication No. US20030219861A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; APPLICANT: Wu, Dayang
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 1087-37
; CURRENT APPLICATION NUMBER: US/10/308,817
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 172
; LENGTH: 112
; TYPE: PRT
; ORGANISM: mouse
US-10-308-817-172

Query Match      100.0%; Score 56; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FQGSHPVPT 9
DB      94 FQGSHPVPT 102

RESULT 10
US-10-308-817-179
; Sequence 179, Application US/10308817
; Publication No. US20030219861A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; APPLICANT: Wu, Dayang
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 1087-37
; CURRENT APPLICATION NUMBER: US/10/308,817
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 179
; LENGTH: 112
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: hybrid humanized antibody light chain
US-10-308-817-179

Query Match      100.0%; Score 56; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FQGSHPVPT 9
DB      94 FQGSHPVPT 102
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RESULT 11
US-10-308-817-180
; Sequence 180, Application US/10308817
; Publication No. US20030219861A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 1087-37
; CURRENT APPLICATION NUMBER: US/10/308,817
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 180
; LENGTH: 112
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: hybrid humanized antibody light chain
US-10-308-817-180
Query Match      100.0%; Score 56; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FQGSHPVPT 9
Db      94 FQGSHPVPT 102

RESULT 12
US-10-308-817-181
; Sequence 181, Application US/10308817
; Publication No. US20030219861A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 1087-37
; CURRENT APPLICATION NUMBER: US/10/308,817
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 181
; LENGTH: 112
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: hybrid humanized antibody light chain
US-10-308-817-181
Query Match      100.0%; Score 56; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FQGSHPVPT 9
Db      94 FQGSHPVPT 102

RESULT 13
US-10-308-817-182
; Sequence 182, Application US/10308817
; Publication No. US20030219861A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 1087-37
; CURRENT APPLICATION NUMBER: US/10/308,817
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 182
; LENGTH: 112
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: hybrid humanized antibody light chain
US-10-308-817-182
Query Match      100.0%; Score 56; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FQGSHPVPT 9
Db      94 FQGSHPVPT 102

RESULT 14
US-10-453-698-172
; Sequence 172, Application US/10453698
; Publication No. US20040038308A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 82 CIP (1087-37 CIP)
; CURRENT APPLICATION NUMBER: US/10/453,698
; CURRENT FILING DATE: 2003-06-03
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 172
; LENGTH: 112
; TYPE: PRT
; ORGANISM: mouse
; OTHER INFORMATION:
US-10-453-698-172
Query Match      100.0%; Score 56; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FQGSHPVPT 9
Db      94 FQGSHPVPT 102

RESULT 15
US-10-453-698-179
; Sequence 179, Application US/10453698
; Publication No. US20040038308A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 82 CIP (1087-37 CIP)
; CURRENT APPLICATION NUMBER: US/10/453,698
; CURRENT FILING DATE: 2003-06-03
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 179
; LENGTH: 112
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: hybrid humanized antibody light chain
US-10-453-698-179
Query Match      100.0%; Score 56; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FQGSHPVPT 9
Db      94 FQGSHPVPT 102

Search completed: December 30, 2005, 14:14:52
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Job time : 67.9194 secs

2006/01/03 11:16:51

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GenCore version 5.1.6
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OM protein' - protein search, using sw model

Run on: December 30, 2005, 13:35:07 ; Search time 3.33871 Seconds
(without alignments)
20.187 Million cell updates/sec

Title: US-10-735-916A-6

Perfect score: 56

Sequence: 1 FQGSHPWT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 57103

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB pep:**
- 2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep:**
- 3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep:**
- 4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep:**
- 5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep:**
- 6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep:**
- 7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB pep:**
- 8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	9	7	US-11-012-353-6
2	56	100.0	9	7	US-11-125-837-15
3	56	100.0	9	7	US-11-105-708-19
4	56	100.0	112	7	US-11-012-353-54
5	56	100.0	112	7	US-11-012-353-56
6	56	100.0	112	7	US-11-012-353-61
7	56	100.0	112	7	US-11-012-353-65
8	56	100.0	122	7	US-11-012-353-49
9	56	100.0	131	7	US-11-012-353-63
10	56	100.0	131	7	US-11-012-353-67
11	56	100.0	131	7	US-11-125-837-23
12	47	83.9	113	6	US-10-932-334-59
13	47	83.9	113	6	US-10-932-334-61
14	47	83.9	251	6	US-10-512-184-30
15	47	83.9	320	6	US-10-512-184-67
16	47	83.9	569	6	US-10-512-184-66
17	47	83.9	618	6	US-10-512-184-48
18	46	82.1	112	7	US-11-012-353-55
19	46	82.1	113	6	US-10-932-334-66
20	46	82.1	113	6	US-10-932-334-68
21	46	82.1	116	7	US-11-065-943-49
22	45	80.4	113	6	US-10-932-334-65
23	44	78.6	112	7	US-11-012-353-57
24	43	76.8	113	6	US-10-932-334-69
25	43	76.8	131	6	US-10-789-273-14

26 42 75.0 113 6 US-10-932-334-62 Sequence 62, Appl
27 41 73.2 9 6 US-10-932-334-6 Sequence 6, Appl
28 41 73.2 113 6 US-10-932-334-8 Sequence 8, Appl
29 41 73.2 113 6 US-10-932-334-9 Sequence 9, Appl
30 41 73.2 113 6 US-10-932-334-10 Sequence 10, Appl
31 41 73.2 113 6 US-10-932-334-11 Sequence 11, Appl
32 41 73.2 113 6 US-10-932-334-12 Sequence 12, Appl
33 41 73.2 113 6 US-10-932-334-58 Sequence 58, Appl
34 41 73.2 113 6 US-10-932-334-63 Sequence 63, Appl
35 41 73.2 113 6 US-10-932-334-64 Sequence 64, Appl
36 41 73.2 113 6 US-10-932-334-82 Sequence 82, Appl
37 41 73.2 113 6 US-10-932-334-83 Sequence 83, Appl
38 41 73.2 113 6 US-10-932-334-84 Sequence 84, Appl
39 41 73.2 113 6 US-10-932-334-85 Sequence 85, Appl
40 41 73.2 113 6 US-10-932-334-86 Sequence 86, Appl
41 41 73.2 113 6 US-10-932-334-90 Sequence 90, Appl
42 41 73.2 113 6 US-10-932-334-94 Sequence 94, Appl
43 41 73.2 132 6 US-10-932-334-50 Sequence 50, Appl
44 40 71.4 100 6 US-10-932-334-56 Sequence 56, Appl
45 40 71.4 113 6 US-10-932-334-60 Sequence 60, Appl

ALIGNMENTS

RESULT 1
US-11-012-353-6
; Sequence 6, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOTSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFIOS, ALAIN
; APPLICANT: HAEUM, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-012-353-6

Query Match 100.0%; Score 56; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.3e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FQGSHPWT 9
| | | | |
Db 1 FQGSHPWT 9

RESULT 2
US-11-125-837-15
; Sequence 15, Application US/11125837

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; Publication No. US20050266003A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Rong-Hwa
; APPLICANT: Chang, Chung Nan
; APPLICANT: Chen, Pei-Jiun
; APPLICANT: Huang, Chiu-Chen
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 13062-011001
; CURRENT APPLICATION NUMBER: US/11/125,837
; CURRENT FILING DATE: 2005-05-10
; PRIOR APPLICATION NUMBER: US 60/569,892
; PRIOR FILING DATE: 2004-05-10
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-125-837-15

Query Match          100.0%; Score 56; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.3e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FQGSHPVPT 9
Db      1 FQGSHPVPT 9
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RESULT 3
US-11-105-708-19
; Sequence 19, Application US/11105708
; Publication No. US20050281821A1
; GENERAL INFORMATION:
; APPLICANT: Pernasetti, Flavia
; APPLICANT: Freimark, Bruce
; APPLICANT: Van Epps, Dennis
; APPLICANT: Brooks, Peter C
; TITLE OF INVENTION: Method and Composition for Angiogenesis Inhibition
; FILE REFERENCE: 30797-704.501
; CURRENT APPLICATION NUMBER: US/11/105,708
; CURRENT FILING DATE: 2005-04-13
; PRIOR APPLICATION NUMBER: 09/478,977
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: 60/152,496
; PRIOR FILING DATE: 1999-09-02
; PRIOR APPLICATION NUMBER: 60/143,534
; PRIOR FILING DATE: 1999-09-02
; PRIOR APPLICATION NUMBER: 60/114,878
; PRIOR FILING DATE: 1999-01-06
; PRIOR APPLICATION NUMBER: 60/114,877
; PRIOR FILING DATE: 1999-01-06
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-105-708-19

Query Match          100.0%; Score 56; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.3e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FQGSHPVPT 9
Db      1 FQGSHPVPT 9
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RESULT 4
US-11-012-353-54

; Sequence 54, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 54
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-012-353-54

Query Match          100.0%; Score 56; DB 7; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.00059;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FQGSHPVPT 9
Db      94 FQGSHPVPT 102
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RESULT 5
US-11-012-353-56
; Sequence 56, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
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; SEQ ID NO 56
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-012-353-56

Query Match 100.0%; Score 56; DB 7; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.00059;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQGSHPVPT 9
Db 94 FQGSHPVPT 102

RESULT 6

US-11-012-353-61
; Sequence 61, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN

; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353

; PRIORITY FILING DATE: 2004-12-16
; PRIORITY FILING DATE: 2003-12-16
; PRIORITY FILING DATE: 2003-07-11
; PRIORITY FILING DATE: 2003-07-11
; PRIORITY FILING DATE: 2003-01-20
; PRIORITY FILING DATE: 2003-01-20
; PRIORITY FILING DATE: 2002-05-07
; PRIORITY FILING DATE: 2002-05-07
; PRIORITY FILING DATE: 2002-01-18
; PRIORITY FILING DATE: 2002-01-18
; PRIORITY FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 61
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens

US-11-012-353-61
Query Match 100.0%; Score 56; DB 7; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.00059;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQGSHPVPT 9
Db 94 FQGSHPVPT 102

RESULT 7

US-11-012-353-65
; Sequence 65, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN

; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353

; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; PRIORITY FILING DATE: 2004-12-16
; PRIORITY FILING DATE: 2003-12-16
; PRIORITY FILING DATE: 2003-07-11
; PRIORITY FILING DATE: 2003-07-11
; PRIORITY FILING DATE: 2003-01-20
; PRIORITY FILING DATE: 2003-01-20
; PRIORITY FILING DATE: 2002-05-07
; PRIORITY FILING DATE: 2002-05-07
; PRIORITY FILING DATE: 2002-01-18
; PRIORITY FILING DATE: 2002-01-18
; PRIORITY FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 65
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-012-353-65

Query Match 100.0%; Score 56; DB 7; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.00059;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQGSHPVPT 9
Db 94 FQGSHPVPT 102

RESULT 8

US-11-012-353-49
; Sequence 49, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN

; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353

; PRIORITY FILING DATE: 2004-12-16
; PRIORITY FILING DATE: 2003-12-16
; PRIORITY FILING DATE: 2003-12-16
; PRIORITY FILING DATE: 2003-07-11
; PRIORITY FILING DATE: 2003-07-11
; PRIORITY FILING DATE: 2003-01-20
; PRIORITY FILING DATE: 2003-01-20
; PRIORITY FILING DATE: 2002-05-07
; PRIORITY FILING DATE: 2002-05-07
; PRIORITY FILING DATE: 2002-01-18
; PRIORITY FILING DATE: 2002-01-18
; PRIORITY FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 49
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-012-353-49

Query Match 100.0%; Score 56; DB 7; Length 122;
Best Local Similarity 100.0%; Pred. No. 0.00064;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQGSHPVPT 9

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Db          104 FQGSHPWT 112
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; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 67
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-012-353-67

Query Match          100.0%; Score 56; DB 7; Length 131;
Best Local Similarity 100.0%; Pred. No. 0.00068;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 FQGSHPWT 9
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Db          113 FQGSHPWT 121
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RESULT 11
US-11-125-837-23
; Sequence 23, Application US/11125837
; Publication No. US20050266003A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Rong-Hwa
; APPLICANT: Chang, Chung Nan
; APPLICANT: Chen, Pei-Jiun
; APPLICANT: Huang, Chiu-Chen
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 13062-011001
; CURRENT APPLICATION NUMBER: US/11/125,837
; CURRENT FILING DATE: 2005-05-10
; PRIOR APPLICATION NUMBER: US 60/569,892
; PRIOR FILING DATE: 2004-05-10
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-125-837-23

Query Match          100.0%; Score 56; DB 7; Length 131;
Best Local Similarity 100.0%; Pred. No. 0.00068;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 FQGSHPWT 9
|||||
Db          113 FQGSHPWT 121
|||||

RESULT 12
US-10-932-334-59
; Sequence 59, Application US/10932334
; Publication No. US20050249728A1
; GENERAL INFORMATION:
; APPLICANT: ImmunoGen, Inc.
; TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
; FILE REFERENCE: A8689
; CURRENT APPLICATION NUMBER: US/10/932,334
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US/10/729,441
; PRIOR FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: 10/170,390
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 59
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence
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Db          104 FQGSHPWT 112
|||||
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 67
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-012-353-63

Query Match          100.0%; Score 56; DB 7; Length 131;
Best Local Similarity 100.0%; Pred. No. 0.00068;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 FQGSHPWT 9
|||||
Db          113 FQGSHPWT 121
|||||

RESULT 10
US-11-012-353-67
; Sequence 67, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 63
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-012-353-63

Query Match          100.0%; Score 56; DB 7; Length 131;
Best Local Similarity 100.0%; Pred. No. 0.00068;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 FQGSHPWT 9
|||||
Db          113 FQGSHPWT 121
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RESULT 10
US-11-012-353-67
; Sequence 67, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
```

```

; FEATURE:
; OTHER INFORMATION: synthetic antibody structure
US-10-932-334-59

```

Query Match 83.9%; Score 47; DB 6; Length 113;
Best Local Similarity 88.9%; Pred. No. 0.027;
Matches 8; Conservative 1; Mismatches 0; Indels

Qy 1 FQGSHPWT 9
Db 94 FQGSHPVT 102

```

RESULT 13
US-10-932-334-61
; Sequence 61, Application US/10932334
; Publication No. US20050249728A1
; GENERAL INFORMATION:
; APPLICANT: ImmunoGen, Inc.
; TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
; FILE REFERENCE: A8689
; CURRENT APPLICATION NUMBER: US/10/932,334
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US/10/729,441
; PRIOR FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: 10/170,390
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody structure
US-10-932-334-61

```

Query Match 83.9%; Score 47; DB 6; Length 113;
Best Local Similarity 88.9%; Pred. No. 0.027;
Matches 8: Conservative 1: Mismatches 0: Indels

QY 1 FQGSHPWT 9
94 FQGSHPYT 102
Db

```

RESULT 14
US-10-512-184-30
; Sequence 30, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scPv VD2 with
; OTHER INFORMATION: specificity against Verticillium dahliae;
; OTHER INFORMATION: originates from Mus musculus.
US-10-512-184-30

```

```
Query Match      83.9%; Score 47; DB 6; Length 251;
Best Local Similarity 88.9%; Pred. No. 0.056;
Matches      8; Conservative      1; Mismatches      0; Indels      0; Gaps      0;
```

Qy 1 FQGSHPVPT 9
Db 231 FQGSHPVPT 239

```

RESULT 15
US-512-194-67
; Sequence 67, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft
; TITLE OF INVENTION: Antibodies, rec
; TITLE OF INVENTION: antibody fragm
; TITLE OF INVENTION: resistance aga
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/5
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 67
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of f
; OTHER INFORMATION: fusion protein
US-512-194-67

```

Query Match	83.9%	Score 47;	DB 6;	Length 320;
Best Local Similarity	88.9%;	Pred. No. 0.07;		
Matches 8;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 1 FQGSHPWT 9
D_b 300 FQGSHPYT 308

Search completed: December 30, 2005, 14:15:21
Job time : 4.33871 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2005, 14:52:54 ; Search time 182 Seconds
(without alignments)
21.728 Million cell updates/sec

Title: US-10-735-916A-6

Perfect score: 56

Sequence: 1 FQGSHPWT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 203235

Minimum DB seq length: 9

Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_21:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	9	5	ABP52345 Fv region
2	56	100.0	9	7	ADD94151 Mouse HUI
3	56	100.0	9	7	ADJ76840 CDR seque
4	56	100.0	9	9	ADZ67010 Murine in
5	55	98.2	9	8	ADS88735
6	52	92.9	9	7	ADD94253 Mouse HUI
7	52	92.9	9	7	ADD94243
8	52	92.9	9	7	ADD94247
9	51	91.1	9	7	ADD94260 Mouse HUI
10	51	91.1	9	7	ADD94256
11	51	91.1	9	7	ADD94254
12	51	91.1	9	7	ADD94258
13	51	91.1	9	7	ADD94257
14	51	91.1	9	7	ADD94255
15	50	89.3	9	7	ADD94242
16	50	89.3	9	7	ADD94241
17	50	89.3	9	7	ADD94245
18	49	87.5	9	7	ADD94246
19	49	87.5	9	7	ADD94244
20	48	85.7	9	7	ADD94252
21	47	83.9	9	2	AAR40218
22	47	83.9	9	2	AAR70455
23	47	83.9	9	6	ABP72122
24	7	83.9	9	7	ADD28190

25	47	83.9	9	7	ADD94250
26	47	83.9	9	7	ADZ67010
27	47	83.9	9	7	ADL35324
28	47	83.9	9	8	ADP84870
29	47	83.9	9	9	ABP03714
30	46	82.1	9	7	ADD94251
31	46	82.1	9	7	ADD94249
32	46	82.1	9	8	ADM78083
33	46	82.1	9	8	ADM78107
34	46	82.1	9	8	ADM78125
35	46	82.1	9	8	ADM78131
36	45	80.4	9	4	AAB86296
37	45	80.4	9	7	ADD94473
38	45	80.4	9	7	ADD94248
39	45	80.4	9	9	AEA34943
40	45	80.4	9	9	AEI17184
41	45	80.4	9	9	AEA42984
42	43	76.8	9	6	ABP58278
43	43	76.8	9	7	ADH61994
44	43	76.8	9	8	ADR19274
45	42	75.0	9	2	AAW70922

ALIGNMENTS

RESULT 1
ABP52345
ID ABP52345 standard; peptide; 9 AA.
XX
AC ABP52345;
XX
DT 17-OCT-2002 (first entry)
XX
DE Fv region SC100 antibody CDR-L3 amino acid sequence.
XX
KW Cytotoxic T lymphocyte; CTL; T helper; MAGE3; cytotoxic T cell response;
KW tumour; immune response; cancer; vaccine; antibody.
XX
OS Mus musculus.
OS Synthetic.
XX
PN WO200258728-A2.
XX
PD 01-AUG-2002.
XX
PF 28-JAN-2002; 2002WO-GB000354.
XX
PR 26-JAN-2001; 2001GB-00002145.
XX
XX (SCAN-) SCANCELL LTD.
XX (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
Durrant LG, Parsons T, Robins A;
WPI; 2002-608418/65.
Use of polypeptides and nucleic acids encoding the polypeptides, in
manufacturing medicament for stimulating a cytotoxic T cell response and
for preventing or treating cancer, e.g. colorectal, lung, breast or
ovarian cancer.
Example 11; Page 46; 87pp; English.
The present invention describes the use of a polypeptide (I) in the
manufacture of a medicament for stimulating a cytotoxic T cell response,
where (I) comprises a first portion comprising the part of human Fc that
binds to CD64 and a second portion comprising one or more heterologous T
cell epitopes. Also described is a method of stimulating a cytotoxic T
cell response in a patient such as a mammal, preferably human, by
administering (I) to the patient. (I) has cytostatic activity and can be
used in vaccine production. (I) and the nucleic acid encoding (I) are
useful in the manufacture of a medicament for stimulating cytotoxic T

CC cell response. The medicament is useful for preventing and/or treating
 CC cancer, e.g. colorectal, lung, breast, gastric or ovarian cancer. The
 CC medicament stimulates cytotoxic and helper T cell responses. The
 CC antibodies are useful as vaccines to stimulate helper and cytotoxic T
 CC cell responses. The polypeptides and nucleic acids are useful in
 CC optimising immunisation schedules for enhancing a protective immune
 CC response against cancer. The present sequence represents an Fv region
 CC SC100 antibody CDR-L3 amino acid sequence which is used in an example
 CC from the present invention

XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 56; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPVPT 9
 DB 1 FQGSHPVPT 9
 |||||

RESULT 2
 ADD94151
 ID ADD94151 standard; peptide; 9 AA.
 AC ADD94151;
 DT 29-JAN-2004 (first entry)
 XX
 DE Mouse HUI77 light chain CDR3 partial amino acid sequence SeqID36.
 XX
 KW grafted antibody; complementarity determining region; CDR; light CDR;
 KW heavy CDR; cryptic collagen epitope; solid tumour;
 KW new blood vessel growth; angiogenesis; tumour growth; cytostatic;
 KW collagen agonist; collagen antagonist; cancer metastasis;
 KW anti-cryptic collagen; antibody; HUI77; variable region light chain;
 KW mouse; murine.
 XX
 OS Mus musculus.
 XX
 PN WO2003046204-A2.
 XX
 PD 05-JUN-2003.
 XX
 PF 26-NOV-2002; 2002WO-US038147.
 XX
 PR 26-NOV-2001; 2001US-00995529.
 PR 06-DEC-2001; 2001US-00011250.
 XX
 PA (CELL-) CELL MATRIX INC.
 XX
 PI Watking JD, Huse WD, Tang Y, Broek D, Brooks PC;
 XX
 DR WPI; 2003-513649/48.
 DR N-PSDB; ADD94150.
 XX
 PT New cryptic collagen antibody with one or more complementarity
 PT determining regions, useful for diagnosing and treating disorders
 PT associated with angiogenesis, tumor growth and/or cancer metastasis.
 XX
 PS Claim 25; SEQ ID NO 36; 232pp; English.

XX
 CC This invention relates to a novel grafted antibody or its functional
 CC fragment comprising one or more complementarity determining regions
 CC (CDRs) of a defined light CDR and a heavy CDR with at least one amino
 CC acid (aa) substitution where the antibody has specific binding activity
 CC for a cryptic collagen epitope. The growth of all solid tumours requires
 CC new blood vessel growth, angiogenesis, inhibition of which is an approach
 CC to limiting tumour growth. The invention may allow development of
 CC therapeutics with a cytostatic activity as a collagen agonist or
 CC antagonist. The invention is useful for diagnosing and treating disorders
 CC associated with angiogenesis, tumour growth and/or cancer metastasis. The
 CC present sequence is the partial amino acid sequence of a mouse anti-

CC cryptic collagen site antibody HUI77 variable region light chain CDR
 CC which is related to the invention.

XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 56; DB 7; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPVPT 9
 DB 1 FQGSHPVPT 9
 |||||

RESULT 3
 ADJ76840
 ID ADJ76840 standard; peptide; 9 AA.
 XX
 AC ADJ76840;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE CDR sequence for anti-IGF-1R antibody.
 XX
 KW cytostatic; antipneumatic; antibody;
 KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;
 KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;
 KW CDR.
 XX
 OS Mus musculus.
 XX
 PN WO2003059951-A2.
 XX
 PD 24-JUL-2003.
 XX
 PF 20-JAN-2003; 2003WO-FR000178.
 XX
 PR 18-JAN-2002; 2002FR-00000653.
 PR 18-JAN-2002; 2002FR-00000654.
 PR 07-MAY-2002; 2002FR-00005753.
 XX
 PA (FABR) FABRE MEDICAMENT SA PIERRE.
 XX
 PI Goetsch L, Corvaia N, Leger O;
 XX
 DR WPI; 2003-569653/53.
 DR N-PSDB; ADJ76839.
 XX
 PT New antibodies that bind to human insulin-like growth factor receptor,
 PT useful for treatment, prevention and diagnosis of cancers.
 XX
 PS Claim 1; SEQ ID NO 6; 164pp; French.

XX
 CC The invention relates to an isolated antibody (Ab), and its functional
 CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-
 CC 1R) and optionally: (i) inhibit natural binding of insulin-like growth
 CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine
 CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or
 CC treat diseases associated with overexpression and/or abnormal activity of
 CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with
 CC hyperactivity of signal transduction pathways mediated by interaction of
 CC these receptors with their ligands. Especially they inhibit
 CC transfection of normal cells to tumor cells, inhibit growth and/or
 CC proliferation of tumor cells, so are useful against cancers of the
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents an
 CC CDR sequence used to generate the Ab of the invention.

XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 56; DB 7; Length 9;

Best Local Similarity 100.0%; Pred. No. 2e+06; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPVPT 9
 DB 1 FQGSHPVPT 9

RESULT 4
 ADZ67010
 ID ADZ67010 standard; peptide; 9 AA.
 AC ADZ67010;
 XX
 DT 30-JUN-2005 (first entry)
 XX
 DE Murine insulin-like growth factor T receptor IGF-IR CDR SEQ ID NO:6.
 XX
 KW Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
 KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;
 KW musculoskeletal disease; respiratory disease; lung tumor;
 KW endocrine disease; gynecology and obstetrics; breast tumor;
 KW endometrial carcinoma; gastrointestinal disease; colon tumor;
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder.
 XX
 OS Mus musculus.
 XX
 PN US2005084906-A1.
 XX
 PD 21-APR-2005.
 XX
 PF 16-DEC-2003; 2003US-00735916.
 XX
 PR 18-JAN-2002; 2002FR-00000653.
 PR 18-JAN-2002; 2002FR-00000654.
 PR 07-MAY-2002; 2002FR-00005753.
 PR 20-JAN-2003; 2003WO-FR000178.
 PR 11-JUL-2003; 2003PR-00008538.
 XX
 PA (GOET/) GOETSCH L.
 PA (CORV/) CORVAIA N.
 PA (LEGE/) LEGER O.
 PA (DUFL/) DUFLOS A.
 PA (HAUW/) HAEUW J.
 PA (BECK/) BECK A.
 XX
 PI Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;
 XX
 WPI; 2005-321968/33.
 DR N-PSDB; ADZ67009.
 XX
 XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)
 PT antibody or its functional fragment, being capable of binding human IGF-
 PT IR and specifically inhibiting tyrosine kinase activity of receptor,
 PT useful for treating cancer.
 XX
 PS Claim 1; SEQ ID NO 6; 125pp; English.
 XX
 XX The invention relates to a novel isolated anti-insulin-like growth factor
 CC I receptor (IGF-IR) antibody (I) or its functional fragment, being
 CC capable of binding to human IGF-IR and, if necessary, capable of
 CC specifically inhibiting tyrosine kinase activity of the receptor,
 CC comprising a light or heavy chain having at least one complementary
 CC determining region (CDR) consisting of one of two fully defined 16 amino
 CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in
 CC the preparation of a medicament intended for the prevention or treatment
 CC of an illness connected with an overexpression and/or an abnormal
 CC activation of the IGF-IR and/or EGFR, and/or connected with a
 CC hyperactivation of the transduction pathway of the signal mediated by the
 CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where
 CC the administration of the medicament does not induce or only slightly
 CC induces secondary effects connected with inhibition of the insulin
 CC receptor. The antibody is useful for preparation of a medicament intended

CC to inhibit the transformation of normal cells into cells with tumoral
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is
 CC useful for preparation of a medicament intended to inhibit the growth
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a
 CC medicament intended for prevention or for the treatment of cancer, where
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the
 CC preparation of a medicament intended for the prevention or for the
 CC treatment of psoriasis. (I) is useful in preparation of a medicament
 CC intended for the specific targeting of a biologically active compound to
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)
 CC is useful for in vitro diagnosis of illnesses induced by an
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor
 CC scarring from a biological sample in which the abnormal presence, of IGF-
 CC IR and/or EGFR receptor is suspected, which involves contacting the
 CC biological sample with (I), which is optionally labeled. The present
 CC sequence is used in the exemplification of the invention.
 XX
 SQ Sequence 9 AA;
 Query Match 100.0%; Score 56; DB 9; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPVPT 9
 DB 1 FQGSHPVPT 9

RESULT 5
 ADZ67010
 ID ADZ67010 standard; peptide; 9 AA.
 AC ADZ67010;
 XX
 DT 16-DEC-2004 (first entry)
 XX
 DE CDR derived from the VL region of an anti RSV G glycoprotein antibody.
 XX
 KW G glycoprotein; respiratory syncytial virus;
 KW respiratory syncytial virus infection; RSV; RSV infection;
 KW complementarity determining region; CDR.
 XX
 OS Unidentified.
 XX
 PN WO2004083373-A2.
 XX
 PD 30-SEP-2004.
 XX
 PF 22-MAR-2004; 2004WO-GB001239.
 XX
 PR 22-MAR-2003; 2003GB-00006618.
 XX
 PA (TYNE-) UNIV NEWCASTLE-UPON-TYNE.
 XX
 PI Toms G, Routledge E, Mekseepalard C;
 XX
 WPI; 2004-691033/67.
 DR N-PSDB; ADS88741.
 XX
 PT New antibody against the G glycoprotein of RSV with a variable region
 PT having a first and second domain from a VL and VH region, respectively,
 PT useful for treating respiratory syncytial virus (RSV) infections.
 XX
 PS Claim 1; SEQ ID NO 3; 93pp; English.
 XX
 XX The specification describes an against the G glycoprotein of respiratory
 CC syncytial virus, with a variable region comprising a first domain from a
 CC variable light chain region and a second domain a variable heavy chain
 CC region. The antibodies of the invention are useful for treating and

CC preventing the development of infections caused by the respiratory
 CC syncytial virus (RSV). The present sequence represents a complementarity
 CC determining region (CDR) derived from the variable light chain (VL)
 CC region of an antibody directed against the G glycoprotein of RSV. This
 CC peptide is used to construct antibodies of the invention.

XX Sequence 9 AA;

Query Match 98.2%; Score 55; DB 8; Length 9;
 Best Local Similarity 88.9%; Pred. No. 2e+06;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPVPT 9
 DB 1 FQGSHPVPT 9
 |||||

RESULT 6
 ADD94253
 ID ADD94253 standard; peptide; 9 AA.

XX ADD94253;

XX 29-JAN-2004 (first entry)

DE Mouse HUI77 mutant light chain CDR amino acid sequence SeqID138.

XX grafted antibody; complementarity determining region; CDR; light CDR;
 KW heavy CDR; cryptic collagen epitope; solid tumour;
 KW new blood vessel growth; angiogenesis; tumour growth; cytostatic;
 KW collagen agonist; collagen antagonist; cancer metastasis;
 KW anti-cryptic collagen; HUI77; variable region light chain; mouse; murine;
 KW mutant; mutein.

XX Synthetic.
 OS Mus musculus.

XX WO2003046204-A2.

XX 05-JUN-2003.

XX 26-NOV-2002; 2002WO-US038147.

XX 26-NOV-2001; 2001US-00995529.

XX 06-DEC-2001; 2001US-00011250.

XX (CELL-) CELL MATRIX INC.

XX Watking JD, Huse WD, Tang Y, Broek D, Brooks PC;

XX WPI; 2003-513649/48.

XX New cryptic collagen antibody with one or more complementarity
 PT determining regions, useful for diagnosing and treating disorders
 PT associated with angiogenesis, tumor growth and/or cancer metastasis.

XX Claim 24; SEQ ID NO 138; 232pp; English.

XX This invention relates to a novel grafted antibody or its functional
 CC fragment comprising one or more complementarity determining regions
 CC (CDRs) of a defined light CDR and a heavy CDR with at least one amino
 CC acid (aa) substitution where the antibody has specific binding activity
 CC for a cryptic collagen epitope. The growth of all solid tumours requires
 CC new blood vessel growth, angiogenesis, inhibition of which is an approach
 CC to limiting tumour growth. The invention may allow development of
 CC therapeutics with a cytostatic activity as a collagen agonist or
 CC antagonist. The invention is useful for diagnosing and treating disorders
 CC associated with angiogenesis, tumour growth and/or cancer metastasis. The
 CC present sequence is the amino acid sequence of a mutant mouse anti-
 CC cryptic collagen site antibody HUI77 variable region light chain CDR
 CC which may be used during the creation of an antibody of the invention.

XX Sequence 9 AA;

Query Match 92.9%; Score 52; DB 7; Length 9;
 Best Local Similarity 88.9%; Pred. No. 2e+06;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FQGSHPVPT 9
 DB 1 FQGSHPVPT 9
 |||||

RESULT 7
 ADD94243
 ID ADD94243 standard; peptide; 9 AA.

XX ADD94243;

XX 29-JAN-2004 (first entry)

DE Mouse HUI77 mutant light chain CDR amino acid sequence SeqID128.

XX grafted antibody; complementarity determining region; CDR; light CDR;
 KW heavy CDR; cryptic collagen epitope; solid tumour;
 KW new blood vessel growth; angiogenesis; tumour growth; cytostatic;
 KW collagen agonist; collagen antagonist; cancer metastasis;
 KW anti-cryptic collagen; HUI77; variable region light chain; mouse; murine;
 KW mutant; mutein.

XX Synthetic.
 OS Mus musculus.

XX WO2003046204-A2.

XX 05-JUN-2003.

XX 26-NOV-2002; 2002WO-US038147.

XX 26-NOV-2001; 2001US-00995529.

XX 06-DEC-2001; 2001US-00011250.

XX (CELL-) CELL MATRIX INC.

XX Watking JD, Huse WD, Tang Y, Broek D, Brooks PC;

XX WPI; 2003-513649/48.

XX New cryptic collagen antibody with one or more complementarity
 PT determining regions, useful for diagnosing and treating disorders
 PT associated with angiogenesis, tumor growth and/or cancer metastasis.

XX Claim 24; SEQ ID NO 128; 232pp; English.

XX This invention relates to a novel grafted antibody or its functional
 CC fragment comprising one or more complementarity determining regions
 CC (CDRs) of a defined light CDR and a heavy CDR with at least one amino
 CC acid (aa) substitution where the antibody has specific binding activity
 CC for a cryptic collagen epitope. The growth of all solid tumours requires
 CC new blood vessel growth, angiogenesis, inhibition of which is an approach
 CC to limiting tumour growth. The invention may allow development of
 CC therapeutics with a cytostatic activity as a collagen agonist or
 CC antagonist. The invention is useful for diagnosing and treating disorders
 CC associated with angiogenesis, tumour growth and/or cancer metastasis. The
 CC present sequence is the amino acid sequence of a mutant mouse anti-
 CC cryptic collagen site antibody HUI77 variable region light chain CDR
 CC which may be used during the creation of an antibody of the invention.

XX Sequence 9 AA;

Query Match 92.9%; Score 52; DB 7; Length 9;
 Best Local Similarity 88.9%; Pred. No. 2e+06;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPVPT 9
 DB 1 FQGSHPVPT 9
 |||||

KW heavy CDR; cryptic collagen epitope; solid tumour;
 KW new blood vessel growth; angiogenesis; tumour growth; cytostatic;
 KW collagen agonist; collagen antagonist; cancer metastasis;
 KW anti-cryptic collagen; HUI77; variable region light chain; mouse; murine;
 KW mutant; mutein.
 XX
 OS Synthetic.
 OS Mus musculus.
 XX
 PN WO2003046204-A2.
 XX
 PD 05-JUN-2003.
 XX
 PF 26-NOV-2002; 2002WO-US038147.
 XX
 PR 26-NOV-2001; 2001US-00995529.
 PR 06-DEC-2001; 2001US-00011250.
 XX
 XX (CELL-) CELL MATRIX INC.
 PA
 PI Watking JD, Huse WD, Tang Y, Broek D, Brooks PC;
 PI WPI; 2003-513649/48.
 DR
 XX
 XX New cryptic collagen antibody with one or more complementarity
 PT determining regions, useful for diagnosing and treating disorders
 PT associated with angiogenesis, tumor growth and/or cancer metastasis.
 XX
 XX Claim 24; SEQ ID NO 141; 232pp; English.
 XX
 CC This invention relates to a novel grafted antibody or its functional
 CC fragment comprising one or more complementarity determining regions
 CC (CDRs) of a defined light CDR and a heavy CDR with at least one amino
 CC acid (aa) substitution where the antibody has specific binding activity
 CC for a cryptic collagen epitope. The growth of all solid tumours requires
 CC new blood vessel growth, angiogenesis, inhibition of which is an approach
 CC to limiting tumour growth. The invention may allow development of
 CC therapeutics with a cytostatic activity as a collagen agonist or
 CC antagonist. The invention is useful for diagnosing and treating disorders
 CC associated with angiogenesis, tumour growth and/or cancer metastasis. The
 CC present sequence is the amino acid sequence of a mutant mouse anti-
 CC cryptic collagen site antibody HUI77 variable region light chain CDR
 CC which may be used during the creation of an antibody of the invention.
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 91.1%; Score 51; DB 7; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FQGSHPVW 8
 Db 1 FQGSHPVW 8
 |||||
 |||||
 RESULT 11
 ADD94254
 ID ADD94254 standard; peptide; 9 AA.
 AC ADD94254;
 XX
 XX 29-JAN-2004 (first entry)
 DT
 DE Mouse HUI77 mutant light chain CDR amino acid sequence SeqID139.
 XX
 XX grafted antibody; complementarity determining region; CDR; light CDR;
 KW heavy CDR; cryptic collagen epitope; solid tumour;
 KW new blood vessel growth; angiogenesis; tumour growth; cytostatic;
 KW collagen agonist; collagen antagonist; cancer metastasis;
 KW anti-cryptic collagen; HUI77; variable region light chain; mouse; murine;
 KW mutant; mutein.
 XX
 OS Synthetic.

OS Mus musculus.
 XX WO2003046204-A2.
 PN
 PD 05-JUN-2003.
 XX
 PF 26-NOV-2002; 2002WO-US038147.
 XX
 PR 26-NOV-2001; 2001US-00995529.
 PR 06-DEC-2001; 2001US-00011250.
 XX
 XX (CELL-) CELL MATRIX INC.
 PA
 PI Watking JD, Huse WD, Tang Y, Broek D, Brooks PC;
 PI WPI; 2003-513649/48.
 DR
 XX
 XX New cryptic collagen antibody with one or more complementarity
 PT determining regions, useful for diagnosing and treating disorders
 PT associated with angiogenesis, tumor growth and/or cancer metastasis.
 XX
 XX Claim 24; SEQ ID NO 139; 232pp; English.
 XX
 CC This invention relates to a novel grafted antibody or its functional
 CC fragment comprising one or more complementarity determining regions
 CC (CDRs) of a defined light CDR and a heavy CDR with at least one amino
 CC acid (aa) substitution where the antibody has specific binding activity
 CC for a cryptic collagen epitope. The growth of all solid tumours requires
 CC new blood vessel growth, angiogenesis, inhibition of which is an approach
 CC to limiting tumour growth. The invention may allow development of
 CC therapeutics with a cytostatic activity as a collagen agonist or
 CC antagonist. The invention is useful for diagnosing and treating disorders
 CC associated with angiogenesis, tumour growth and/or cancer metastasis. The
 CC present sequence is the amino acid sequence of a mutant mouse anti-
 CC cryptic collagen site antibody HUI77 variable region light chain CDR
 CC which may be used during the creation of an antibody of the invention.
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 91.1%; Score 51; DB 7; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FQGSHPVW 8
 Db 1 FQGSHPVW 8
 |||||
 |||||
 RESULT 12
 ADD94258
 ID ADD94258 standard; peptide; 9 AA.
 AC ADD94258;
 XX
 XX 29-JAN-2004 (first entry)
 DT
 DE Mouse HUI77 mutant light chain CDR amino acid sequence SeqID143.
 XX
 XX grafted antibody; complementarity determining region; CDR; light CDR;
 KW heavy CDR; cryptic collagen epitope; solid tumour;
 KW new blood vessel growth; angiogenesis; tumour growth; cytostatic;
 KW collagen agonist; collagen antagonist; cancer metastasis;
 KW anti-cryptic collagen; HUI77; variable region light chain; mouse; murine;
 KW mutant; mutein.
 XX
 OS Synthetic.
 OS Mus musculus.
 XX
 PN WO2003046204-A2.
 XX
 PD 05-JUN-2003.
 XX
 PF 26-NOV-2002; 2002WO-US038147.

XX PR 26-NOV-2001; 2001US-00995529.
XX PR 06-DEC-2001; 2001US-00011250.
XX PA (CELL-) CELL MATRIX INC.
XX PI Watking JD, Huse WD, Tang Y, Broek D, Brooks PC;
XX DR WPI; 2003-513649/48.
XX XX
XX PR New cryptic collagen antibody with one or more complementarity
XX PT determining regions, useful for diagnosing and treating disorders
XX PT associated with angiogenesis, tumor growth and/or cancer metastasis.
XX PS Claim 24; SEQ ID NO 143; 232pp; English.
XX XX
XX CC This invention relates to a novel grafted antibody or its functional
XX CC fragment comprising one or more complementarity determining regions
XX CC (CDRs) of a defined light CDR and a heavy CDR with at least one amino
XX CC acid (aa) substitution where the antibody has specific binding activity
XX CC for a cryptic collagen epitope. The growth of all solid tumours requires
XX CC new blood vessel growth, angiogenesis, inhibition of which is an approach
XX CC to limiting tumour growth. The invention may allow development of
XX CC therapeutics with a cytostatic activity as a collagen agonist or
XX CC antagonist. The invention is useful for diagnosing and treating disorders
XX CC associated with angiogenesis, tumour growth and/or cancer metastasis. The
XX CC present sequence is the amino acid sequence of a mutant mouse anti-
XX CC cryptic collagen site antibody HUI77 variable region light chain CDR
XX CC which may be used during the creation of an antibody of the invention.
XX SQ Sequence 9 AA;
Query Match 91.1%; Score 51; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FQSGHVPW 8
Db 1 FQSGHVPW 8
RESULT 13
ID ADD94257
AC ADD94257 standard; peptide; 9 AA.
AC ADD94257;
XX
XX DT 29-JAN-2004 (first entry)
XX Mouse HUI77 mutant light chain CDR amino acid sequence SeqID142.
XX DE
XX KW grafted antibody; complementarity determining region; CDR; light CDR;
XX KW heavy CDR; cryptic collagen epitope; solid tumour;
XX KW new blood vessel growth; angiogenesis; tumour growth; cytostatic;
XX KW collagen agonist; collagen antagonist; cancer metastasis;
XX KW anti-cryptic collagen; HUI77; variable region light chain; mouse; murine;
XX KW mutant; mutein.
XX OS Synthetic.
XX OS Mus musculus.
XX XX
XX PN W02003046204-A2.
XX XX
XX PD 05-JUN-2003.
XX XX
XX PF 26-NOV-2002; 2002WO-US038147.
XX PR 26-NOV-2001; 2001US-00995529.
XX PR 06-DEC-2001; 2001US-00011250.
XX XX
XX PA (CELL-) CELL MATRIX INC.
XX PI Watking JD, Huse WD, Tang Y, Broek D, Brooks PC;

XX DR WPI; 2003-513649/48.
XX XX
XX PT New cryptic collagen antibody with one or more complementarity
XX PT determining regions, useful for diagnosing and treating disorders
XX PT associated with angiogenesis, tumor growth and/or cancer metastasis.
XX PS Claim 24; SEQ ID NO 142; 232pp; English.
XX XX
XX CC This invention relates to a novel grafted antibody or its functional
XX CC fragment comprising one or more complementarity determining regions
XX CC (CDRs) of a defined light CDR and a heavy CDR with at least one amino
XX CC acid (aa) substitution where the antibody has specific binding activity
XX CC for a cryptic collagen epitope. The growth of all solid tumours requires
XX CC new blood vessel growth, angiogenesis, inhibition of which is an approach
XX CC to limiting tumour growth. The invention may allow development of
XX CC therapeutics with a cytostatic activity as a collagen agonist or
XX CC antagonist. The invention is useful for diagnosing and treating disorders
XX CC associated with angiogenesis, tumour growth and/or cancer metastasis. The
XX CC present sequence is the amino acid sequence of a mutant mouse anti-
XX CC cryptic collagen site antibody HUI77 variable region light chain CDR
XX CC which may be used during the creation of an antibody of the invention.
XX SQ Sequence 9 AA;
Query Match 91.1%; Score 51; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FQSGHVPW 8
Db 1 FQSGHVPW 8
RESULT 14
ID ADD94255
AC ADD94255 standard; peptide; 9 AA.
AC ADD94255;
XX
XX DT 29-JAN-2004 (first entry)
XX Mouse HUI77 mutant light chain CDR amino acid sequence SeqID140.
XX DE
XX KW grafted antibody; complementarity determining region; CDR; light CDR;
XX KW heavy CDR; cryptic collagen epitope; solid tumour;
XX KW new blood vessel growth; angiogenesis; tumour growth; cytostatic;
XX KW collagen agonist; collagen antagonist; cancer metastasis;
XX KW anti-cryptic collagen; HUI77; variable region light chain; mouse; murine;
XX KW mutant; mutein.
XX OS Synthetic.
XX OS Mus musculus.
XX XX
XX PN W02003046204-A2.
XX XX
XX PD 05-JUN-2003.
XX XX
XX PF 26-NOV-2002; 2002WO-US038147.
XX PR 26-NOV-2001; 2001US-00995529.
XX PR 06-DEC-2001; 2001US-00011250.
XX XX
XX PA (CELL-) CELL MATRIX INC.
XX PI Watking JD, Huse WD, Tang Y, Broek D, Brooks PC;
XX WPI; 2003-513649/48.
XX XX
XX PT New cryptic collagen antibody with one or more complementarity
XX PT determining regions, useful for diagnosing and treating disorders
XX PT associated with angiogenesis, tumor growth and/or cancer metastasis.
XX XX

PS Claim 24; SEQ ID NO 140; 232pp; English.
 XX
 CC This invention relates to a novel grafted antibody or its functional
 CC fragment comprising one or more complementarity determining regions
 CC (CDRs) of a defined light CDR and a heavy CDR with at least one amino
 CC acid (aa) substitution where the antibody has specific binding activity
 CC for a cryptic collagen epitope. The growth of all solid tumours requires
 CC new blood vessel growth, angiogenesis, inhibition of which is an approach
 CC to limiting tumour growth. The invention may allow development of
 CC therapeutics with a cytostatic activity as a collagen agonist or
 CC antagonist. The invention is useful for diagnosing and treating disorders
 CC associated with angiogenesis, tumour growth and/or cancer metastasis. The
 CC present sequence is the amino acid sequence of a mutant mouse anti-
 CC cryptic collagen site antibody HUI77 variable region light chain CDR
 CC which may be used during the creation of an antibody of the invention.

XX Sequence 9 AA;

Query Match 91.1%; Score 51; DB 7; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPVW 8

DB 1 FQGSHPVW 8

RESULT 15

ADD94242

ID ADD94242 standard; peptide; 9 AA.

XX AC ADD94242;

XX DT 29-JAN-2004 (first entry)

XX DE

Mouse HUI77 mutant light chain CDR amino acid sequence SeqID127.

XX KW

grafted antibody; complementarity determining region; CDR; light CDR;
 heavy CDR; cryptic collagen epitope; solid tumour;

new blood vessel growth; angiogenesis; tumour growth; cytostatic;

collagen agonist; collagen antagonist; cancer metastasis;

anti-cryptic collagen; HUI77; variable region light chain; mouse; murine;
 mutant; mutein.

XX OS

Synthetic.

OS Mus musculus.

XX PN

WO2003046204-A2.

XX PD

05-JUN-2003.

XX PF

26-NOV-2002; 2002WO-US038147.

XX PR

26-NOV-2001; 2001US-00995529.

XX PR

06-DEC-2001; 2001US-00011250.

XX PA

(CELL-) CELL MATRIX INC.

XX PI

Watking JD, Huse WD, Tang Y, Broek D, Brooks PC;

XX DR

WPI; 2003-513649/48.

XX PT

New cryptic collagen antibody with one or more complementarity
 determining regions, useful for diagnosing and treating disorders

XX PT

associated with angiogenesis, tumor growth and/or cancer metastasis.

XX PS

Claim 24; SEQ ID NO 127; 232pp; English.

XX CC

This invention relates to a novel grafted antibody or its functional
 fragment comprising one or more complementarity determining regions

XX CC

(CDRs) of a defined light CDR and a heavy CDR with at least one amino
 acid (aa) substitution where the antibody has specific binding activity
 for a cryptic collagen epitope. The growth of all solid tumours requires

CC new blood vessel growth, angiogenesis, inhibition of which is an approach
 CC to limiting tumour growth. The invention may allow development of
 CC therapeutics with a cytostatic activity as a collagen agonist or
 CC antagonist. The invention is useful for diagnosing and treating disorders
 CC associated with angiogenesis, tumour growth and/or cancer metastasis. The
 CC present sequence is the amino acid sequence of a mutant mouse anti-
 CC cryptic collagen site antibody HUI77 variable region light chain CDR
 CC which may be used during the creation of an antibody of the invention.

XX SQ

Sequence 9 AA;

Query Match

89.3%; Score 50; DB 7; Length 9;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QGSHVPWT 9

DB 2 QGSHVPWT 9

Search completed: December 30, 2005, 15:08:40

Job time : 183 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2005, 15:05:21 ; Search time 37 Seconds
(without alignments)
23.404 Million cell updates/sec

Title: US-10-735-916A-6

Perfect score: 56

Sequence: 1 FQGSHPVWT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 185

Minimum DB seq length: 9

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80:*

1: Pirl1.*

2: Pirl2.*

3: Pirl3.*

4: Pirl4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	32.1	9	2 JS0302	xenopsin-related p
2	18	32.1	9	2 A60320	xenopsin-related p
3	18	32.1	9	2 T31612	hypothetical prote
4	18	32.1	9	2 I46023	growth hormone rec
5	18	32.1	9	2 A60522	sperm-activating p
6	16	28.6	9	2 A43848	cell surface adhes
7	16	28.6	9	2 D57444	neuropeptide Grb-A
8	15	26.8	9	2 S77984	cytochrome-c oxida
9	13	23.2	9	1 AKLQIM	locustamyoinhibiti
10	13	23.2	9	2 A61230	calsequestrin, car
11	13	23.2	9	2 D28894	fibrinopeptide B -
12	12	21.4	9	2 C24180	fibrinogen beta ch
13	12	21.4	9	2 E28854	fibrinopeptide B -
14	12	21.4	9	2 C60070	gastrin - domestic
15	12	21.4	9	2 S65913	pyrimidine synthe
16	12	21.4	9	2 S36850	ig heavy chain V r
17	12	21.4	9	2 G41946	T-cell receptor ga
18	12	21.4	9	2 A42266	peptidylglycine mo
19	12	21.4	9	2 A12872	transaldolase (EC
20	12	21.4	9	2 A11497	transaldolase (EC
21	12	21.4	9	2 A61620	locustamyotropin I
22	12	21.4	9	2 PC7078	unidentified 48.7K
23	12	21.4	9	2 S39437	D-amino-acid oxida
24	11	19.6	9	1 YPPG	thymic factor - pi
25	11	19.6	9	2 A61364	isotocin - common
26	11	19.6	9	2 A60957	thymocyte growth p
27	11	19.6	9	2 A24244	adipokinetic hormo
28	11	19.6	9	2 S07205	litorin 2-Glu - Au
29	11	19.6	9	2 S07204	litorin I - Austra

30	11	19.6	9	2 S07241	litorin - Rohde's
31	11	19.6	9	2 A61357	phyllocaerulein -
32	11	19.6	9	2 S70334	endosperm protein,
33	11	19.6	9	2 S39766	cardioactive pepti
34	11	19.6	9	2 PT0231	ig heavy chain CDR
35	11	19.6	9	2 PT0270	ig heavy chain CDR
36	11	19.6	9	2 PT0272	ig heavy chain CDR
37	11	19.6	9	2 PT0288	ig heavy chain CDR
38	11	19.6	9	2 PT0299	ig heavy chain CDR
39	11	19.6	9	2 PT0324	ig heavy chain CDR
40	11	19.6	9	2 PH1591	ig H chain V-D-J r
41	11	19.6	9	2 PT0634	T-cell receptor be
42	11	19.6	9	2 PT0562	T-cell receptor be
43	11	19.6	9	2 I58350	gene c-mpl protein
44	11	19.6	9	2 S78426	52.5K protein - sp
45	11	19.6	9	2 S39767	cardioactive pepti

ALIGNMENTS

RESULT 1

JS0302
xenopsin-related peptide 2 - turkey
N:Contains: xenopsin-related peptide 1
C:Species: Meleagris gallopavo (common turkey)
C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C:Accession: JS0302
R:Carraway, R.E.; Cochran, D.E.; Mitra, S.P.
Regul. Pept. 22, 303-314, 1988
A:Title: Xenopsin-related peptide generated in avian gastric extracts.
A:Reference number: JS0302; MUID:89042995; PMID:2460902
A:Accession: JS0302
A:Molecule type: protein
A:Residues: 1-9 <CAR>
A:Cross-references: UNIPROT:Q7LZ66; UNIPARC:UPI0000178409
C:Comment: The peptides are present within several tissues primarily in large molecular
C:Superfamily: yeast coatomer complex alpha chain; WD repeat homology
C:Keywords: neuropeptide
F:1-9/Product: xenopsin-related peptide 2 #status experimental <XP2>
F:2-9/Product: xenopsin-related peptide 1 #status experimental <XP1>

Query Match 32.1%; Score 18; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PW 8
Db 6 PW 7

RESULT 2

A60320
xenopsin-related peptide 2 - rat
N:Contains: xenopsin-related peptide 1
C:Species: Rattus norvegicus (Norway rat)
C>Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 09-Jul-2004
C:Accession: A60320
R:Carraway, R.E.; Mitra, S.P.; Muraki, K.
Regul. Pept. 23, 229-239, 1990
A:Title: Isolation and structures of xenopsin-related peptides from rat stomach, liver
A:Reference number: A60320; MUID:91018491; PMID:2217904
A:Accession: A60320
A:Molecule type: protein
A:Residues: 1-9 <CAR>
A:Cross-references: UNIPROT:Q7M078; UNIPARC:UPI0000178409
A:Note: the authors purified these peptides from pepsin-treated extracts of stomach, li
C:Comment: Xenopsin and xenopsin-related peptides are similar to neurotensin in sequenc
C:Superfamily: yeast coatomer complex alpha chain; WD repeat homology
C:Keywords: neuropeptide
F:1-9/Product: xenopsin-related peptide 2 #status experimental <MAT1>
F:2-9/Product: xenopsin-related peptide 1 #status experimental <MAT2>

Query Match 32.1%; Score 18; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PW 8
DB 6 PW 7

RESULT 3

T31612
hypothetical protein Y50E8A.h - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T31612
R;Steward, C.
submitted to the EMBL Data Library, September 1999
A;Reference number: Z21047
A;Accession: T31612
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-9 <WIL>
A;Cross-references: UNIPARC:UPI000017BCA0; EMBL:AL117200; NID:el549770; PIDN:CAB55051.1;
A;Experimental source: clone Y50E8A
C;Genetics:
A;Gene: CESP:Y50E8A.h

Query Match 32.1%; Score 18; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GSH 5
DB 3 GSH 5

RESULT 4

I46023
growth hormone receptor - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: I46023
R;Hauser, S.D.; McGrath, M.F.; Collier, R.J.; Krivi, G.G.
Mol. Cell. Endocrinol. 72, 187-200, 1990
A;Title: Cloning and in vivo expression of bovine growth hormone receptor mRNA.
A;Reference number: I46023; MUID:91146804; PMID:2289631
A;Accession: I46023
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-9 <HNA>
A;Cross-references: UNIPROT:Q28121; UNIPARC:UPI0000086CAB; EMBL:U24113; NID:g775221; PID
C;Genetics:
A;Gene: GHR

Query Match 32.1%; Score 18; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PW 8
DB 4 PW 5

RESULT 5

A60522
sperm-activating peptide SAP-IV - sea urchin (Diadema setosum)
C;Species: Diadema setosum
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 05-Oct-2004
C;Accession: A60522
R;Yoshino, K.I.; Kurita, M.; Yamaguchi, M.; Nomura, K.; Takao, T.; Shimonishi, Y.; Suzuki
Comp. Biochem. Physiol. B 95, 423-429, 1990
A;Title: A species-specific sperm-activating peptide from the egg jelly of the sea urchin
A;Reference number: A60522; MUID:90227916; PMID:2158412

A;Accession: A60522
A;Molecule type: protein
A;Residues: 1-9 <YOS>
A;Cross-references: UNIPROT:Q7M4D5; UNIPARC:UPI000017A4D9
F;2-9/Disulfide bonds: #status experimental

Query Match 32.1%; Score 18; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PW 8
DB 3 PW 4

RESULT 6

A43848
cell surface adhesin for heparan sulfate, 66K - Staphylococcus aureus (fragment)
C;Species: Staphylococcus aureus
C;Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A43848
R;Liang, O.D.; Ascencio, F.; Fransson, L.A.; Wadstrom, T.
Infect. Immun. 60, 899-906, 1992
A;Title: Binding of heparan sulfate to Staphylococcus aureus.
A;Reference number: A43848; MUID:92176005; PMID:1541563
A;Accession: A43848
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <LTA>
A;Cross-references: UNIPROT:Q9R5M1; UNIPARC:UPI0000089726
A;Note: sequence extracted from NCBI backbone (NCBIP:85442)

Query Match 28.6%; Score 16; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 WT 9
DB 2 WT 3

RESULT 7

D57444
neuropeptide Grb-AST B4 - two-spotted cricket
C;Species: Gryllus bimaculatus (two-spotted cricket)
C;Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 09-Jul-2004
C;Accession: D57444
R;Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.
J. Biol. Chem. 270, 21103-21108, 1995
A;Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the cr
A;Reference number: A57444; MUID:95403341; PMID:7673141
A;Accession: D57444
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <LOR>
A;Cross-references: UNIPROT:Q7M3N6; UNIPARC:UPI000017BE1A

Query Match 28.6%; Score 16; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FQGS 4
DB 5 FHGS 8

RESULT 8

S77984
cytochrome-c oxidase (EC 1.9.3.1) chain Via - bigeye tuna (fragment)
C;Species: Thunnus obesus (bigeye tuna)
C;Date: 17-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C;Accession: S77984
R;Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lottspeich, F.; Kadenbach, B.

submitted to the Protein Sequence Database, June 1997

A;Reference number: S77980
A;Accession: S77984
A;Molecule type: protein
A;Residues: 1-9 <ARN>
A;Cross-references: UNIPROT:P80975; UNIPARC:UPI0000128149
A;Experimental source: heart
C;Genetics:
A;Genome: nuclear
C;Function:

A;Pathway: oxidative phosphorylation; respiratory chain
C;Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane

Query Match 26.8%; Score 15; DB 2; Length 9;

Best Local Similarity 42.9%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 QGSHVPW 8
| : | : |
Db 3 QPEFVPY 9

RESULT 9

AKUQIM

locustamyoinhibiting peptide - migratory locust

C;Species: Locusta migratoria (migratory locust)

C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004

A;Accession: A60065

R;Schooofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; De Loof, A.

Regul. Pept. 36, 111-119, 1991

A;Title: Isolation, identification and synthesis of locustamyoinhibiting peptide (LOM-MIP)

A;Reference number: A60065; MUID:92179466; PMID:1796179

A;Accession: A60065

A;Molecule type: protein

A;Residues: 1-9 <SCH>

A;Cross-references: UNIPROT:P31799; UNIPARC:UPI000012877A

C;Comment: This peptide hormone suppresses spontaneous contractions of the hindgut and d

C;Superfamily: locustamyoinhibiting peptide

C;Keywords: amidated carboxyl end; hormone

F;9/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 23.2%; Score 13; DB 1; Length 9;

Best Local Similarity 25.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 FQSHVPW 8
| : | : |
Db 2 WQDLNAGW 9

RESULT 10

A61230

calsequestrin, cardiac and slow skeletal muscle - northern leopard frog (fragment)

N;Alternate names: 58k dihydropyridine-binding protein; aspartactin; calmitine; laminin-

C;Species: Rana pipiens (northern leopard frog)

C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004

A;Accession: A61230

R;McLeod, A.G.; Shen, A.C.Y.; Campbell, K.P.; Michalak, M.; Jorgensen, A.O.

Circ. Res. 69, 344-359, 1991

A;Title: Frog cardiac calsequestrin. Identification, characterization, and subcellular d
rdium.

A;Reference number: A61230; MUID:91316784; PMID:1860177

A;Accession: A61230

A;Molecule type: protein

A;Residues: 1-9 <MCL>

A;Cross-references: UNIPROT:Q71LZ81; UNIPARC:UPI00001776B8

C;Comment: Calsequestrin is a high-capacity and moderate-affinity calcium binding protei

C;Comment: Calsequestrin acts as a calcium buffer, and the release of calcium bound to c

C;Comment: The fast skeletal muscle isoform of calsequestrin can be phosphorylated in vi

C;Superfamily: calsequestrin

C;Keywords: calcium binding; cardiac muscle; glycoprotein; heart; phosphoprotein; skelet

Query Match 23.2%; Score 13; DB 2; Length 9;

Best Local Similarity 33.3%; Pred. No. 2.8e+05;

Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 QGSHVP 7
| : | : |
Db 2 EGLNFP 7

RESULT 11

D28854

fibrinopeptide B - olive baboon

C;Species: Papio anubis, Papio hamadryas anubis (olive baboon)

C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 09-Jul-2004

C;Accession: D28854

R;Nakamura, S.; Takenaka, O.; Takahashi, K.

J. Biochem. 94, 1973-1978, 1983

A;Title: Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropi

A;Reference number: A91973; MUID:84161822; PMID:6423621

A;Accession: D28854

A;Molecule type: protein

A;Residues: 1-9 <NAK>

A;Cross-references: UNIPROT:P19344; UNIPARC:UPI000012A77F

C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulf

Query Match 23.2%; Score 13; DB 2; Length 9;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQG 3
| : | : |
Db 6 FRG 8

RESULT 12

C24180

fibrinogen beta chain - Japanese macaque (fragment)

N;Contents: fibrinopeptide B

C;Species: Macaca fuscata (Japanese macaque)

C;Date: 05-Jun-1988 #sequence_revision 10-Mar-1994 #text_change 09-Jul-2004

C;Accession: C24180

R;Nakamura, S.; Takenaka, O.; Takahashi, K.

J. Biochem. 97, 1487-1492, 1985

A;Title: Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and patas monkey (

uenons. and baboons.

A;Reference number: A91990; MUID:85289140; PMID:3928610

A;Accession: C24180

A;Molecule type: protein

A;Residues: 1-9 <NAK>

A;Cross-references: UNIPROT:P19345; UNIPARC:UPI000012A77B

C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulf

Query Match 21.4%; Score 12; DB 2; Length 9;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FQG 3
| : | : |
Db 6 FSG 8

RESULT 13

E28854

fibrinopeptide B - hamadryas baboon

C;Species: Papio hamadryas (hamadryas baboon)

C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 09-Jul-2004

C;Accession: E28854

R;Nakamura, S.; Takenaka, O.; Takahashi, K.

J. Biochem. 94, 1973-1978, 1983

A;Title: Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropi

A;Reference number: A91973; MUID:84161822; PMID:6423621

A;Accession: E28854

A;Molecule type: protein

A;Residues: 1-9 <NAK>

A;Cross-references: UNIPROT:P19343; UNIPARC:UPI000012A780
 C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide

Query Match 21.4%; Score 12; DB 2; Length 9;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FQG 3
 Db 6 FHG 8

RESULT 14

C60070
 gastrin - domestic ferret (fragment)
 C;Species: Mustela putorius furo (domestic ferret)
 C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 18-Jun-1993
 C;Accession: C60070
 R;Desmond, H.; Varro, A.; Young, J.; Gregory, H.; Nemeth, J.; Dockray, G.J.
 Regul. Pept. 25, 223-233, 1989
 A;Title: The constitution and properties of phosphorylated and unphosphorylated C-terminal
 A;Reference number: A60070; PMID:89331947; PMID:2756156
 A;Accession: C60070
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-9 <DES>
 A;Cross-references: UNIPARC:UPI000017C439

Query Match 21.4%; Score 12; DB 2; Length 9;
 Best Local Similarity 33.3%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 QGSHVP 7
 Db 4 EGDERP 9

RESULT 15

S65913
 pyrimidine synthesis multifunctional protein CAD - golden hamster (fragment)
 C;Species: Mesocricetus auratus (golden hamster)
 C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
 C;Accession: S65913
 R;Hemmings, B.; Carrey, E.A.
 Eur. J. Biochem. 231, 220-225, 1995
 A;Title: Mammalian dihydroorotase; secondary structure, and interactions with other proteins
 A;Reference number: S65913; PMID:95354692; PMID:7628474
 A;Accession: S65913
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-9 <HEM>
 A;Cross-references: UNIPARC:UPI000017C614

Query Match 21.4%; Score 12; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 HV 6
 Db 1 HV 2

Search completed: December 30, 2005, 15:14:17
 Job time : 38 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2005, 15:02:14 ; Search time 230 Seconds
(without alignments)

27.608 Million cell updates/sec

Title: US-10-735-916A-6

Perfect score: 56

Sequence: 1 FQGSHPWT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 873

Minimum DB seq length: 9

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	39.3	9	2	Q9UCQ9_HUMAN
2	19	33.9	9	2	Q6QF45_HUMAN
3	19	33.9	9	2	Q924N8_MOUSE
4	18	32.1	9	1	COW_CONVE
5	18	32.1	9	2	Q9UMF3_HUMAN
6	18	32.1	9	2	Q9UQW0_HUMAN
7	18	32.1	9	2	Q7M4D5_DIASE
8	18	32.1	9	2	Q28121_BOVIN
9	18	32.1	9	2	Q38366_BPPHX
10	18	32.1	9	2	Q7M078_RAT
11	18	32.1	9	2	Q7LZ66_MELGA
12	17	30.4	9	2	Q51LX3_MAGGR
13	17	30.4	9	2	Q67AR4_HUMAN
14	17	30.4	9	2	Q67AR6_HUMAN
15	17	30.4	9	2	Q67AR7_HUMAN
16	17	30.4	9	2	Q67AT1_HUMAN
17	17	30.4	9	2	Q67AT2_HUMAN
18	16	28.6	9	2	Q7M3N6_GRYBI
19	16	28.6	9	2	Q6LAP5_WACEU
20	16	28.6	9	2	Q47410_ECOLI
21	16	28.6	9	2	Q9RSM1_STAAU
22	16	28.6	9	2	Q673W5_TYTRA
23	16	28.6	9	2	Q673W6_9CORV
24	16	28.6	9	2	Q673W7_9CORV
25	16	28.6	9	2	Q673W8_9CORV
26	16	28.6	9	2	Q673W9_9CORV
27	16	28.6	9	2	Q673X0_9CORV
28	16	28.6	9	2	Q673X1_9CORV
29	16	28.6	9	2	Q673X2_9CORV
30	16	28.6	9	2	Q673X3_9CORV
31	16	28.6	9	2	Q673X4_9CORV

32	16	28.6	9	2	Q673X5_9CORV	Q673x5 platysteira
33	16	28.6	9	2	Q673X6_ORIXA	Q673x6 oriolus xan
34	16	28.6	9	2	Q673X7_9CORV	Q673x7 nilaus afer
35	16	28.6	9	2	Q673X8_9CORV	Q673x8 bias flammu
36	16	28.6	9	2	Q673X9_9CORV	Q673x9 malaconotus
37	16	28.6	9	2	Q673Y0_LANCL	Q673y0 lanius coll
38	16	28.6	9	2	Q673Y1_9CORV	Q673y1 lanioturdus
39	16	28.6	9	2	Q673Y2_9CORV	Q673y2 laniarius f
40	16	28.6	9	2	Q673Y3_9CORV	Q673y3 laniarius b
41	16	28.6	9	2	Q673Y4_9CORV	Q673y4 laniarius a
42	16	28.6	9	2	Q673Y5_9CORV	Q673y5 laniarius a
43	16	28.6	9	2	Q673Y6_9CORV	Q673y6 platysteira
44	16	28.6	9	2	Q673Y7_9CORV	Q673y7 dryoscopus
45	16	28.6	9	2	Q673Y8_9CORV	Q673y8 dryoscopus

ALIGNMENTS

RESULT 1

Q9UCQ9_HUMAN
ID Q9UCQ9_HUMAN PRELIMINARY; PRT; 9 AA.
AC Q9UCQ9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE AUTOTAXIN (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=9219337; PubMed=1733949;
RA Stracke M.L., Kruttsch H.C., Unsworth E.J., Arestad A., Cioce V.,
RA Schifmann E., Liotta L.A.;
RT "Identification, purification, and partial sequence analysis of
RT autotaxin, a novel motility-stimulating protein.",
RL J. Biol. Chem. 267:2524-2529(1992).
DR GO; GO:0006928; P:cell motility; NAS.
FT NON_TER 1 1
FT TER 9 9
SQ SEQUENCE 9 AA; 1136 MW; 9A3CAB14536772CA CRC64;
Query Match 39.3%; Score 22; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. NO. 2.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VPW 8

Db 3 VPW 5

RESULT 2

Q6QF45_HUMAN
ID Q6QF45_HUMAN PRELIMINARY; PRT; 9 AA.
AC Q6QF45;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Cytochrome P450 4F12 (Fragment).
GN Names-CYP4F12;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Cauffiez C., Klinzig F., Rat E., Tournel G., Allorge D., Chevalier D.,
RA Lovecchio T., Pottier N., Colombel J.-F., Lhermitte M.,
RA D'halluin J.-C., Broly F., Lo-Guidice J.-M.;

```

RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY544783; AAS49384.1; -; Genomic DNA.
DR EMBL; AY544784; AAS49385.1; -; Genomic DNA.
DR EMBL; AY544785; AAS49386.1; -; Genomic DNA.
DR EMBL; AY544782; AAS49383.1; -; Genomic DNA.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1059 MW; 970A676735B72735 CRC64;

Query Match 33.9%; Score 19; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.2e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 VPW 8
DB 6 LPW 8

RESULT 3
Q924N8 MOUSE PRELIMINARY; PRT; 9 AA.
AC Q924N8
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Niemann Pick type C1 protein (Fragment).
GN Name=Npcl;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BLKS;
RA Gevry N.Y., Lacroix D.A., Murphy B.D.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF184964; AAK83683.1; -; Genomic DNA.
FT NON_TER 9
SQ SEQUENCE 9 AA; 890 MW; 2C4E2DC761E1EDD8 CRC64;

Query Match 33.9%; Score 19; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 3 GSHVP 7
DB 2 GAHHP 6

RESULT 4
COW_CONVE STANDARD; PRT; 9 AA.
AC PB3047;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Contryphan-Vn.
OS Conus ventricosus (Mediterranean cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=117992;
RN [1]
RP PROTEIN SEQUENCE, SYNTHESIS, DISULFIDE BONDS, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RA Maesilia G.R., Schinina M.E., Ascenzi P., Polticelli F.;
RX MEDLINE=21547785; PubMed=11688995; DOI=10.1006/bbrc.2001.5833;
RT "Contryphan-Vn: a novel peptide from the venom of the Mediterranean
RT snail Conus ventricosus."
RT Biochem. Biophys. Res. Commun. 288:908-913(2001).
RN [2]
RP STRUCTURE BY NMR, SYNTHESIS, DISULFIDE BONDS, AND FUNCTION.
RX PubMed=12646193; DOI=10.1016/S0006-291X(03)00331-0;

RA Masilia G.R., Eliseo T., Grolleau F., Lapiere B., Barbier J.,
RA Bournaud R., Molgo J., Cicero D.O., Paci M., Schinina M.E.,
RA Ascenzi P., Polticelli F.;
RT "Contryphan-Vn: a modulator of Ca2+-dependent K+ channels."
RL Biochem. Biophys. Res. Commun. 303:238-246(2003).
CC -!- FUNCTION: Affects both voltage-gated and calcium-dependent
CC potassium channel activities, with composite and diversified
CC effects in invertebrate and vertebrate systems.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- PTM: The cis isomer is the most abundant and is thus thought to be
CC the functionally relevant conformer.
CC -!- MASS SPECTROMETRY: MW=1088.6; METHOD=MALDI; RANGE=1-9; NOTE=Ref.1.
CC -!- SIMILARITY: Belongs to the contryphan family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PDB; 1NKN; NMR; A=1-9.
KW 3D-structure; Amidation; D-amino acid; Direct protein sequencing;
KW Ionic channel inhibitor; Neurotoxin; Potassium channel inhibitor;
KW Toxin.
FT MOD_RES 5 5 D-tryptophan.
FT MOD_RES 9 9 Cysteine amide.
FT DISULFID 3 9
SQ SEQUENCE 9 AA; 1091 MW; 8D38676323676EBA CRC64;

Query Match 32.1%; Score 18; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PW 8
DB 4 PW 5

RESULT 5
Q9UMF3 HUMAN PRELIMINARY; PRT; 9 AA.
AC Q9UMF3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PD-1 protein (Fragment).
GN Name=PD-1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta;
RX MEDLINE=97473511; PubMed=9332365; DOI=10.1016/S0378-1119(97)00260-6;
RA Finger L.R., Pu J., Wasserman R., Vibhakar R., Louie E., Hardy R.R.,
RA Burrows P.D., Billips L.D.;
RT "The human PD-1 gene: complete cDNA, genomic organization, and
RT developmentally regulated expression in B cell progenitors."
RT Gene 197:177-187(1997).
DR EMBL; U64864; AAC51774.1; -; Genomic DNA.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1067 MW; DD4A676DC6C76046 CRC64;

Query Match 32.1%; Score 18; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PW 8
DB 7 PW 8

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```
RESULT 6
O9UQW0_HUMAN
ID O9UQW0_HUMAN PRELIMINARY; PRT; 9 AA.
AC Q9UQW0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Prolactin precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=84182507; PubMed=6325171;
RA Truong A.T., Duez C., Belayew A., Renard A., Pictet R.L., Bell G.I.,
RA Martial J.A.;
RT "Isolation and characterization of the human prolactin gene.";
RL EMBO J. 3:429-437(1984).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93076813; PubMed=1332868;
RA Peers B., Nalida A.M., Monget P., Voz M.L., Belayew A., Martial J.A.;
RT "Binding of a 100-kDa ubiquitous factor to the human prolactin
RT promoter is required for its basal and hormone-regulated activity.";
RL Eur. J. Biochem. 210:53-58(1992).
DR EMBL; X00368; CAA25108.1; -; Genomic_DNA.
KW Signal.
FT SIGNAL.
FT NON_TER 1 1 Potential.
FT NON_TER 1 1
SQ SEQUENCE 9 AA; 1060 MW; 0A1A6775B8733054 CRC64;

Query Match 32.1%; Score 18; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PW 8
DB 7 PW 8

RESULT 7
Q7M4D5_DIASE
ID Q7M4D5_DIASE PRELIMINARY; PRT; 9 AA.
AC Q7M4D5;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Sperm-activating peptide SAP-IV.
OS Diadema setosum (Sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Diadematacea; Diadematoida; Diadematidae;
OC Diadema.
OX NCBI_TaxID=31175;
RN [1]
RP PROTEIN SEQUENCE.
RA Yoshino K.I., Kurita M., Yamaguchi M., Nomura K., Takao T.,
RA Shimonishi Y., Suzuki N.;
RT "A species-specific sperm-activating peptide from the egg jelly of the
RT sea urchin Diadema setosum.";
RL Comp. Biochem. Physiol. 95:423-429(1990).
RN [2]
RP PROTEIN SEQUENCE.
RX PubMed=2158412;
RA Yoshino K., Kurita M., Yamaguchi M., Nomura K., Takao T.,
RA Shimonishi Y., Suzuki N.;
RT "A species-specific sperm-activating peptide from the egg jelly of the
RT sea urchin Diadema setosum.";
RL Comp. Biochem. Physiol. B, Comp. Biochem. 95:423-429(1990).
DR PIR; A60522; A60522.
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SQ SEQUENCE 9 AA; 849 MW; 9639CDD87863676E CRC64;

Query Match 32.1%; Score 18; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PW 8
DB 3 PW 4

RESULT 8
Q28121_BOVIN
ID Q28121_BOVIN PRELIMINARY; PRT; 9 AA.
AC Q28121;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Growth hormone receptor (Fragment).
GN Name=GHR;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96043217; PubMed=7486254;
RA Moody D.B., Pomp D., Barendse W., Womack J.E.;
RT "Assignment of the growth hormone receptor gene to bovine chromosome
RT 20 using linkage analysis and somatic cell mapping.";
RL Anim. Genet. 26:341-343(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91146804; PubMed=2289631; DOI=10.1016/0303-7207(90)90143-V;
RA Hauser S.D., McGrath M.F., Collier R.J., Krivi G.G.;
RT "Cloning and in vivo expression of bovine growth hormone receptor
RT mRNA.";
RL Mol. Cell. Endocrinol. 72:187-200(1990).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Moody D.M., Pomp D.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U24113; AAA91014.1; -; Genomic_DNA.
DR PIR; I46023; I46023.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 9 9
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1182 MW; D11E42C9D36769D6 CRC64;

Query Match 32.1%; Score 18; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PW 8
DB 4 PW 5

RESULT 9
Q38366_BPHX
ID Q38366_BPHX PRELIMINARY; PRT; 9 AA.
AC Q38366;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DSC-2001 (TrEMBLrel. 19, Last annotation update)
DE E gene product (Fragment).
OS Bacteriophage phi-X174.
OC Viruses; ssDNA viruses; Microviridae; Microvirus.
OX NCBI_TaxID=10847;
RN [1]
RP NUCLEOTIDE SEQUENCE.
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RX MEDLINE=88118956; PubMed=2963134;
RA Buckley K.J., Hayashi M.;
RT "Role of premature translational termination in the regulation of
RT expression of the phi X174 lysis gene.";
RL J. Mol. Biol. 198;599-607(1987).
DR EMBL; X07809; CAA30668.1; -; Genomic_DNA.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1207 MW; C093B37731B36412 CRC64;

Query Match 32.1%; Score 18; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 VPWT 9
DB 2 VWT 5

RESULT 10
Q7M078 RAT PRELIMINARY; PRT; 9 AA.
AC Q7M078_
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DE 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Xenopsin-related peptide 2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=91018491; PubMed=2217904; DOI=10.1016/0167-0115(90)90085-B;
RA Carraway R.E., Mitra S.P., Muraki K.;
RT "Isolation and structures of xenopsin-related peptides from rat
RT stomach, liver and brain.";
RL Regul. Pept. 29:229-239(1990).
DR PIR; A60320; A60320.
SQ SEQUENCE 9 AA; 1193 MW; E9FE436774032761 CRC64;

Query Match 32.1%; Score 18; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PW 8
DB 6 PW 7

RESULT 11
Q7LZ66 MELGA PRELIMINARY; PRT; 9 AA.
AC Q7LZ66_
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Xenopsin-related peptide 2.
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Meleagris.
OX NCBI_TaxID=9103;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=89042995; PubMed=2460902; DOI=10.1016/0167-0115(88)90107-3;
RA Carraway R.E., Cochran D.E., Mitra S.P.;
RT "Xenopsin-related peptide generated in avian gastric extracts.";
RL Regul. Pept. 22:303-314(1988).
DR PIR; JS0302; JS0302.
SQ SEQUENCE 9 AA; 1193 MW; E9FE436774032761 CRC64;

Query Match 32.1%; Score 18; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
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Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PW 8
DB 6 PW 7

RESULT 12
Q51LX3 MAGGR PRELIMINARY; PRT; 9 AA.
AC Q51LX3_
DT 13-SEP-2005 (TReMBLrel. 31, Created)
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
DE Hypothetical protein.
DE ORFNames=MG02768.4;
GN Magnaporthe grisea 70-15,
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthae.
OX NCBI_TaxID=242507;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
RA Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
RA Arachchi H., Armbruster J., Bachantsang P., Baldwin J., Barry A.,
RA Bayul T., Blitshteyn B., Bloom T., Blye J., Boguslavsky L.,
RA Borowsky M., Boukhaltier B., Brunache A., Butler J., Calixte N.,
RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
RA Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
RA Fitzgerald M., Foley K., Gage D., Galagan J., Galtsova E., Gnerre S.,
RA Gnikre A., Goette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
RA Jaffe D., Jones C., Kamal M., Kamat A., Kamysseles M., Karlsson E.,
RA Kells C., Kieu A., Kisner P., Kodira C., Kulbokas E., Labutti K.,
RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
RA Lindblad-toh K., Liu X., Lokyitsang T., Lokyitsang Y., Lucien O.,
RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
RA Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,
RA McCarthy M., McDonough S., Mcghee T., Meldrim J., Meneus L.,
RA Mesirov J., Mihalev A., Mihova T., Mikkelsen T., Mlenga V., Moru K.,
RA Mozes J., Multain L., Munson G., Naylor J., News C., Nguyen C.,
RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
RA Norbu N., O'donnell P., Okoawo O., O'leary S., Omotosho B.,
RA O'Neill K., Osman S., Parker S., Perrin D., Phunkhang P., Pignani B.,
RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
RA Rutman M., Schupbach R., Seaman C., Settipalli S., Sharpe T.,
RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,
RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
RA Stenson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,
RA Tensing P., Tesfaye S., Theodore J., Thoulutsang Y., Topham K.,
RA Towey S., Tsamla T., Tsomo N., Vallee D., Vassiliev H.,
RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
RA Vengataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
RA Zimmer A., Zody M., Lander E.;
RT "The genome sequence of Magnaporthe grisea.";
RN Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Dean R., Mitchell T., Brown D., Pan H., Thon M.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Zhu H., Blackmon B.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
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CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACU01001555; EAA47525.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 9 AA; 1003 MW; DF9FCSA6D1F5BDC6 CRC64;

Query Match 30.4%; Score 17; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QGSH 5
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|
|
Db 2 QASH 5

RESULT 13
Q67AR4 HUMAN
ID Q67AR4_HUMAN PRELIMINARY; PRT; 9 AA.
AC Q67AR4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE MHC class II antigen (Fragment).
GN Name=HLA-DPB1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wood J.M., Simons M.J., Ashdown M.L.;
RT "HLA-DPB1 3' intron 1.\"",
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY375795; AAQ88089.1; -; Genomic_DNA.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1154 MW; 1AF0C40866D9C73B CRC64;

Query Match 30.4%; Score 17; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQG 3
|
|
|
Db 4 FQG 6

RESULT 14
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ID Q67AR6_HUMAN PRELIMINARY; PRT; 9 AA.
AC Q67AR6;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE MHC class II antigen (Fragment).
GN Name=HLA-DPB1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wood J.M., Simons M.J., Ashdown M.L.;
RT "HLA-DPB1 3' intron 1.\"",
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY375793; AAQ88087.1; -; Genomic_DNA.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1154 MW; 1AF0C40866D9C73B CRC64;

Query Match 30.4%; Score 17; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQG 3
|
|
|
Db 4 FQG 6

RESULT 15
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ID Q67AR7_HUMAN PRELIMINARY; PRT; 9 AA.
AC Q67AR7;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE MHC class II antigen (Fragment).
GN Name=HLA-DPB1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wood J.M., Simons M.J., Ashdown M.L.;
RT "HLA-DPB1 3' intron 1.\"",
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY375792; AAQ88086.1; -; Genomic_DNA.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1154 MW; 1AF0C40866D9C73B CRC64;

Query Match 30.4%; Score 17; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQG 3
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|
|
Db 4 FQG 6

Search completed: December 30, 2005, 15:12:37
Job time : 232 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2005, 15:02:40 ; Search time 50 Seconds
(without alignments)
14.882 Million cell updates/sec

Title: US-10-735-916A-6
Perfect score: 56
Sequence: 1 FQSHVPWT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 25369

Minimum DB seq length: 9
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	94.6	9	1	US-07-977-696C-72
2	53	94.6	9	1	US-08-129-330B-72
3	53	94.6	9	2	US-08-976-288A-72
4	53	94.6	9	2	US-09-947-839B-72
5	47	83.9	9	1	US-07-977-696C-34
6	47	83.9	9	1	US-08-129-330B-34
7	47	83.9	9	1	US-08-560-558E-31
8	47	83.9	9	2	US-08-134-346A-21
9	47	83.9	9	2	US-08-976-288A-34
10	47	83.9	9	2	US-09-217-268B-31
11	47	83.9	9	2	US-09-947-839B-34
12	46	82.1	9	1	US-08-053-171-29
13	39	69.6	9	2	US-09-724-409-5
14	39	69.6	9	2	US-09-724-530-5
15	39	69.6	9	2	US-09-328-296-5
16	37	66.1	9	2	US-08-649-100-15
17	37	66.1	9	2	US-08-649-100-31
18	36	64.3	9	2	US-10-226-795-30
19	35	62.5	9	2	US-09-771-415-15
20	34	60.7	9	1	US-08-488-161-6
21	34	60.7	9	2	US-09-273-685-6
22	34	60.7	9	2	US-09-440-781-24
23	34	60.7	9	4	PCT-US95-11934-6
24	32	57.1	9	2	US-09-440-781-26
25	32	57.1	9	2	US-09-771-415-14
26	32	57.1	9	2	US-09-518-737-10
27	32	57.1	9	2	US-09-996-288-61

28	57.1	9	2	US-09-996-265-61	Sequence 61, Appl
29	55.4	9	2	US-08-836-561-39	Sequence 39, Appl
30	55.4	9	2	US-09-434-122-39	Sequence 39, Appl
31	55.4	9	2	US-09-440-781-25	Sequence 25, Appl
32	55.4	9	2	US-09-771-415-5	Sequence 5, Appl
33	55.4	9	2	US-09-771-415-16	Sequence 16, Appl
34	55.4	9	2	US-09-996-288-6	Sequence 6, Appl
35	55.4	9	2	US-09-996-265-6	Sequence 6, Appl
36	55.4	9	2	US-08-908-469-6	Sequence 10, Appl
37	55.4	9	2	US-10-135-636-10	Sequence 10, Appl
38	53.6	9	1	US-08-350-260A-364	Sequence 364, App
39	53.6	9	1	US-08-350-260A-425	Sequence 425, App
40	53.6	9	2	US-09-104-337A-364	Sequence 364, App
41	53.6	9	2	US-09-104-337A-425	Sequence 425, App
42	53.6	9	2	US-09-889-480A-6	Sequence 6, Appl
43	48.2	9	1	US-08-244-626-8	Sequence 8, Appl
44	48.2	9	2	US-09-440-781-23	Sequence 23, Appl
45	48.2	9	2	US-08-908-469-125	Sequence 125, App

ALIGNMENTS

RESULT 1
US-07-977-696C-72
; Sequence 72, Application US/07977696C
; Patent No. 5792852
; GENERAL INFORMATION:
; APPLICANT: do Couto, Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides with Specificity
; TITLE OF INVENTION: for Carcinomas and Kit and Diagnostic Vaccination
; TITLE OF INVENTION: and Therapeutic Methods.
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/977,696C
; FILING DATE: 11-16-92
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel Ph.D., Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P66 38227
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 748-6686
; TELEFAX: (510) 748-6688
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-977-696C-72

Query Match 94.6%; Score 53; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 FQSHVPWT 9

Db 1 FQGHVPWT 9
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RESULT 2

US-08-129-930B-72
; Sequence 72, Application US/08129930B
; Patent No. 5804187
; GENERAL INFORMATION:
; APPLICANT: do Couto Dr., Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides With Broad
; TITLE OF INVENTION: Carcinoma Specificity, and Kit and
; TITLE OF INVENTION: Diagnostic Vaccination and
; TITLE OF INVENTION: Therapeutic Methods
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: V. AMZEL & ASSOC.
; STREET: 2055 No. 5804187th Broadway, Suite 201
; CITY: Walnut Creek
; STATE: California
; COUNTRY: USA
; ZIP: 94596
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/129,930B
; FILING DATE: September 30, 1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel Ph.D., Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: CRFCC-008A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 521-1333
; TELEFAX: (510) 521-3541
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-129-930B-72

Query Match 94.6%; Score 53; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. NO. 4.6e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQGHVPWT 9
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Db

RESULT 3

US-08-976-288A-72
; Sequence 72, Application US/08976288A
; Patent No. 6315997
; GENERAL INFORMATION:
; APPLICANT: do Couto Dr., Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides With Broad
; TITLE OF INVENTION: Carcinoma Specificity, and Kit and
; TITLE OF INVENTION: Diagnostic Vaccination and
; TITLE OF INVENTION: Therapeutic Methods
; NUMBER OF SEQUENCES: 96

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder & Poplawski
; STREET: 444 South Flower St., 19th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976,288A
; FILING DATE: No. 6315997ember 21, 1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/129,930
; FILING DATE: September 30, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/977,696
; FILING DATE: No. 6315997ember 16, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel Ph.D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P6639938
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 622-7700
; TELEFAX: (213) 489-4210
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-976-288A-72

Query Match 94.6%; Score 53; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. NO. 4.6e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQGHVPWT 9
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Db 1 FQGHVPWT 9

RESULT 4

US-09-947-839B-72
; Sequence 72, Application US/09947839B
; Patent No. 6936706
; GENERAL INFORMATION:
; APPLICANT: do Couto, Fernando J.R.
; Ceriani Dr., Roberto L.
; Peterson Dr., Jerry A.
; Padlan Dr., Eduardo A.

TITLE OF INVENTION: Analogue Peptides with Specificity
for Carcinomas and Kit and Diagnostic Vaccination
and Therapeutic Methods.

NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: V. Amzel & Assoc.
STREET: P.O.Box 159
CITY: Gladwyne
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19035

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/947,839B
FILING DATE: 06-Sep-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Amzel Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: CRFC-083
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-649-0609
TELEFAX: 240-359-0299
TELEX: n.a.
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 72:
US-09-947-839B-72

Query Match 94.6%; Score 53; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQSHVPT 9
Db 1 FQSHVPT 9

RESULT 5
US-07-977-696C-34
Sequence 34, Application US/07977696C
Patent No. 5792852
GENERAL INFORMATION:
APPLICANT: do Couto, Fernando J.R.
APPLICANT: Ceriani Dr., Roberto L.
APPLICANT: Peterson Dr., Jerry A.
APPLICANT: Padlan Dr., Eduardo A.
TITLE OF INVENTION: Analogue Peptides with Specificity
TITLE OF INVENTION: for Carcinomas and Kit and Diagnostic Vaccination
TITLE OF INVENTION: and Therapeutic Methods.
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/977,696C
FILING DATE: 11-16-92
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Amzel Ph.D., Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38227
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 748-6868
TELEFAX: (510) 748-6688
TELEX: n.a.
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-977-696C-34

Query Match 83.9%; Score 47; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQSHVPT 9
Db 1 FQSHVPT 9

RESULT 6
US-08-129-930B-34
Sequence 34, Application US/08129930B
Patent No. 5804187
GENERAL INFORMATION:
APPLICANT: do Couto Dr., Fernando J.R.
APPLICANT: Ceriani Dr., Roberto L.
APPLICANT: Peterson Dr., Jerry A.
APPLICANT: Padlan Dr., Eduardo A.
TITLE OF INVENTION: Analogue Peptides with Broad
TITLE OF INVENTION: Carcinoma Specificity, and Kit and
TITLE OF INVENTION: Diagnostic Vaccination and
TITLE OF INVENTION: Therapeutic Methods
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: V. AMZEL & ASSOC.
STREET: 2055 No. 5804187th Broadway, Suite 201
CITY: Walnut Creek
STATE: California
COUNTRY: USA
ZIP: 94596
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/129,930B
FILING DATE: September 30, 1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Amzel Ph.D., Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: CRFCC-008A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 521-1333
TELEFAX: (510) 521-3541
TELEX: n.a.
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-129-930B-34

Query Match 83.9%; Score 47; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQSHVPT 9
Db 1 FQSHVPT 9

RESULT 7
US-08-560-558E-31
Sequence 31, Application US/08560558E
Patent No. 5891996
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Humanized and chimeric monoclonal
TITLE OF INVENTION: antibodies that recognize epidermal growth factor receptor

;/ TITLE OF INVENTION: EGF-R; diagnostic and therapeutic use.
;/ NUMBER OF SEQUENCES: 34
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Allen C. Turner, TRASK, BRITT & ROSSA
;/ STREET: P.O. Box 2250
;/ CITY: Salt Lake City
;/ STATE: Utah
;/ COUNTRY: United States of America
;/ ZIP: 84110
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: WINDOWS95
;/ SOFTWARE: WordPerfect 5.1/5.2
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/560,558E
;/ FILING DATE: No. 5891996ember 17, 1995
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Turner, Allen C.
;/ REGISTRATION NUMBER: 33,041
;/ REFERENCE/DOCKET NUMBER: 2720US
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (801) 532-1922
;/ TELEFAX: (801) 531-9168
;/ INFORMATION FOR SEQ ID NO: 31:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 9 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: unknown
;/ TOPOLOGY: unknown
;/ MOLECULE TYPE: protein
;/ HYPOTHETICAL: NO
;/ US-08-560-558E-31

Query Match 83.9%; Score 47; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FQSHVPWT 9
Db 1 FQSHVPWT 9

RESULT 8
US-08-134-346A-21
; Sequence 21, Application US/08134346A
; Patent No. 6281335
; GENERAL INFORMATION:
; APPLICANT: do Couto, F.J.R.
; APPLICANT: Cexiani, R.L.C.
; APPLICANT: Petersen, J.A.
; TITLE OF INVENTION: HYBRIDOMA AND ANTI-KC-4 HUMANIZED
; TITLE OF INVENTION: MONOCLONAL ANTIBODY AND DNA AND RNA ENCODING IT, KIT AND
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ostrager, Chong & Flaherty
; STREET: 300 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10022-7499
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette-3.50 inch, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/134,346A
; FILING DATE: 08-OCT-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Onofrio, Dara L.

;/ REGISTRATION NUMBER: 34,889
;/ REFERENCE/DOCKET NUMBER: CLT 149,608
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 212-826-6565
;/ TELEFAX: 212-826-5909
;/ INFORMATION FOR SEQ ID NO: 21:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 9 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS:
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
;/ US-08-134-346A-21

Query Match 83.9%; Score 47; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQSHVPWT 9
Db 1 FQSHVPWT 9

RESULT 9
US-08-976-288A-34
; Sequence 34, Application US/08976288A
; Patent No. 6315997
; GENERAL INFORMATION:
; APPLICANT: do Couto Dr., Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides With Broad
; TITLE OF INVENTION: Carcinoma Specificity, and Kit and
; TITLE OF INVENTION: Diagnostic Vaccination and
; TITLE OF INVENTION: Therapeutic Methods
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder & Poplawski
; STREET: 444 South Flower St., 19th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976,288A
; FILING DATE: No. 6315997ember 21, 1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/129,930
; FILING DATE: September 30, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/977,696
; FILING DATE: No. 6315997ember 16, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel Ph.D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P6639938
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 622-7700
; TELEFAX: (213) 489-4210
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-976-288A-34

Query Match 83.9%; Score 47; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQSHVPWT 9
Db 1 FQSHVPYT 9

RESULT 10

US-09-217-268B-31

; Sequence 31, Application US/09217268B

; Patent No. 6506883

; GENERAL INFORMATION:

; APPLICANT: Mateo de Acosta del Rio, Christina M

; APPLICANT: Rodriguez, Rolando P

; APPLICANT: Frias, Ernesto M

; TITLE OF INVENTION: Humanized and Chimeric Monoclonal Antibodies That Recognize Epide

; TITLE OF INVENTION: Growth Factor Receptor (EGF-R); Diagnostic and Therapeutic Use

; FILE REFERENCE: 2720.1US

; CURRENT APPLICATION NUMBER: US/09/217,268B

; CURRENT FILING DATE: 1998-12-21

; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 31

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Murine

; FEATURE:

; NAME/KEY: MISC FEATURE

; OTHER INFORMATION: CDR of murine R3 antibody

US-09-217-268B-31

Query Match

Best Local Similarity 83.9%; Score 47; DB 2; Length 9;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FQSHVPWT 9
Db 1 FQSHVPYT 9

RESULT 11

US-09-947-839B-34

; Sequence 34, Application US/09947839B

; Patent No. 6936706

; GENERAL INFORMATION:

; APPLICANT: do Couto, Fernando J.R.

; APPLICANT: Ceriani Dr., Roberto L.

; APPLICANT: Peterson Dr., Jerry A.

; APPLICANT: Padlan Dr., Eduardo A.

; TITLE OF INVENTION: Analogue Peptides with Specificity

; TITLE OF INVENTION: Analogue Peptides with Specificity

; TITLE OF INVENTION: Analogue Peptides with Specificity

; TITLE OF INVENTION: Analogue Peptides with Specificity

; TITLE OF INVENTION: Analogue Peptides with Specificity

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; TITLE OF INVENTION: Analogue Peptides with Specificity

; TITLE OF INVENTION: Analogue Peptides with Specificity

; TITLE OF INVENTION: Analogue Peptides with Specificity

ATTORNEY/AGENT INFORMATION:

NAME: Amzel Viviana

REGISTRATION NUMBER: 30,930

REFERENCE/DOCKET NUMBER: CRFC-083

TELEPHONE: 610-649-0609

TELEFAX: 240-359-0299

TELEX: n.a.

INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 34:

US-09-947-839B-34

Query Match

Best Local Similarity 83.9%; Score 47; DB 2; Length 9;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQSHVPWT 9
Db 1 FQSHVPYT 9

RESULT 12

US-08-053-171-29

; Sequence 29, Application US/08053171

; Patent No. 5562903

; GENERAL INFORMATION:

; APPLICANT: Co. Loibner

; TITLE OF INVENTION: Antibody Derivatives

; NUMBER OF SEQUENCES: 32

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend Kourie and Crew

; STREET: 379 Lytton Avenue

; CITY: Palo Alto

; STATE: California

; COUNTRY: US

; ZIP: 94301

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/053,171

; FILING DATE: 22-APR-1993

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Smith, William M

; REGISTRATION NUMBER: 30,223

; REFERENCE/DOCKET NUMBER: 11823-54-1

; TELEPHONE: (415) 326-2400

; TELEFAX: (415) 326-2422

; INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

FEATURE:

.NAME/KEY: Peptide

LOCATION: 1..9

OTHER INFORMATION: /note= "Third

OTHER INFORMATION: complementarity-determining region (CDR3) of

OTHER INFORMATION: BR55-2 antibody light chain"

US-08-053-171-29

Query Match

82.1%; Score 46; DB 1; Length 9;

Best Local Similarity 88.9%; Pred. No. 4.6e+05; Indels 0; Gaps 0;
Matches 8; Conservative 1; Mismatches 0;

QY 1 FQSHVPWT 9
|:|||||:
Db 1 FQSHVPWT 9

RESULT 13

US-09-724-409-5
; Sequence 5, Application US/09724409
; Patent No. 6838261
; GENERAL INFORMATION:
; APPLICANT: Siegall, Clay
; APPLICANT: Wahl, Alan
; APPLICANT: Francisco, Joseph
; APPLICANT: Fell, H. Perry
; TITLE OF INVENTION: RECOMBINANT ANTI-CD40 ANTIBODY AND USES THEREOF
; FILE REFERENCE: 9632-005
; CURRENT APPLICATION NUMBER: US/09/724,409
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/328,296
; PRIOR FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-724-409-5

Query Match 69.6%; Score 39; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QGSHVPWT 9
|:|||||:
Db 2 QTTHVPWT 9

RESULT 14

US-09-724-530-5
; Sequence 5, Application US/09724530
; Patent No. 6843989
; GENERAL INFORMATION:
; APPLICANT: Siegall, Clay
; APPLICANT: Wahl, Alan
; APPLICANT: Francisco, Joseph
; APPLICANT: Fell, H. Perry
; TITLE OF INVENTION: RECOMBINANT ANTI-CD40 ANTIBODY AND USES THEREOF
; FILE REFERENCE: 9632-005
; CURRENT APPLICATION NUMBER: US/09/724,530
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/328,296
; PRIOR FILING DATE: CURRENT FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-724-530-5

Query Match 69.6%; Score 39; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QGSHVPWT 9
|:|||||:
Db 2 QTTHVPWT 9

RESULT 15

US-09-328-296-5
; Sequence 5, Application US/09328296
; Patent No. 6946129
; GENERAL INFORMATION:
; APPLICANT: Siegall, Clay
; APPLICANT: Wahl, Alan
; APPLICANT: Francisco, Joseph
; APPLICANT: Fell, H. Perry
; TITLE OF INVENTION: RECOMBINANT ANTI-CD40 ANTIBODY AND USES THEREOF
; FILE REFERENCE: 9632-005
; CURRENT APPLICATION NUMBER: US/09/328,296
; CURRENT FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-328-296-5

Query Match 69.6%; Score 39; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QGSHVPWT 9
|:|||||:
Db 2 QTTHVPWT 9

Search completed: December 30, 2005, 15:13:33
Job time : 50 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2005, 15:12:47 ; Search time 160 Seconds
(without alignments)
23.503 Million cell updates/sec

Title: US-10-735-916A-6

Perfect score: 56

Sequence: 1 FQGSHPVWT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 68385

Minimum DB seq length: 9

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	9	3	US-09-995-529-36
2	56	100.0	9	3	US-09-995-529-36
3	56	100.0	9	4	US-10-470-045-48
4	56	100.0	9	5	US-10-735-916A-6
5	53	94.6	9	3	US-09-947-839-72
6	52	92.9	9	3	US-09-995-529-128
7	52	92.9	9	3	US-09-995-529-132
8	52	92.9	9	3	US-09-995-529-138
9	52	92.9	9	3	US-09-995-529-128
10	52	92.9	9	3	US-09-995-529-132
11	52	92.9	9	3	US-09-995-529-138
12	51	91.1	9	3	US-09-995-529-139
13	51	91.1	9	3	US-09-995-529-140
14	51	91.1	9	3	US-09-995-529-141
15	51	91.1	9	3	US-09-995-529-142
16	51	91.1	9	3	US-09-995-529-143
17	51	91.1	9	3	US-09-995-529-145
18	51	91.1	9	3	US-09-995-529-139
19	51	91.1	9	3	US-09-995-529-140
20	51	91.1	9	3	US-09-995-529-141
21	51	91.1	9	3	US-09-995-529-142
22	51	91.1	9	3	US-09-995-529-143
23	51	91.1	9	3	US-09-995-529-145
24	50	89.3	9	3	US-09-995-529-126
25	50	89.3	9	3	US-09-995-529-127
26	50	89.3	9	3	US-09-995-529-130
27	50	89.3	9	3	US-09-995-529-126

Sequence 127, App
Sequence 130, App
Sequence 129, App
Sequence 131, App
Sequence 129, App
Sequence 131, App
Sequence 131, App
Sequence 137, App
Sequence 137, App
Sequence 31, Appl
Sequence 135, App
Sequence 34, Appl
Sequence 135, App
Sequence 12, Appl
Sequence 10, Appl
Sequence 81, Appl
Sequence 23, Appl
Sequence 12, Appl
Sequence 6, Appl

28 50 89.3 9 3 US-09-995-529-127
29 50 89.3 9 3 US-09-995-529-130
30 49 87.5 9 3 US-09-995-529-129
31 49 87.5 9 3 US-09-995-529-131
32 49 87.5 9 3 US-09-995-529-129
33 49 87.5 9 3 US-09-995-529-131
34 48 85.7 9 3 US-09-995-529-137
35 48 85.7 9 3 US-09-995-529-137
36 47 83.9 9 3 US-09-217-268B-31
37 47 83.9 9 3 US-09-995-529-135
38 47 83.9 9 3 US-09-947-839-34
39 47 83.9 9 3 US-09-995-529-135
40 47 83.9 9 4 US-10-434-469-12
41 47 83.9 9 5 US-10-482-105-10
42 47 83.9 9 5 US-10-409-611-81
43 47 83.9 9 5 US-10-409-608A-23
44 47 83.9 9 5 US-10-500-207A-12
45 47 83.9 9 6 US-11-009-443-6

ALIGNMENTS

RESULT 1
US-09-995-529-36
; Sequence 36, Application US/09995529
; Publication No. US2003009655A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; TITLE OF INVENTION: Related Methods
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-995-529-36

Query Match 100.0%; Score 56; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQGSHPVWT 9
| | | | | | | | |
Db 1 FQGSHPVWT 9

RESULT 2
US-09-995-529-36
; Sequence 36, Application US/09995529
; Publication No. US20040091482A9
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; TITLE OF INVENTION: Related Methods
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-995-529-36

Query Match 100.0%; Score 56; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPWT 9
| | | | |
DB 1 FQGSHPWT 9

RESULT 3
US-10-470-045-48
; Sequence 48, Application US/10470045
; Publication No. US20040146505A1
; GENERAL INFORMATION:
; APPLICANT: Scancell Limited
; APPLICANT: Durrant, Linda Gillian
; APPLICANT: Parsons, Tina
; TITLE OF INVENTION: Substances
; FILE REFERENCE: P32181WQ/NJL
; CURRENT APPLICATION NUMBER: US/10/470,045
; CURRENT FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: GB 0102145.0
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 48
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-470-045-48

Query Match 100.0%; Score 56; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPWT 9
| | | | |
DB 1 FQGSHPWT 9

RESULT 4
US-10-735-916A-6
; Sequence 6, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GORTSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFILOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10/735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-735-916A-6

Query Match 100.0%; Score 56; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPWT 9
| | | | |
DB 1 FQGSHPWT 9

RESULT 5
US-09-947-839-72
; Sequence 72, Application US/09947839
; Publication No. US20030138428A1
; GENERAL INFORMATION:
; APPLICANT: do Couto Dr., Fernando J.R.
; Ceriani Dr., Roberto L.
; Padern Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides With Broad
; Carcinoma Specificity, and Kit and
; Diagnostic Vaccination and
; Therapeutic Methods
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder & Poplawski
; STREET: 444 South Flower St., 19th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/09/947,839
; FILING DATE: 06-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/976,288
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 07/977,696
; FILING DATE: No. US20030138428A1ember 16, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel Ph.D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P6639938
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 622-7700
; TELEFAX: (213) 489-4210
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 72:
US-09-947-839-72

Query Match 94.6%; Score 53; DB 3; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPWT 9
| | | | |
DB 1 FQGSHPWT 9

RESULT 6
US-09-995-529-128

; Sequence 128, Application US/09995529
; Publication No. US20030099655A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 128
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody mutation
US-09-995-529-128

Query Match 92.9%; Score 52; DB 3; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQGSHPVPT 9
Db 1 FQGSHPVPT 9

RESULT 7

US-09-995-529-132
; Sequence 132, Application US/09995529
; Publication No. US20030099655A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 132
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody mutation
US-09-995-529-132

Query Match 92.9%; Score 52; DB 3; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FQGSHPVPT 9
Db 1 FQGSHPVPT 9

RESULT 8

US-09-995-529-138
; Sequence 138, Application US/09995529
; Publication No. US20030099655A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; FILE REFERENCE: P-IX 4976

; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 138
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody mutation
US-09-995-529-138

Query Match 92.9%; Score 52; DB 3; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FQGSHPVPT 9
Db 1 FQGSHPVPT 9

RESULT 9

US-09-995-529-128
; Sequence 128, Application US/09995529
; Publication No. US20040091482A9
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 128
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody mutation
US-09-995-529-128

Query Match 92.9%; Score 52; DB 3; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQGSHPVPT 9
Db 1 FQGSHPVPT 9

RESULT 10

US-09-995-529-132
; Sequence 132, Application US/09995529
; Publication No. US20040091482A9
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 132
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

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; OTHER INFORMATION: synthetic antibody mutation
US-09-995-529-132

Query Match          92.9%; Score 52; DB 3; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FQGSHPWT 9
DB 1 FQGSHPWT 9

RESULT 11
US-09-995-529-138
; Sequence 138, Application US/09995529
; Publication No. US20040091482A9
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; TITLE OF INVENTION: Related Methods
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 138
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody mutation
US-09-995-529-138

Query Match          92.9%; Score 52; DB 3; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FQGSHPWT 9
DB 1 FQGSHPWT 9

RESULT 12
US-09-995-529-139
; Sequence 139, Application US/09995529
; Publication No. US2003009655A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; TITLE OF INVENTION: Related Methods
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 139
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody mutation
US-09-995-529-139

Query Match          91.1%; Score 51; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPW 8
DB 1 FQGSHPW 8

RESULT 13
US-09-995-529-140
; Sequence 140, Application US/09995529
; Publication No. US2003009655A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; TITLE OF INVENTION: Related Methods
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 140
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody mutation
US-09-995-529-140

Query Match          91.1%; Score 51; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPW 8
DB 1 FQGSHPW 8

RESULT 14
US-09-995-529-141
; Sequence 141, Application US/09995529
; Publication No. US2003009655A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; TITLE OF INVENTION: Related Methods
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 141
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody mutation
US-09-995-529-141

Query Match          91.1%; Score 51; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FQGSHPW 8
DB 1 FQGSHPW 8

RESULT 15
US-09-995-529-142
; Sequence 142, Application US/09995529
; Publication No. US2003009655A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.

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; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; TITLE OF INVENTION: Related Methods
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 142
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody mutation
US-09-995-529-142
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```
Query Match          91.1%; Score 51; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 FQGSHPVW 8
        |||||
Db      1 FQGSHPVW 8
```

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Search completed: December 30, 2005, 15:26:42
Job time : 161 secs
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OM protein - protein search, using sw model

Run on: December 30, 2005, 15:13:42 ; Search time 13 seconds
(without alignments)

5.185 Million cell updates/sec

Title: US-10-735-916A-6

Perfect score: 56

Sequence: 1 FQGSHPWT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 6541

Minimum DB seq length: 9

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pap:*
- 2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pap:*
- 3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pap:*
- 4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pap:*
- 5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pap:*
- 6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pap:*
- 7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pap:*
- 8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	9	7 US-11-012-353-6	Sequence 6, Appl
2	56	100.0	9	7 US-11-125-837-15	Sequence 15, Appl
3	56	100.0	9	7 US-11-105-708-19	Sequence 19, Appl
4	41	73.2	9	6 US-10-932-334-6	Sequence 6, Appl
5	39	69.6	9	7 US-11-102-743-5	Sequence 5, Appl
6	37	66.1	9	7 US-11-125-837-3	Sequence 3, Appl
7	32	57.1	9	7 US-11-009-939-40	Sequence 40, Appl
8	32	57.1	9	7 US-11-097-812-196	Sequence 196, Appl
9	31	55.4	9	7 US-11-193-512-39	Sequence 39, Appl
10	29	51.8	9	6 US-10-473-037-8	Sequence 8, Appl
11	27	48.2	9	6 US-10-507-662-60	Sequence 60, Appl
12	26	46.4	9	6 US-10-507-662-59	Sequence 59, Appl
13	24	42.9	9	7 US-11-045-024-46	Sequence 46, Appl
14	24	42.9	9	7 US-11-045-024-3770	Sequence 3770, Ap
15	24	42.9	9	7 US-11-045-024-7048	Sequence 7048, Ap
16	24	42.9	9	7 US-11-045-024-13595	Sequence 13595, A
17	23	41.1	9	7 US-11-009-939-20	Sequence 20, Appl
18	22	39.3	9	7 US-11-010-748A-303	Sequence 303, Appl
19	22	39.3	9	7 US-11-010-748A-304	Sequence 304, Appl
20	22	39.3	9	7 US-11-045-024-45	Sequence 45, Appl
21	22	39.3	9	7 US-11-045-024-47	Sequence 47, Appl
22	22	39.3	9	7 US-11-045-024-3769	Sequence 3769, Ap
23	22	39.3	9	7 US-11-045-024-3771	Sequence 3771, Ap
24	22	39.3	9	7 US-11-045-024-6971	Sequence 6971, Ap
25	22	39.3	9	7 US-11-045-024-7067	Sequence 7067, Ap

Sequence 13572, A
Sequence 13594, A
Sequence 13597, A
Sequence 13604, A
Sequence 13630, A
Sequence 13638, A
Sequence 45, Appl
Sequence 301, Appl
Sequence 302, Appl
Sequence 305, Appl
Sequence 306, Appl
Sequence 10563, A
Sequence 12365, A
Sequence 13976, A
Sequence 1135, Ap
Sequence 4056, Ap
Sequence 4058, Ap
Sequence 12607, A
Sequence 13736, A
Sequence 72, Appl

ALIGNMENTS

RESULT 1
US-11-012-353-6
; Sequence 6, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GORTSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFILOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-012-353-6

Query Match 100.0%; Score 56; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.3e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FQGSHPWT 9
| | | | | | | | |
Db 1 FQGSHPWT 9

RESULT 2
US-11-125-837-15
; Sequence 15, Application US/11125837

```
; Publication No. US20050266003A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Rong-Hwa
; APPLICANT: Chang, Chung Nan
; APPLICANT: Chen, Pei-Jiun
; APPLICANT: Huang, Chiu-Chen
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 13062-011001
; CURRENT APPLICATION NUMBER: US/11/125,837
; CURRENT FILING DATE: 2005-05-10
; PRIOR APPLICATION NUMBER: US 60/569,892
; PRIOR FILING DATE: 2004-05-10
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-125-837-15

Query Match      100.0%; Score 56; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.3e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FQGSHPVPT 9
Db      1 FQGSHPVPT 9
|||||

RESULT 3
US-11-105-708-19
; Sequence 19, Application US/11105708
; Publication No. US20050281821A1
; GENERAL INFORMATION:
; APPLICANT: Pernasetti, Flavia
; APPLICANT: Freimark, Bruce
; APPLICANT: Van Epps, Dennis
; APPLICANT: Brooks, Peter C
; TITLE OF INVENTION: Method and Composition for Angiogenesis Inhibition
; FILE REFERENCE: 30797-704.501
; CURRENT APPLICATION NUMBER: US/11/105,708
; CURRENT FILING DATE: 2005-04-13
; PRIOR APPLICATION NUMBER: 09/478,977
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: 60/152,496
; PRIOR FILING DATE: 1999-09-02
; PRIOR APPLICATION NUMBER: 60/143,534
; PRIOR FILING DATE: 1999-09-02
; PRIOR APPLICATION NUMBER: 60/114,878
; PRIOR FILING DATE: 1999-01-06
; PRIOR APPLICATION NUMBER: 60/114,877
; PRIOR FILING DATE: 1999-01-06
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-105-708-19

Query Match      100.0%; Score 56; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.3e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FQGSHPVPT 9
Db      1 FQGSHPVPT 9
|||||

RESULT 4
US-10-932-334-6
; Sequence 6, Application US/10932334
; Publication No. US20050249728A1
; GENERAL INFORMATION:
; APPLICANT: ImmunoGen, Inc.
; TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
; FILE REFERENCE: A8689
; CURRENT APPLICATION NUMBER: US/10/932,334
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US/10/729,441
; PRIOR FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: 10/170,390
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antibody light chain complementarity determining region
US-10-932-334-6

Query Match      73.2%; Score 41; DB 6; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.3e+04;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 FQGSHPVPT 9
Db      1 FQGSHPVPT 9
|||||

RESULT 5
US-11-102-743-5
; Sequence 5, Application US/11102743
; Publication No. US20050266002A1
; GENERAL INFORMATION:
; APPLICANT: Siegall, Clay
; APPLICANT: Wahl, Alan
; APPLICANT: Francisco, Joseph
; APPLICANT: Fell, H. Perry
; TITLE OF INVENTION: RECOMBINANT ANTI-CD40 ANTIBODY AND USES THEREOF
; FILE REFERENCE: 9632-005
; CURRENT APPLICATION NUMBER: US/11/102,743
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US/09/328,296
; PRIOR FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-102-743-5

Query Match      69.6%; Score 39; DB 7; Length 9;
Best Local Similarity 75.0%; Pred. No. 4.3e+04;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 QGSHPVPT 9
Db      2 QTHVPT 9
|:|||||

RESULT 6
US-11-125-837-3
; Sequence 3, Application US/11125837
; Publication No. US20050266003A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Rong-Hwa
; APPLICANT: Chang, Chung Nan
; APPLICANT: Chen, Pei-Jiun
; APPLICANT: Huang, Chiu-Chen
; TITLE OF INVENTION: ANTIBODIES
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FILE REFERENCE: 13062-011001
CURRENT APPLICATION NUMBER: US/11/125,837
CURRENT FILING DATE: 2005-05-10
PRIOR APPLICATION NUMBER: US 60/569,892
PRIOR FILING DATE: 2004-05-10
NUMBER OF SEQ ID NOS: 100
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 9
TYPE: PRT
ORGANISM: Mus musculus
US-11-125-837-3

Query Match 66.1%; Score 37; DB 7; Length 9;
Best Local Similarity 77.8%; Pred. No. 4.3e+04;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FQSHVPWT 9
Db 1 FQGSYVELT 9

RESULT 7
US-11-009-939-40
Sequence 40, Application US/11009939
Publication No. US20050265998A1
GENERAL INFORMATION:
APPLICANT: Elson, Greg Christopher Andrew
TITLE OF INVENTION: Neutralizing Antibodies and Methods of Use Thereof
FILE REFERENCE: 23135-402
CURRENT APPLICATION NUMBER: US/11/009,939
CURRENT FILING DATE: 2005-12-10
PRIOR APPLICATION NUMBER: 60/528,811
PRIOR FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 60/528,812
PRIOR FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 60/528,962
PRIOR FILING DATE: 2003-12-10
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 40
LENGTH: 9
TYPE: PRT
ORGANISM: Mus musculus
US-11-009-939-40

Query Match 57.1%; Score 32; DB 7; Length 9;
Best Local Similarity 62.5%; Pred. No. 4.3e+04;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QGSHVPWT 9
Db 2 QGNTFPWT 9

RESULT 8
US-11-097-812-196
Sequence 196, Application US/11097812
Publication No. US20050281828A1
GENERAL INFORMATION:
APPLICANT: Bowdish, Katherine S.
APPLICANT: Kretz-Rommel, Anke
APPLICANT: Dakapagari, Naveen
TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
CURRENT APPLICATION NUMBER: US/11/097,812
CURRENT FILING DATE: 2005-04-01
PRIOR APPLICATION NUMBER: US 11/016,647
PRIOR FILING DATE: 2004-12-17
PRIOR APPLICATION NUMBER: PCT/US04/06570
PRIOR FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: US 60/548,385

PRIOR FILING DATE: 2004-02-28
PRIOR APPLICATION NUMBER: US 60/529,500
PRIOR FILING DATE: 2003-12-15
PRIOR APPLICATION NUMBER: US 60/451,816
PRIOR FILING DATE: 2003-03-04
NUMBER OF SEQ ID NOS: 207
SOFTWARE: PatentIn version 3.2
SEQ ID NO 196
LENGTH: 9
TYPE: PRT
ORGANISM: mouse
US-11-097-812-196

Query Match 57.1%; Score 32; DB 7; Length 9;
Best Local Similarity 62.5%; Pred. No. 4.3e+04;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 QGSHVPWT 9
Db 2 QSKVEPWT 9

RESULT 9
US-11-193-512-39
Sequence 39, Application US/11193512
Publication No. US20050272918A1
GENERAL INFORMATION:
APPLICANT: KOIKE, Masamichi
FURUYA, Akiko
NAKAMURA, Kazuyasu
IIDA, Akihiro
ANAZAWA, Hideharu
HANAI, Nobuo
TAKATSU, Kiyoshi
TITLE OF INVENTION: Antibody Against Human Interleukin-5
Receptor Alpha Chain
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/193,512
FILING DATE: 01-Aug-2005
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/283,349
FILING DATE: 29-Oct-2002
APPLICATION NUMBER: US/08/836,561
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: JP 232384/95
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lawrence, III, Stanton T
REGISTRATION NUMBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-115-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single

```

; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-11-193-512-39

Query Match      55.4%; Score 31; DB 7; Length 9;
Best Local Similarity 62.5%; Pred. No. 4.3e+04;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 QGSHVPWT 9
DB 2 QSKDVPWT 9

RESULT 10
US-10-473-037-8
; Sequence 8, Application US/10473037
; Publication No. US20050260206A1
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
; TITLE OF INVENTION: Agents for treatment of cancer using recombinant anti-GD3 antibody
; TITLE OF INVENTION: the antibody fragments
; FILE REFERENCE: 11374WO1
; CURRENT APPLICATION NUMBER: US/10/473,037
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: JP2001-097483
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-473-037-8

Query Match      51.8%; Score 29; DB 6; Length 9;
Best Local Similarity 62.5%; Pred. No. 4.3e+04;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 QGSHVPWT 9
DB 2 QYSKLPWT 9

RESULT 11
US-10-507-662-60
; Sequence 60, Application US/10507662
; Publication No. US20050255102A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; TITLE OF INVENTION: ANTI-ALPHA-V BETA-6 ANTIBODIES
; FILE REFERENCE: A136PCT
; CURRENT APPLICATION NUMBER: US/10/507,662
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: 60/364,991
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/426,286
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-507-662-60

Query Match      48.2%; Score 27; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.3e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VPWT 9
   ||||

```

```

DB 6 VPWT 9

RESULT 12
US-10-507-662-59
; Sequence 59, Application US/10507662
; Publication No. US20050255102A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; TITLE OF INVENTION: ANTI-ALPHA-V BETA-6 ANTIBODIES
; FILE REFERENCE: A136PCT
; CURRENT APPLICATION NUMBER: US/10/507,662
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: 60/364,991
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/426,286
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-507-662-59

Query Match      46.4%; Score 26; DB 6; Length 9;
Best Local Similarity 75.0%; Pred. No. 4.3e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 VPWT 9
DB 6 IPWT 9

RESULT 13
US-11-045-024-46
; Sequence 46, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060, 0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 46
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-46

Query Match      42.9%; Score 24; DB 7; Length 9;
Best Local Similarity 60.0%; Pred. No. 4.3e+04;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      4 SHVPW 8
       :||||
Db      5 TNVPW 9
```

RESULT 14

```
US-11-045-024-3770
; Sequence 3770, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3770
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-3770
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```
Query Match      42.9%; Score 24; DB 7; Length 9;
Best Local Similarity 60.0%; Pred. No. 4.3e+04;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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Qy      4 SHVPW 8
       :||||
Db      5 TNVPW 9
```

RESULT 15

```
US-11-045-024-7048
; Sequence 7048, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7048
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-7048
```

```
Query Match      42.9%; Score 24; DB 7; Length 9;
Best Local Similarity 60.0%; Pred. No. 4.3e+04;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      4 SHVPW 8
       :||||
Db      5 TNVPW 9
```

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Search completed: December 30, 2005, 15:27:03
Job time : 16 secs
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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:14:26 ; Search time 13.4516 Seconds
(without alignments)
36.877 Million cell updates/sec

Title: US-10-735-916A-8
Perfect score: 40
Sequence: 1 GGYLWN 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
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4: /cgn2_6/ptodata/1/iaa/PCUS_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	90.0	480	2	US-09-252-991A-19202
2	35	87.5	275	2	US-09-489-039A-12128
3	35	87.5	277	2	US-09-583-110-2944
4	35	87.5	278	2	US-09-769-787-19
5	35	87.5	290	2	US-09-107-433-4262
6	35	87.5	550	2	US-09-252-991A-17547
7	35	87.5	739	2	US-09-540-236-3594
8	34	85.0	144	1	US-09-108-051-2
9	34	85.0	144	2	US-09-440-833-2
10	34	85.0	180	2	US-08-913-159-13
11	34	85.0	301	2	US-09-328-352-7439
12	34	85.0	326	2	US-09-489-039A-9700
13	34	85.0	349	2	US-09-270-767-45401
14	34	85.0	516	2	US-09-489-039A-12893
15	34	85.0	609	2	US-09-949-016-6846
16	34	85.0	984	2	US-09-171-461-14
17	34	85.0	984	2	US-09-970-711-14
18	34	85.0	1091	2	US-09-328-352-5758
19	33	82.5	324	2	US-09-549-848B-34
20	33	82.5	324	2	US-09-688-069-34
21	33	82.5	347	2	US-09-902-540-13914
22	33	82.5	601	2	US-09-902-540-12462
23	32	80.0	114	1	US-08-741-437-3
24	32	80.0	114	1	US-09-134-593-3
25	32	80.0	143	2	US-09-270-767-33503
26	32	80.0	143	2	US-09-270-767-48720
27	32	80.0	289	1	US-08-741-437-1

28	32	80.0	289	1	US-08-741-437-4	Sequence 4, Appli
29	32	80.0	289	1	US-09-134-593-1	Sequence 1, Appli
30	32	80.0	289	1	US-09-134-593-4	Sequence 4, Appli
31	32	80.0	289	2	US-09-538-092-1335	Sequence 1335, Ap
32	32	80.0	339	2	US-09-583-110-3067	Sequence 3067, Ap
33	32	80.0	348	2	US-09-107-433-2966	Sequence 2966, Ap
34	32	80.0	411	2	US-09-540-236-3549	Sequence 3549, Ap
35	32	80.0	533	2	US-09-252-991A-25841	Sequence 25841, A
36	32	80.0	545	2	US-08-976-0638-10	Sequence 10, Appl
37	32	80.0	613	1	US-08-484-101B-46	Sequence 46, Appl
38	32	80.0	613	1	US-08-484-101B-48	Sequence 48, Appl
39	32	80.0	613	2	US-08-714-524D-46	Sequence 46, Appl
40	32	80.0	613	2	US-08-714-524D-48	Sequence 48, Appl
41	32	80.0	738	2	US-09-328-352-4315	Sequence 4315, Ap
42	32	80.0	886	2	US-09-769-787-126	Sequence 126, App
43	32	80.0	2504	2	US-09-328-352-5821	Sequence 5821, Ap
44	31	77.5	94	2	US-09-543-681A-7919	Sequence 7919, App
45	31	77.5	120	2	US-09-991-181-199	Sequence 199, App

ALIGNMENTS

RESULT 1
US-09-252-991A-19202
; Sequence 19202, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19202
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19202

Query Match 90.0%; Score 36; DB 2; Length 480;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGYLWN 6
Db 194 GGFLWN 199

RESULT 2
US-09-489-039A-12128
; Sequence 12128, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12128
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12128

Query Match 87.5%; Score 35; DB 2; Length 275;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGYLWN 6
||| ||
DB 103 GGYTWN 108

RESULT 3
US-09-583-110-2944
; Sequence 2944, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 2944
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-2944

Query Match 87.5%; Score 35; DB 2; Length 277;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGYLWN 6
||| ||
DB 66 GGYTWN 71

RESULT 4
US-09-769-787-19
; Sequence 19, Application US/09769787
; Patent No. 6936252
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics Limited
; APPLICANT: Gilbert, Christophe FG
; APPLICANT: Hansbro, Philip M
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21129WO
; CURRENT APPLICATION NUMBER: US/09/769,787
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: GB 9816337.1
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/125164
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-769-787-19

Query Match 87.5%; Score 35; DB 2; Length 278;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGYLWN 6
||| ||

DB 67 GGYTWN 72
RESULT 5
US-09-107-433-4262
; Sequence 4262, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 4262:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 290 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...290
; SEQUENCE DESCRIPTION: SEQ ID NO: 4262:
US-09-107-433-4262

Query Match 87.5%; Score 35; DB 2; Length 290;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGYLWN 6
||| ||
DB 79 GGYTWN 84

RESULT 6
US-09-252-991A-17547
; Sequence 17547, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: ASERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17547
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17547

Query Match 87.5%; Score 35; DB 2; Length 550;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGYLWN 6
|||
Db 257 GGYWYN 262

RESULT 7
US-09-540-236-3594
; Sequence 3594, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 3594
; LENGTH: 739
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-3594

Query Match 87.5%; Score 35; DB 2; Length 739;
Best Local Similarity 83.3%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGYLWN 6
|||
Db 339 GGYLWH 344

RESULT 8
US-09-108-051-2
; Sequence 2, Application US/09108051
; Patent No. 5985576
; GENERAL INFORMATION:
; APPLICANT: Ellingson, Jay L.E.
; APPLICANT: Stabel, Judith R.
; TITLE OF INVENTION: Species-Specific Genetic Identification
; TITLE OF INVENTION: of Mycobacterium Paratuberculosis
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis P. Ribando
; STREET: 1815 N. University Street
; CITY: Peoria
; STATE: IL
; COUNTRY: US
; ZIP: 61604
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/108,051

; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ribando, Curtis P.
; REGISTRATION NUMBER: 27,976
; REFERENCE/DOCKET NUMBER: 0229.97
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 309/681-6513
; TELEFAX: 309/681-6688
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 144 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-108-051-2

Query Match 85.0%; Score 34; DB 1; Length 144;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GYLWN 6
|||
Db 30 GYLWN 34

RESULT 9
US-09-440-833-2
; Sequence 2, Application US/09440833
; Patent No. 6277580
; GENERAL INFORMATION:
; APPLICANT: Ellingson, Jay L.E.
; APPLICANT: Stabel, Judith R.
; TITLE OF INVENTION: Species-Specific Genetic Identification
; TITLE OF INVENTION: of Mycobacterium Paratuberculosis
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis P. Ribando
; STREET: 1815 N. University Street
; CITY: Peoria
; STATE: IL
; COUNTRY: US
; ZIP: 61604
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/440,833
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/108,051
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ribando, Curtis P.
; REGISTRATION NUMBER: 27,976
; REFERENCE/DOCKET NUMBER: 0229.97
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 309/681-6513
; TELEFAX: 309/681-6688
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 144 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-440-833-2

Query Match 85.0%; Score 34; DB 2; Length 144;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      2 GYLWN 6
      |||||
Db     30 GYLWN 34

RESULT 10
US-08-913-159-13
; Sequence 13, Application US/08913159
; Patent No. 6300109
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Plasmid-derived type II
; TITLE OF INVENTION: restriction-modification systems from Lactococcus lactis
; NUMBER OF SEQUENCES: 14
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,159
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0179/95
; FILING DATE: 17-FEB-1995
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-913-159-13

Query Match      85.0%; Score 34; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GYLWN 6
      |||||
Db     57 GYLWN 61

RESULT 11
US-09-328-352-7439
; Sequence 7439, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 7439
; LENGTH: 301
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7439

Query Match      85.0%; Score 34; DB 2; Length 301;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GYLWN 6
      |||||
Db     215 GYLWN 219

RESULT 12
US-09-489-039A-9700
; Sequence 9700, Application US/09489039A
```

```
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 9700
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9700

Query Match      85.0%; Score 34; DB 2; Length 326;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GYLWN 6
      |||||
Db     240 GYLWN 244

RESULT 13
US-09-270-767-45401
; Sequence 45401, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45401
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-45401

Query Match      85.0%; Score 34; DB 2; Length 349;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGYLW 5
      |||||
Db     57 GGYLW 61

RESULT 14
US-09-489-039A-12893
; Sequence 12893, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12893
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12893
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Query Match 85.0%; Score 34; DB 2; Length 516;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGYLW 5
|
|
|
|
Db 491 GGYLW 495

RESULT 15
US-09-949-016-6846
; Sequence 6846, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6846
; LENGTH: 609
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(609)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-949-016-6846

Query Match 85.0%; Score 34; DB 2; Length 609;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GYLWN 6
|
|
|
|
Db 294 GYLWN 298

Search completed: December 30, 2005, 13:37:18
Job time : 14.4516 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:02:01 ; Search time 53.3226 Seconds
(without alignments)
49.440 Million cell updates/sec

Title: US-10-735-916A-8

Perfect score: 40

Sequence: 1 GGYLWN 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq_21.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	40	100.0	6	7	ADJ76842 CDR seque
2	40	100.0	6	9	ADZ67012 Murine in
3	40	100.0	117	7	ADJ76903
4	40	100.0	117	7	ADJ76909 Anti-IGF-
5	40	100.0	117	7	ADJ76917 Anti-IGF-
6	40	100.0	117	7	ADJ76913 Anti-IGF-
7	40	100.0	117	9	ADZ67083 Human ant
8	40	100.0	117	9	ADZ67087 Human ant
9	40	100.0	117	9	ADZ67073 Murine im
10	40	100.0	117	9	ADZ67079 Human ant
11	40	100.0	127	7	ADJ76886 Anti-IGF-
12	40	100.0	127	9	ADZ67056 Murine im
13	40	100.0	135	7	ADJ76911 Anti-IGF-
14	40	100.0	135	7	ADJ76919 Anti-IGF-
15	40	100.0	135	9	ADZ67091 Human ant
16	40	100.0	135	9	ADZ67089 Human ant
17	40	100.0	135	9	ADZ67081 Human ant
18	40	100.0	135	9	ADZ67085 Human ant
19	40	100.0	544	7	ADB70198 C. neofo
20	37	92.5	1471	4	ABBS8739 Drosophil
21	36	90.0	480	7	ABO70456 Pseudomon
22	35	87.5	83	5	ABU05763 M. tuberc
23	35	87.5	121	7	ADJ80377 Antibody
24	35	87.5	125	7	ADP03868 Murine-ex

25	35	87.5	125	7	ADP03876 Murine-ex
26	35	87.5	257	7	ADB75644 TM1 scFv
27	35	87.5	275	7	ABO65611 Klebsiell
28	35	87.5	277	8	ADK46429 Streptoco
29	35	87.5	279	3	AY81519 Streptoco
30	35	87.5	285	6	ABU02392 S. pneumo
31	35	87.5	290	8	ADR95627 Novel S.
32	35	87.5	290	9	AEA59497 Streptoco
33	35	87.5	400	7	ADC87483 Human GPC
34	35	87.5	550	7	ABO68801 Pseudomon
35	35	87.5	739	8	ADL05908 M. catarr
36	34	85.0	57	5	ABG80748 C-type le
37	34	85.0	71	4	ABBI7537 Human ner
38	34	85.0	72	4	AAG73998 Human col
39	34	85.0	96	4	AAM92258 Human dig
40	34	85.0	103	3	AAG29147 Arabidops
41	34	85.0	107	3	AAG29146 Arabidops
42	34	85.0	109	4	AAU20236 Human nov
43	34	85.0	137	4	ABB59022 Drosophil
44	34	85.0	139	3	AAB41367 Human ORF
45	34	85.0	139	5	ABP34716 Human ORF

ALIGNMENTS

RESULT 1
ADJ76842

ID ADJ76842 standard; peptide; 6 AA.

AC ADJ76842;

DT 06-MAY-2004 (first entry)

DE CDR sequence for anti-IGF-1R antibody.

KW cytostatic; antipsoriatic; antibody;

KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;

KW or epidermal growth factor receptor; EGFR; signal transduction pathway;

KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;

KW CDR.

OS Mus musculus.

PN WO2003059951-A2.

PD 24-JUL-2003.

PF 20-JAN-2003; 2003WO-FR000178.

PR 18-JAN-2002; 2002FR-00000653.

PR 18-JAN-2002; 2002FR-00000654.

PR 07-MAY-2002; 2002FR-000005753.

PA (FABR) FABRE MEDICAMENT SA PIERRE.

PI Goetech L, Corvaia N, Leger O;

DR WPI; 2003-569653/53.

DR N-PSDB; ADJ76841.

PT New antibodies that bind to human insulin-like growth factor receptor,

PT useful for treatment, prevention and diagnosis of cancers.

XX Claim 1; SEQ ID NO 8; 164pp; French.

XX The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-1R) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-1R. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with

CC hyperactivity of signal transduction pathways mediated by interaction of
 CC these receptors with their ligands. Especially they inhibit
 CC transfection of normal cells to tumor cells, inhibit growth and/or
 CC proliferation of tumor cells, so are useful against cancers of the
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused
 CC by abnormal expression of IGF-IR and/or EGFR. This sequence represents an
 CC CDR sequence used to generate the Ab of the invention.

XX Sequence 6 AA;

Query Match 100.0%; Score 40; DB 7; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0;

QY 1 GGYLWN 6
 |||||
 Db 1 GGYLWN 6

RESULT 2

ID ADZ67012 standard; peptide; 6 AA.

XX ADZ67012;

AC ADZ67012;

XX 30-JUN-2005 (first entry)

DE Marine insulin-like growth factor T receptor IGF-IR CDR SEQ ID NO:8.

XX Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
 KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;
 KW musculoskeletal disease; respiratory disease; lung tumor;
 KW endocrine disease; gynecology and obstetrics; breast tumor;
 KW endometroid carcinoma; gastrointestinal disease; colon tumor;
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder.

XX Mus musculus.

XX US2005084906-A1.

XX 21-APR-2005.

XX 16-DEC-2003; 2003US-00735916.

XX 18-JAN-2002; 2002FR-00000653.

XX 18-JAN-2002; 2002FR-00000654.

XX 07-MAY-2002; 2002FR-00005753.

XX 20-JAN-2003; 2003WO-FR000178.

XX 11-JUL-2003; 2003FR-00008538.

XX (GOET/) GOETSCH L.

XX (CORV/) CORVAIA N.

XX (LEGE/) LEGER O.

XX (DUFLO/) DUFLOS A.

XX (HAEU/) HAEUW J.

XX (BECK/) BECK A.

XX Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;

XX WPI; 2005-321968/33.

XX N-PSDB; ADZ67011.

XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)

XX antibody or its functional fragment, being capable of binding human IGF-

XX IR and specifically inhibiting tyrosine kinase activity of receptor,

XX useful for treating cancer.

CC specifically inhibiting tyrosine kinase activity of the receptor,
 CC comprising a light or heavy chain having at least one complementary
 CC determining region (CDR) consisting of one of two fully defined 16 amino
 CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in
 CC the preparation of a medicament intended for the prevention or treatment
 CC of an illness connected with an overexpression and/or an abnormal
 CC activation of the IGF-IR and/or EGFR, and/or connected with a
 CC hyperactivation of the transduction pathway of the signal mediated by the
 CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where
 CC the administration of the medicament does not induce or only slightly
 CC induces secondary effects connected with inhibition of the insulin
 CC receptor. The antibody is useful for preparation of a medicament intended
 CC to inhibit the transformation of normal cells into cells with tumoral
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is
 CC useful for preparation of a medicament intended to inhibit the growth
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a
 CC medicament intended for prevention or for the treatment of cancer, where
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the
 CC preparation of a medicament intended for the prevention or for the
 CC treatment of psoriasis. (I) is useful in preparation of a medicament
 CC intended for the specific targeting of a biologically active compound to
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)
 CC is useful for in vitro diagnosis of illnesses induced by an
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor
 CC starting from a biological sample in which the abnormal presence, of IGF-
 CC IR and/or EGFR receptor is suspected, which involves contacting the
 CC biological sample with (I), which is optionally labeled. The present
 CC sequence is used in the exemplification of the invention.

XX Sequence 6 AA;

Query Match 100.0%; Score 40; DB 9; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0;

QY 1 GGYLWN 6
 |||||
 Db 1 GGYLWN 6

RESULT 3

ADJ76903

ID ADJ76903 standard; protein; 117 AA.

XX AC ADJ76903;

XX 06-MAY-2004 (first entry)

XX Anti-IGF-1R related protein #16.

XX cytostatic; antipsoriatic; antibody;

XX insulin-like growth factor-1 receptor; IGF-IR; tyrosine kinase activity;
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;
 KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;
 KW CDR.

XX Homo sapiens.

XX WO2003059951-A2.

XX 24-JUL-2003.

XX 20-JAN-2003; 2003WO-FR000178.

XX 18-JAN-2002; 2002FR-00000653.

XX 18-JAN-2002; 2002FR-00000654.

XX 07-MAY-2002; 2002FR-00005753.

XX (FABR) FABRE MEDICAMENT SA PIERRE.

XX Goetsch L, Corvaia N, Leger O;
 XX WPI; 2003-569653/53.
 XX New antibodies that bind to human insulin-like growth factor receptor,
 XX useful for treatment, prevention and diagnosis of cancers.
 XX Disclosure; SEQ ID NO 69; 164pp; French.
 XX
 CC The invention relates to an isolated antibody (Ab), and its functional
 CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-
 CC IR) and optionally: (i) inhibit natural binding of insulin-like growth
 CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine
 CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or
 CC treat diseases associated with overexpression and/or abnormal activity of
 CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with
 CC hyperactivity of signal transduction pathways mediated by interaction of
 CC these receptors with their ligands. Especially they inhibit
 CC transformation of normal cells to tumor cells, inhibit growth and/or
 CC proliferation of tumor cells, so are useful against cancers of the
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a
 CC protein sequence used to generate the Ab of the invention.
 XX
 SQ Sequence 117 AA;

Query Match 100.0%; Score 40; DB 7; Length 117;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLMN 6
 DB 31 GGYLMN 36
 |||||

RESULT 4
 ADJ76909
 ID ADJ76909 standard; protein; 117 AA.

XX AC ADJ76909;
 XX DT 06-MAY-2004 (first entry)
 XX DE Anti-IGF-1R related protein #22.
 XX
 KW cytosolic; antipsoriatic; antibody;
 KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;
 KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;
 KW CDR.

XX OS Homo sapiens.

XX PN WO2003059951-A2.

XX PD 24-JUL-2003.

XX PF 20-JAN-2003; 2003WO-FR000178.

XX PR 18-JAN-2002; 2002FR-00000653.

XX PR 18-JAN-2002; 2002FR-00000654.

XX PR 07-MAY-2002; 2002FR-00005753.

XX PA (FABR) FABRE MEDICAMENT SA PIERRE.

XX PI Goetsch L, Corvaia N, Leger O;

XX WPI; 2003-569653/53.

XX New antibodies that bind to human insulin-like growth factor receptor,
 XX useful for treatment, prevention and diagnosis of cancers.

XX Disclosure; SEQ ID NO 75; 164pp; French.
 XX
 CC The invention relates to an isolated antibody (Ab), and its functional
 CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-
 CC IR) and optionally: (i) inhibit natural binding of insulin-like growth
 CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine
 CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or
 CC treat diseases associated with overexpression and/or abnormal activity of
 CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with
 CC hyperactivity of signal transduction pathways mediated by interaction of
 CC these receptors with their ligands. Especially they inhibit
 CC transformation of normal cells to tumor cells, inhibit growth and/or
 CC proliferation of tumor cells, so are useful against cancers of the
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a
 CC protein sequence used to generate the Ab of the invention.
 XX
 SQ Sequence 117 AA;

Query Match 100.0%; Score 40; DB 7; Length 117;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLMN 6
 DB 31 GGYLMN 36
 |||||

RESULT 5
 ADJ76917
 ID ADJ76917 standard; protein; 117 AA.

XX AC ADJ76917;

XX DT 06-MAY-2004 (first entry)

XX DE Anti-IGF-1R related protein #26.

XX
 KW cytosolic; antipsoriatic; antibody;
 KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;
 KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;
 KW CDR.

XX OS Homo sapiens.

XX PN WO2003059951-A2.

XX PD 24-JUL-2003.

XX PF 20-JAN-2003; 2003WO-FR000178.

XX PR 18-JAN-2002; 2002FR-00000653.

XX PR 18-JAN-2002; 2002FR-00000654.

XX PR 07-MAY-2002; 2002FR-00005753.

XX PA (FABR) FABRE MEDICAMENT SA PIERRE.

XX PI Goetsch L, Corvaia N, Leger O;

XX WPI; 2003-569653/53.

XX New antibodies that bind to human insulin-like growth factor receptor,
 XX useful for treatment, prevention and diagnosis of cancers.

XX Disclosure; SEQ ID NO 83; 164pp; French.

XX
 CC The invention relates to an isolated antibody (Ab), and its functional
 CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-
 CC IR) and optionally: (i) inhibit natural binding of insulin-like growth
 CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine

CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or
 CC treat diseases associated with overexpression and/or abnormal activity of
 CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with
 CC hyperactivity of signal transduction pathways mediated by interaction of
 CC these receptors with their ligands. Especially they inhibit
 CC transformation of normal cells to tumor cells, inhibit growth and/or
 CC proliferation of tumor cells, so are useful against cancers of the
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a
 CC protein sequence used to generate the Ab of the invention.

XX SQ Sequence 117 AA;

Query Match 100.0%; Score 40; DB 7; Length 117;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6
 |||||
 Db 31 GGYLWN 36

RESULT 6

ADJ76913
 ID ADJ76913 standard; protein; 117 AA.

XX AC ADJ76913;

XX DT 06-MAY-2004 (first entry)

XX DE Anti-IGF-1R related protein #24.

XX KW cytostatic; antipsoriatic; antibody;

KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;
 KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;
 KW CDR.

XX OS Homo sapiens.

XX PN WO2003059951-A2.

XX PD 24-JUL-2003.

XX PF 20-JAN-2003; 2003WO-FR000178.

XX PR 18-JAN-2002; 2002FR-00000653.

XX PR 18-JAN-2002; 2002FR-00000654.

XX PR 07-MAY-2002; 2002FR-00005753.

XX PA (FABR) FABRE MEDICAMENT SA PIERRE.

XX PI Goetsch L, Corvaia N, Leger O;

XX PF WPI; 2003-569653/53.

XX PT New antibodies that bind to human insulin-like growth factor receptor,
 PT useful for treatment, prevention and diagnosis of cancers.

XX PS Disclosure; SEQ ID NO 79; 164pp; French.

XX CC The invention relates to an isolated antibody (Ab), and its functional
 CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-
 CC 1R) and optionally: (i) inhibit natural binding of insulin-like growth
 CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine
 CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or
 CC treat diseases associated with overexpression and/or abnormal activity of
 CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with
 CC hyperactivity of signal transduction pathways mediated by interaction of
 CC these receptors with their ligands. Especially they inhibit
 CC transformation of normal cells to tumor cells, inhibit growth and/or
 CC proliferation of tumor cells, so are useful against cancers of the

CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a
 CC protein sequence used to generate the Ab of the invention.

XX SQ Sequence 117 AA;

Query Match 100.0%; Score 40; DB 7; Length 117;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6
 |||||
 Db 31 GGYLWN 36

RESULT 7

ADZ67083
 ID ADZ67083 standard; protein; 117 AA.

XX AC ADZ67083;

XX DT 30-JUN-2005 (first entry)

XX DE Human antibody 7C10 2 heavy chain variable region SEQ ID NO:79.

XX KW Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
 KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;
 KW musculoskeletal disease; respiratory disease; lung tumor;
 KW endocrine disease; gynecology and obstetrics; breast tumor;
 KW endometroid carcinoma; gastrointestinal disease; colon tumor;
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder;
 KW heavy chain variable region.

XX OS Homo sapiens.

XX PN US2005084906-A1.

XX PD 21-APR-2005.

XX PF 16-DEC-2003; 2003US-00735916.

XX PR 18-JAN-2002; 2002FR-00000653.

XX PR 18-JAN-2002; 2002FR-00000654.

XX PR 07-MAY-2002; 2002FR-00005753.

XX PR 20-JAN-2003; 2003WO-FR000178.

XX PR 11-JUL-2003; 2003FR-00008538.

XX PA (GOET/) GOETSCH L.

XX PA (CORV/) CORVAIA N.

XX PA (LEGE/) LEGER O.

XX PA (DUFL/) DUFLOS A.

XX PA (HAEU/) HAEUW J.

XX PA (BECK/) BECK A.

XX PI Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;

XX PF WPI; 2005-321968/33.

XX PT Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)
 PT antibody or its functional fragment, being capable of binding human IGF-
 PT IR and specifically inhibiting tyrosine kinase activity of receptor,
 PT useful for treating cancer.

XX PS Example 13; SEQ ID NO 79; 125pp; English.

XX CC The invention relates to a novel isolated anti-insulin-like growth factor
 CC I receptor (IGF-IR) antibody (I) or its functional fragment, being
 CC capable of binding to human IGF-IR and, if necessary, capable of
 CC specifically inhibiting tyrosine kinase activity of the receptor,
 CC comprising a light or heavy chain having at least one complementary
 CC determining region (CDR) consisting of one of two fully defined 16 amino
 CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in

CC the preparation of a medicament intended for the prevention or treatment
 CC of an illness connected with an overexpression and/or an abnormal
 CC activation of the IGF-IR and/or EGFR, and/or connected with a
 CC hyperactivation of the transduction pathway of the signal mediated by the
 CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where
 CC the administration of the medicament does not induce or only slightly
 CC induces secondary effects connected with inhibition of the insulin
 CC receptor. The antibody is useful for preparation of a medicament intended
 CC to inhibit the transformation of normal cells into cells with tumoral
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is
 CC useful for preparation of a medicament intended to inhibit the growth
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a
 CC medicament intended for prevention or for the treatment of cancer, where
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the
 CC preparation of a medicament intended for the prevention or for the
 CC treatment of psoriasis. (I) is useful in preparation of a medicament
 CC intended for the specific targeting of a biologically active compound to
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)
 CC is useful for in vitro diagnosis of illnesses induced by an
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor
 CC starting from a biological sample in which the abnormal presence, of IGF-
 CC IR and/or EGFR receptor is suspected, which involves contacting the
 CC biological sample with (I), which is optionally labeled. The present
 CC sequence is used in the exemplification of the invention.

XX SQ Sequence 117 AA;

Query Match 100.0%; Score 40; DB 9; Length 117;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6
 DB 31 GGYLWN 36
 |||||

RESULT 8

ID ADZ67087 standard; protein; 117 AA.

XX AC ADZ67087;

DT 30-JUN-2005 (first entry)

XX Human antibody 7C10 3 heavy chain variable region SEQ ID NO:83.

XX Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
 KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;
 KW musculoskeletal disease; respiratory disease; lung tumor;
 KW endocrine disease; gynecology and obstetrics; breast tumor;
 KW endometroid carcinoma; gastrointestinal disease; colon tumor;
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder;
 KW heavy chain variable region.

XX OS Homo sapiens.

XX US2005084906-A1.

XX 21-APR-2005.

XX 16-DEC-2003; 2003US-00735916.

XX 18-JAN-2002; 2002FR-00000653.

XX 18-JAN-2002; 2002FR-00000554.

XX 07-MAY-2002; 2002FR-00005753.

XX 20-JAN-2003; 2003WO-FR000178.

XX 11-JUL-2003; 2003FR-00008538.

XX (GOET/) GOETSCH L.

PA (CORV/) CORVAIA N.
 PA (LEGE/) LEGER O.
 PA (DUFLO/) DUFLOS A.
 PA (HAEUW/) HAEUW J.
 XX (BECK/) BECK A.

PI Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;
 DR WPI; 2005-321968/33.

XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)
 PT antibody or its functional fragment, being capable of binding human IGF-
 PT IR and specifically inhibiting tyrosine kinase activity of receptor,
 PT useful for treating cancer.

XX Example 13; SEQ ID NO 83; 125pp; English.

XX The invention relates to a novel isolated anti-insulin-like growth factor
 CC I receptor (IGF-IR) antibody (I) or its functional fragment, being
 CC capable of binding to human IGF-IR and, if necessary, capable of
 CC specifically inhibiting tyrosine kinase activity of the receptor,
 CC comprising a light or heavy chain having at least one complementary
 CC determining region (CDR) consisting of one of two fully defined 16 amino
 CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in
 CC the preparation of a medicament intended for the prevention or treatment
 CC of an illness connected with an overexpression and/or an abnormal
 CC activation of the IGF-IR and/or EGFR, and/or connected with a
 CC hyperactivation of the transduction pathway of the signal mediated by the
 CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where
 CC the administration of the medicament does not induce or only slightly
 CC induces secondary effects connected with inhibition of the insulin
 CC receptor. The antibody is useful for preparation of a medicament intended
 CC to inhibit the transformation of normal cells into cells with tumoral
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is
 CC useful for preparation of a medicament intended to inhibit the growth
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a
 CC medicament intended for prevention or for the treatment of cancer, where
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the
 CC preparation of a medicament intended for the prevention or for the
 CC treatment of psoriasis. (I) is useful in preparation of a medicament
 CC intended for the specific targeting of a biologically active compound to
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)
 CC is useful for in vitro diagnosis of illnesses induced by an
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor
 CC starting from a biological sample in which the abnormal presence, of IGF-
 CC IR and/or EGFR receptor is suspected, which involves contacting the
 CC biological sample with (I), which is optionally labeled. The present
 CC sequence is used in the exemplification of the invention.

XX SQ Sequence 117 AA;

Query Match 100.0%; Score 40; DB 9; Length 117;

Best Local Similarity 100.0%; Pred. No. 21;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6
 DB 31 GGYLWN 36
 |||||

RESULT 9

ID ADZ67073

XX ADZ67073 standard; protein; 117 AA.

XX AC ADZ67073;

XX 30-JUN-2005 (first entry)

XX Murine immunoglobulin heavy chain variable region 7C10 VH SEQ ID NO:69.

XX Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;
KW musculoskeletal disease; respiratory disease; lung tumor;
KW endocrine disease; gynecology and obstetrics; breast tumor;
KW endometroid carcinoma; gastrointestinal disease; colon tumor;
KW antipsoriatic; psoriasis; dermatological disease; immune disorder;
KW immunoglobulin; heavy chain variable region.
XX Mus musculus.
XX US2005084906-A1.
PW 21-APR-2005.
XX 16-DEC-2003; 2003US-00735916.
XX 18-JAN-2002; 2002FR-00000653.
PR 18-JAN-2002; 2002FR-00000654.
PR 07-MAY-2002; 2002FR-00005753.
PR 20-JAN-2003; 2003WO-FR000178.
PR 11-JUL-2003; 2003FR-00008538.
XX (GOET/) GOETSCH L.
PA (CORV/) CORVAIA N.
PA (LEGE/) Leger O.
PA (DUFL/) DUFLOS A.
PA (HAU/) HAEUW J.
PA (BECK/) BECK A.
XX Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;
PI WPI; 2005-321968/33.
XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)
PT antibody or its functional fragment, being capable of binding human IGF-
PT IR and specifically inhibiting tyrosine kinase activity of receptor,
PT useful for treating cancer.
XX Example 13; SEQ ID NO 69; 125pp; English.
XX The invention relates to a novel isolated anti-insulin-like growth factor
XX I receptor (IGF-IR) antibody (I) or its functional fragment, being
CC capable of binding to human IGF-IR and, if necessary, capable of
CC specifically inhibiting tyrosine kinase activity of the receptor,
CC comprising a light or heavy chain having at least one complementary
CC determining region (CDR) consisting of one of two fully defined 16 amino
CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in
CC the preparation of a medicament intended for the prevention or treatment
CC of an illness connected with an overexpression and/or an abnormal
CC activation of the IGF-IR and/or EGFR, and/or connected with a
CC hyperactivation of the transduction pathway of the signal mediated by the
CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where
CC the administration of the medicament does not induce or only slightly
CC induces secondary effects connected with inhibition of the insulin
CC receptor. The antibody is useful for preparation of a medicament intended
CC to inhibit the transformation of normal cells into cells with tumoral
CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-
CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is
CC useful for preparation of a medicament intended to inhibit the growth
CC and/or the proliferation of tumor cells, preferably IGF-dependent,
CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or
CC HER2/neu-dependent cells. (I) is useful in the preparation of a
CC medicament intended for prevention or for the treatment of cancer, where
CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,
CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the
CC preparation of a medicament intended for the prevention or for the
CC treatment of psoriasis. (I) is useful in preparation of a medicament
CC intended for the specific targeting of a biologically active compound to
CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)
CC is useful for in vitro diagnosis of illnesses induced by an
CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor
CC starting from a biological sample in which the abnormal presence, of IGF-

CC IR and/or EGFR receptor is suspected, which involves contacting the
CC biological sample with (I), which is optionally labeled. The present
CC sequence is used in the exemplification of the invention.
XX Sequence 117 AA;
SQ Query Match 100.0%; Score 40; DB 9; Length 117;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGYLWN 6
Db 31 GGYLWN 36
RESULT 10
ADZ67079
ID ADZ67079 standard; protein; 117 AA.
XX AC ADZ67079;
XX 30-JUN-2005 (first entry)
XX Human antibody 7C10 1 heavy chain variable region SEQ ID NO:75.
DE Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
XX neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;
KW musculoskeletal disease; respiratory disease; lung tumor;
KW endocrine disease; gynecology and obstetrics; breast tumor;
KW endometroid carcinoma; gastrointestinal disease; colon tumor;
KW antipsoriatic; psoriasis; dermatological disease; immune disorder;
KW heavy chain variable region.
XX Homo sapiens.
XX US2005084906-A1.
PW 21-APR-2005.
XX 16-DEC-2003; 2003US-00735916.
XX 18-JAN-2002; 2002FR-00000653.
PR 18-JAN-2002; 2002FR-00000654.
PR 07-MAY-2002; 2002FR-00005753.
PR 20-JAN-2003; 2003WO-FR000178.
PR 11-JUL-2003; 2003FR-00008538.
XX (GOET/) GOETSCH L.
PA (CORV/) CORVAIA N.
PA (LEGE/) Leger O.
PA (DUFL/) DUFLOS A.
PA (HAU/) HAEUW J.
PA (BECK/) BECK A.
XX Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;
PI WPI; 2005-321968/33.
XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)
PT antibody or its functional fragment, being capable of binding human IGF-
PT IR and specifically inhibiting tyrosine kinase activity of receptor,
PT useful for treating cancer.
XX Example 13; SEQ ID NO 75; 125pp; English.
XX The invention relates to a novel isolated anti-insulin-like growth factor
XX I receptor (IGF-IR) antibody (I) or its functional fragment, being
CC capable of binding to human IGF-IR and, if necessary, capable of
CC specifically inhibiting tyrosine kinase activity of the receptor,
CC comprising a light or heavy chain having at least one complementary
CC determining region (CDR) consisting of one of two fully defined 16 amino
CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in
CC the preparation of a medicament intended for the prevention or treatment
CC of an illness connected with an overexpression and/or an abnormal
CC activation of the IGF-IR and/or EGFR, and/or connected with a
CC hyperactivation of the transduction pathway of the signal mediated by the
CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where
CC the administration of the medicament does not induce or only slightly
CC induces secondary effects connected with inhibition of the insulin
CC receptor. The antibody is useful for preparation of a medicament intended
CC to inhibit the transformation of normal cells into cells with tumoral
CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-
CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is
CC useful for preparation of a medicament intended to inhibit the growth
CC and/or the proliferation of tumor cells, preferably IGF-dependent,
CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or
CC HER2/neu-dependent cells. (I) is useful in the preparation of a
CC medicament intended for prevention or for the treatment of cancer, where
CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,
CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the
CC preparation of a medicament intended for the prevention or for the
CC treatment of psoriasis. (I) is useful in preparation of a medicament
CC intended for the specific targeting of a biologically active compound to
CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)
CC is useful for in vitro diagnosis of illnesses induced by an
CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor
CC starting from a biological sample in which the abnormal presence, of IGF-

CC of an illness connected with an overexpression and/or an abnormal
 CC activation of the IGF-IR and/or EGFR, and/or connected with a
 CC hyperactivation of the transduction pathway of the signal mediated by the
 CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where
 CC the administration of the medicament does not induce or only slightly
 CC induces secondary effects connected with inhibition of the insulin
 CC receptor. The antibody is useful for preparation of a medicament intended
 CC to inhibit the transformation of normal cells into cells with tumoral
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is
 CC useful for preparation of a medicament intended to inhibit the growth
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a
 CC medicament intended for prevention or for the treatment of cancer, where
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the
 CC preparation of a medicament intended for the prevention or for the
 CC treatment of psoriasis. (I) is useful in preparation of a medicament
 CC intended for the specific targeting of a biologically active compound to
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)
 CC is useful for in vitro diagnosis of illnesses induced by an
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor
 CC starting from a biological sample in which the abnormal presence, of IGF-
 CC IR and/or EGFR receptor is suspected, which involves contacting the
 CC biological sample with (I), which is optionally labeled. The present
 CC sequence is used in the exemplification of the invention.

XX Sequence 117 AA;

Query Match 100.0%; Score 40; DB 9; Length 117;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6
 DB 31 GGYLWN 36
 |||||

RESULT 11

ADJ76886
 ID ADJ76886 standard; protein; 127 AA.

XX AC ADJ76886;

DT 06-MAY-2004 (first entry)

XX DE Anti-IGF-1R related protein #4.

XX cytotostatic; antipsoriatic; antibody;
 KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;
 KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;
 KW CDR.

XX MSB musculus.

XX W02003059951-A2.

XX 24-JUL-2003.

XX 20-JAN-2003; 2003WO-FR000178.

XX 18-JAN-2002; 2002FR-00000653.

XX 18-JAN-2002; 2002FR-00000654.

XX 07-MAY-2002; 2002FR-00005753.

XX (FABR) FABRE MEDICAMENT SA PIERRE.

XX Goetsch L, Corvala N, Leger O;

XX WPI; 2003-569653/53.

XX

PT New antibodies that bind to human insulin-like growth factor receptor,
 PT useful for treatment, prevention and diagnosis of cancers.
 XX Disclosure; SEQ ID NO 52; 164pp; French.

XX The invention relates to an isolated antibody (Ab), and its functional
 CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-
 CC IR) and optionally: (i) inhibit natural binding of insulin-like growth
 CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine
 CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or
 CC treat diseases associated with overexpression and/or abnormal activity of
 CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with
 CC hyperactivity of signal transduction pathways mediated by interaction of
 CC these receptors with their ligands. Especially they inhibit
 CC transformation of normal cells to tumor cells, inhibit growth and/or
 CC proliferation of tumor cells, so are useful against cancers of the
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a
 CC protein sequence used to generate the Ab of the invention.

XX Sequence 127 AA;

Query Match 100.0%; Score 40; DB 7; Length 127;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6
 DB 41 GGYLWN 46
 |||||

RESULT 12

ADZ67056
 ID ADZ67056 standard; protein; 127 AA.

XX AC ADZ67056;

XX 30-JUN-2005 (first entry)

XX Murine immunoglobulin heavy chain variable region 7C10 VH SEQ ID NO:52.

XX Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
 KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;
 KW musculoskeletal disease; respiratory disease; lung tumor;
 KW endocrine disease; gynecology and obstetrics; breast tumor;
 KW endometrial carcinoma; gastrointestinal disease; colon tumor;
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder;
 KW immunoglobulin; heavy chain variable region.

XX MSB musculus.

Key	Location/Qualifiers
Peptide	1..10 /note= "leader peptide"
Region	41..46 /note= "CDR1"
Region	61..76 /note= "CDR2"
Region	109..116 /note= "CDR3"

XX US2005084906-A1.

XX 21-APR-2005.

XX 16-DEC-2003; 2003US-00735916.

XX 18-JAN-2002; 2002FR-00000653.

XX 18-JAN-2002; 2002FR-00000654.

XX 07-MAY-2002; 2002FR-00005753.

XX 20-JAN-2003; 2003WO-FR000178.

XX 11-JUL-2003; 2003FR-00008538.

XX (GORT/) GOETSCH L.
 PA (CORV/) CORVAIA N.
 PA (LEGE/) LEGER O.
 PA (DUF/) DUFLOS A.
 PA (HAEU/) HAEUW J.
 PA (BECK/) BECK A.
 XX
 PI Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;
 XX
 XX WPI: 2005-321968/33.
 DR N-PSDB; AD267055.
 DR
 XX
 PT Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)
 PT antibody or its functional fragment, being capable of binding human IGF-
 PT IR and specifically inhibiting tyrosine kinase activity of receptor,
 PT useful for treating cancer.
 PT
 XX
 XX Example 8; SEQ ID NO 52; 125pp; English.
 PS
 PS The invention relates to a novel isolated anti-insulin-like growth factor
 CC I receptor (IGF-IR) antibody (I) or its functional fragment, being
 CC capable of binding to human IGF-IR and, if necessary, capable of
 CC specifically inhibiting tyrosine kinase activity of the receptor,
 CC comprising a light or heavy chain having at least one complementary
 CC determining region (CDR) consisting of one of two fully defined 16 amino
 CC acids (AD267006 and AD267014). An antibody of the invention is useful in
 CC the preparation of a medicament intended for the prevention or treatment
 CC of an illness connected with an overexpression and/or an abnormal
 CC activation of the IGF-IR and/or EGFR, and/or connected with a
 CC hyperactivation of the transduction pathway of the signal mediated by the
 CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where
 CC the administration of the medicament does not induce or only slightly
 CC induces secondary effects connected with inhibition of the insulin
 CC receptor. The antibody is useful for preparation of a medicament intended
 CC to inhibit the transformation of normal cells into cells with tumoral
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is
 CC useful for preparation of a medicament intended to inhibit the growth
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a
 CC medicament intended for prevention or for the treatment of cancer, where
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the
 CC preparation of a medicament intended for the prevention or for the
 CC treatment of psoriasis. (I) is useful in preparation of a medicament
 CC intended for the specific targeting of a biologically active compound to
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)
 CC is useful for in vitro diagnosis of illnesses induced by an
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor
 CC starting from a biological sample in which the abnormal presence, of IGF-
 CC IR and/or EGFR receptor is suspected, which involves contacting the
 CC biological sample with (I), which is optionally labeled. The present
 CC sequence is used in the exemplification of the invention.
 XX
 XX Sequence 127 AA;
 SQ
 Query Match 100.0%; Score 40; DB 9; Length 127;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGYLWN 6
 DB 41 GGYLWN 46
 |||||
 RESULT 13
 ID ADJ76911 standard; protein; 135 AA.
 XX
 AC ADJ76911;
 XX

DT 06-MAY-2004 (first entry)
 XX
 DE Anti-IGF-IR related protein #23.
 XX
 KW cytostatic; antipsoriatic; antibody;
 KW insulin-like growth factor-1 receptor; IGF-IR; tyrosine kinase activity;
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;
 KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;
 KW CDR.
 KW
 XX Homo sapiens.
 OS
 XX WO2003059951-A2.
 PN
 XX 24-JUL-2003.
 PD
 XX 20-JAN-2003; 2003WO-FR000178.
 PF
 XX 18-JAN-2002; 2002FR-00000653.
 PR 18-JAN-2002; 2002FR-00000654.
 PR 07-MAY-2002; 2002FR-00005753.
 PR
 XX (FABR) FABRE MEDICAMENT SA PIERRE.
 PA
 XX Goetsch L, Corvaia N, Leger O;
 PI
 PI WPI; 2003-569653/53.
 DR
 XX New antibodies that bind to human insulin-like growth factor receptor,
 PT useful for treatment, prevention and diagnosis of cancers.
 PT
 XX Disclosure; SEQ ID NO 77; 164pp; French.
 PS
 PS The invention relates to an isolated antibody (Ab), and its functional
 CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-
 CC IR) and optionally: (i) inhibit natural binding of insulin-like growth
 CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine
 CC kinase activity of IGF-IR. Ab and its fragments are used to prevent or
 CC treat diseases associated with overexpression and/or abnormal activity of
 CC IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with
 CC hyperactivity of signal transduction pathways mediated by interaction of
 CC these receptors with their ligands. Especially they inhibit
 CC transformation of normal cells to tumor cells, inhibit growth and/or
 CC proliferation of tumor cells, so are useful against cancers of the
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused
 CC by abnormal expression of IGF-IR and/or EGFR. This sequence represents a
 CC protein sequence used to generate the Ab of the invention.
 XX
 XX Sequence 135 AA;
 SQ
 Query Match 100.0%; Score 40; DB 7; Length 135;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGYLWN 6
 DB 49 GGYLWN 54
 |||||
 RESULT 14
 ID ADJ76919 standard; protein; 135 AA.
 XX
 AC ADJ76919;
 XX
 XX 06-MAY-2004 (first entry)
 DT
 XX Anti-IGF-IR related protein #27.
 DE
 XX cytostatic; antipsoriatic; antibody;
 KW insulin-like growth factor-1 receptor; IGF-IR; tyrosine kinase activity;
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;
 KW

KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;
 KW CDR.
 XX Homo sapiens.
 OS
 XX
 XX WO2003059951-A2.
 PN
 XX
 XX 24-JUL-2003.
 PD
 XX
 XX 20-JAN-2003; 2003WO-FR000178.
 PP
 XX
 XX 18-JAN-2002; 2002FR-00000653.
 PR
 XX 18-JAN-2002; 2002FR-00000654.
 PR
 XX 07-MAY-2002; 2002FR-00005753.
 XX
 XX (FABR) FABRE MEDICAMENT SA PIERRE.
 PA
 XX
 XX Goetsch L, Corvaia N, Leger O;
 PI
 XX
 XX WPI; 2003-569653/53.
 DR
 XX
 XX New antibodies that bind to human insulin-like growth factor receptor,
 PT useful for treatment, prevention and diagnosis of cancers.
 PT
 XX
 XX Disclosure; SEQ ID NO 85; 164pp; French.
 PS
 XX
 XX The invention relates to an isolated antibody (Ab), and its functional
 CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-
 CC 1R) and optionally: (i) inhibit natural binding of insulin-like growth
 CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine
 CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or
 CC treat diseases associated with overexpression and/or abnormal activity of
 CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with
 CC hyperactivity of signal transduction pathways mediated by interaction of
 CC these receptors with their ligands. Especially they inhibit
 CC transformation of normal cells to tumor cells, inhibit growth and/or
 CC proliferation of tumor cells, so are useful against cancers of the
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a
 CC protein sequence used to generate the Ab of the invention.
 XX
 SQ Sequence 135 AA;
 Query Match 100.0%; Score 40; DB 7; Length 135;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGYLWN 6
 Db |||||
 49 GGYLWN 54
 RESULT 15
 ADJ76915
 ID ADJ76915 standard; protein; 135 AA.
 XX
 XX ADJ76915;
 AC
 XX
 XX 06-MAY-2004 (first entry)
 DT
 XX
 XX Anti-IGF-1R related protein #25.
 DE
 XX
 KW cytostatic; antiproliferative; antibody;
 KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;
 KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;
 KW CDR.
 XX
 XX Homo sapiens.
 OS
 XX
 XX WO2003059951-A2.
 PN
 XX

PD 24-JUL-2003.
 XX
 XX 20-JAN-2003; 2003WO-FR000178.
 PF
 XX
 XX 18-JAN-2002; 2002FR-00000653.
 PR
 XX 18-JAN-2002; 2002FR-00000654.
 PR
 XX 07-MAY-2002; 2002FR-00005753.
 XX
 XX (FABR) FABRE MEDICAMENT SA PIERRE.
 PA
 XX
 XX Goetsch L, Corvaia N, Leger O;
 PI
 XX
 XX WPI; 2003-569653/53.
 DR
 XX
 XX New antibodies that bind to human insulin-like growth factor receptor,
 PT useful for treatment, prevention and diagnosis of cancers.
 PT
 XX
 XX Disclosure; SEQ ID NO 81; 164pp; French.
 PS
 XX
 XX The invention relates to an isolated antibody (Ab), and its functional
 CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-
 CC 1R) and optionally: (i) inhibit natural binding of insulin-like growth
 CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine
 CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or
 CC treat diseases associated with overexpression and/or abnormal activity of
 CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with
 CC hyperactivity of signal transduction pathways mediated by interaction of
 CC these receptors with their ligands. Especially they inhibit
 CC transformation of normal cells to tumor cells, inhibit growth and/or
 CC proliferation of tumor cells, so are useful against cancers of the
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a
 CC protein sequence used to generate the Ab of the invention.
 XX
 SQ Sequence 135 AA;
 Query Match 100.0%; Score 40; DB 7; Length 135;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGYLWN 6
 Db |||||
 49 GGYLWN 54
 Search completed: December 30, 2005, 13:24:00
 Job time : 55.3226 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:11:41 ; Search time 8.51613 Seconds
(without alignments)
67.789 Million cell updates/sec

Title: US-10-735-916A-8

Perfect score: 40

Sequence: 1 GGYLWN 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	90.0	277	2 D42400	membrane protein M
2	36	90.0	479	2 T44446	D-rhamnose synthase
3	36	90.0	479	2 F82964	phosphomannose iso
4	36	90.0	530	2 S01430	chlorophyll a/b-bi
5	35	87.5	70	2 AF2508	transposase asl724
6	35	87.5	258	2 AD0615	probable membrane
7	35	87.5	259	2 C90754	hypothetical prote
8	35	87.5	259	2 G64831	probable membrane
9	35	87.5	259	2 A85618	hypothetical prote
10	35	87.5	277	2 D98085	hypothetical prote
11	35	87.5	278	2 E95221	sugar ABC transpor
12	35	87.5	440	2 F69322	hypothetical prote
13	35	87.5	481	2 A38598	mannose-6-phosphat
14	35	87.5	481	2 B83201	phosphomannose iso
15	35	87.5	1001	2 AG1979	hypothetical prote
16	34	85.0	107	2 H84839	late embryogenesis
17	34	85.0	155	2 S78774	perlucin - Halioti
18	34	85.0	159	2 AB2051	hypothetical prote
19	34	85.0	167	2 G71548	hypothetical prote
20	34	85.0	274	2 B95912	hypothetical prote
21	34	85.0	286	2 T22354	hypothetical prote
22	34	85.0	304	2 T05587	hypothetical prote
23	34	85.0	318	2 A11945	hypothetical prote
24	34	85.0	323	2 F69454	signal-transducing
25	34	85.0	323	2 T26536	hypothetical prote
26	34	85.0	325	2 AD3140	hypothetical prote
27	34	85.0	325	2 H98147	hypothetical prote
28	34	85.0	330	2 B95900	probable ABC trans
29	34	85.0	356	2 C97265	mannose-1-phosphat

30 34 85.0 390 2 D81289 probable aminotran
31 34 85.0 394 2 AB1870 hypothetical prote
32 34 85.0 395 2 S50986 MAF1 protein - yea
33 34 85.0 406 2 T50894 hydroxynurosporen
34 34 85.0 436 2 H87697 mannose-1-phosphat
35 34 85.0 448 1 H69386 mannose-6-phosphat
36 34 85.0 476 2 AH2968 mannose-1-phosphat
37 34 85.0 476 2 C98314 mannose-1-phosphat
38 34 85.0 494 2 S30187 mannose-6-phosphat
39 34 85.0 667 2 A97176 ba-type ubiquinol
40 34 85.0 667 2 AG2593 cytochrome O ubiq
41 34 85.0 667 2 JC7771 hypoxia inducible
42 34 85.0 705 2 A41322 N-acetylmuramoyl-L
43 34 85.0 736 2 C69451 cationic amino aci
44 34 85.0 798 2 JN0878 100K protein - fow
45 34 85.0 1482 2 T34010 hypothetical prote

ALIGNMENTS

RESULT 1

D42400

membrane protein MemG - Streptococcus mutans

C;Species: Streptococcus mutans

C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C;Accession: D42400

R;Russell, R.R.; Aducci-Opoku, J.; Sutcliffe, I.C.; Tao, L.; Ferretti, J.J.

J. Biol. Chem. 267, 4631-4637, 1992

A;Title: A binding protein-dependent transport system in Streptococcus mutans responsi

A;Reference number: A42400; MUID:92165821; PMID:1537846

A;Accession: D42400

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-277 <RUS>

A;Cross-references: UNIPROT:Q00751; UNIPARC:UPI000012F61F; GB:M77351; GB:M19349; GB:M30

A;Note: sequence extracted from NCBI backbone (NCBIN:83895, NCBI:P:83891)

C;Superfamily: maltose transport protein malG

C;Keywords: transmembrane protein

Query Match 90.0%; Score 36; DB 2; Length 277;
Best Local Similarity 83.3%; Pred. No. 18;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGYLWN 6
Db 66 GGYFWN 71

RESULT 2

T44446

D-rhamnose synthase protein wbpW [imported] - Pseudomonas aeruginosa

C;Species: Pseudomonas aeruginosa

C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004

C;Accession: T44446

R;Rocchetta, H.L.; Pacan, J.C.; Lam, J.S.

Mol. Microbiol. 29, 1419-1434, 1998

A;Title: Synthesis of the A-band polysaccharide sugar D-rhamnose requires Rmd and WbpW;

A;Reference number: Z22772; MUID:98453140; PMID:9781879

A;Accession: T44446

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-479 <ROC>

A;Cross-references: UNIPROT:O87266; UNIPARC:UPI00000BBB2C; EMBL:AF0009956; NID:G3249548;

A;Experimental source: strain PAOI

C;Genetics:

A;Gene: wbpW

C;Superfamily: Helicobacter mannose-6-phosphate isomerase

Query Match 90.0%; Score 36; DB 2; Length 479;
Best Local Similarity 83.3%; Pred. No. 32;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

QY      1 GGYLWN 6
      ||:||||
Db      193 GGFLWN 198

RESULT 3
F82964
phosphomannose isomerase/GDP-mannose WbpW PA5452 [imported] - Pseudomonas aeruginosa (st
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: F82964
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warriner, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A>Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: F82964
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-479 <STO>
A:Cross-references: UNIPROT:Q9HTB7; UNIPARC:UPI00000C6012; GB:AE004958; GB:AE004091; NID
A:Experimental source: strain PA01
C:Genetics:
A:Gene: wbpW; PA5452
C:Superfamily: Helicobacter mannose-6-phosphate isomerase

Query Match      90.0%; Score 36; DB 2; Length 479;
Best Local Similarity 83.3%; Pred. No. 32;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGYLWN 6
      ||:||||
Db      193 GGFLWN 198

RESULT 4
S01430
chlorophyll a/b-binding protein LH38 precursor - Euglena gracilis (fragment)
N;Alternate names: light-harvesting complex I apoprotein
C:Species: Euglena gracilis
C>Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C:Accession: S01430
R:Houlne, G.; Schantz, R.
Mol. Gen. Genet. 213, 479-486, 1988
A>Title: Characterization of cDNA sequences for LHCI apoproteins in Euglena gracilis: Th
A:Reference number: S01429; MUID:89039737; PMID:3141775
A:Accession: S01430
A:Molecule type: mRNA
A:Residues: 1-530 <HOU>
A:Cross-references: UNIPROT:P08976; UNIPARC:UPI000012E61A; EMBL:X12861; NID:g18421; PIDN
F;1-178/Product: chlorophyll a/b-binding protein LH38a (fragment) #status predicted <WAT
F;179-360/Product: chlorophyll a/b-binding protein LH38b #status predicted <WAT>
F;361-530/Product: chlorophyll a/b-binding protein LH38c (fragment) #status predicted <M

Query Match      90.0%; Score 36; DB 2; Length 530;
Best Local Similarity 83.3%; Pred. No. 35;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGYLWN 6
      ||:||||
Db      468 GGFLWN 473

RESULT 5
AF2508
transposase asl7246 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120alpha
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AF2508
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi

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Nakazaki, N.; Shimp, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, T.
DNA Res. 8, 205-213, 2001
A>Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AF2508
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-70 <KUR>
A:Cross-references: UNIPROT:Q8YKP7; UNIPARC:UPI00000CEFA4; GB:BA000020; PIDN:BA078330.1;
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: asl7246
A:Genome: plasmid

Query Match      87.5%; Score 35; DB 2; Length 70;
Best Local Similarity 83.3%; Pred. No. 6; 7;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGYLWN 6
      ||:||||
Db      37 GGHLWN 42

RESULT 6
AD0615
probable membrane protein STY092 [imported] - Salmonella enterica subsp. enterica serov
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 12-Jul-2004
C:Accession: AD0615
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Conner, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
.; S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Barry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A>Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AD0615
A:Molecule type: DNA
A:Residues: 1-258 <PAR>
A:Cross-references: UNIPARC:UPI000005A069; GB:AL513382; PIDN:CAD05390.1; PID:g16502152;
C:Genetics:
A:Gene: STY092
C:Superfamily: conserved hypothetical protein H11262

Query Match      87.5%; Score 35; DB 2; Length 258;
Best Local Similarity 83.3%; Pred. No. 26;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGYLWN 6
      ||:||||
Db      87 GGYTWN 92

RESULT 7
C90754
hypothetical protein ECs1003 [imported] - Escherichia coli (strain O157:H7, substrain R
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 12-Jul-2004
C:Accession: C90754
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A>Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: C90754
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-259 <HAY>
A:Cross-references: UNIPROT:P36565; UNIPARC:UPI000013A5A1; GB:BA000007; PIDN:BA034426.1
A:Experimental source: strain O157:H7, substrain RMD 050952
C:Genetics:

```

A;Gene: ECs1003

C;Superfamily: conserved hypothetical protein HI1262

Query Match 87.5%; Score 35; DB 2; Length 259;
Best Local Similarity 83.3%; Pred. No. 26;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGYLWN 6
||| ||
Db 87 GGYTWN 92

RESULT 8

G64831

probable membrane protein ycbC - Escherichia coli (strain K-12)

C;Species: Escherichia coli

C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 12-Jul-2004

C;Accession: G64831

A.; Røge, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of Escherichia coli K-12.

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Accession: G64831

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-259 <BLAT>

A;Cross-references: UNIPROT:P36565; UNIPARC:UPI000013A5A1; GB:AE000194; GB:U000096; MID:9

A;Experimental source: strain K-12, substrain MG1655

C;Genetics:

A;Gene: ycbC

C;Superfamily: conserved hypothetical protein HI1262

C;Keywords: transmembrane protein

F;13-29/Domain: transmembrane #status predicted <TM1>

F;39-55/Domain: transmembrane #status predicted <TM2>

Query Match 87.5%; Score 35; DB 2; Length 259;

Best Local Similarity 83.3%; Pred. No. 26;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGYLWN 6
||| ||
Db 87 GGYTWN 92

RESULT 9

A85618

hypothetical protein ycbC [imported] - Escherichia coli (strain O157:H7, substrain EDL93

C;Species: Escherichia coli

C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 12-Jul-2004

C;Accession: A85618

R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew

iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,

Nature 409, 529-533, 2001

A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Accession: A85618

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-259 <STO>

A;Cross-references: UNIPROT:P36565; UNIPARC:UPI000013A5A1; GB:AE005174; NID:g12514089; H

A;Experimental source: strain O157:H7, substrain EDL933

C;Genetics:

A;Gene: ycbC

C;Superfamily: conserved hypothetical protein HI1262

Query Match 87.5%; Score 35; DB 2; Length 259;

Best Local Similarity 83.3%; Pred. No. 26;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGYLWN 6
||| ||
Db 87 GGYTWN 92

RESULT 10

D98085

hypothetical protein msmG [imported] - Streptococcus pneumoniae (strain R6)

C;Species: Streptococcus pneumoniae

C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004

C;Accession: D98085

R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Bursgett, S.; DeHoff, B.S.;

e, P.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, S.J.; Lu, J.; Matsushima, P.; McAhren, S.;

Y, P.; Sun, P.M.; Winkler, M.E.

J. Bacteriol. 183, 5709-5717, 2001

A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R

A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.

A;Reference number: A97872; MUID:21429245; PMID:11544234

A;Accession: D98085

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-277 <KUR>

A;Cross-references: UNIPROT:Q8DNI0; UNIPARC:UPI00000E36DD; GB:AE007317; PIDN:AAL00513.1

C;Genetics:

A;Gene: msmG

C;Superfamily: maltose transport protein malG

Query Match 87.5%; Score 35; DB 2; Length 277;

Best Local Similarity 83.3%; Pred. No. 28;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGYLWN 6
||| ||
Db 66 GGYTWN 71

RESULT 11

E95221

sugar ABC transporter, permease protein SP1895 [imported] - Streptococcus pneumoniae (s

C;Species: Streptococcus pneumoniae

C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004

C;Accession: E95221

R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Hei

on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,

son, T.; Hickey, E.K.; Holt, I.E.

Science 293, 498-506, 2001

A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison

A;Title: Complete Genome Sequence of a Virulent isolate of Streptococcus pneumoniae.

A;Reference number: A95000; MUID:21357209; PMID:11463916

A;Accession: E95221

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-278 <KUR>

A;Cross-references: UNIPROT:Q97NW4; UNIPARC:UPI00000C9CFA; GB:AE005672; PIDN:AAK75966.1

A;Experimental source: strain TIGR4

C;Genetics:

A;Gene: SP1895

C;Superfamily: maltose transport protein malG

Query Match 87.5%; Score 35; DB 2; Length 278;

Best Local Similarity 83.3%; Pred. No. 28;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGYLWN 6
||| ||
Db 67 GGYTWN 72

RESULT 12

F69322

hypothetical protein AF0582 - Archaeoglobus fulgidus

C;Species: Archaeoglobus fulgidus

C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C;Accession: F69322

R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodso

.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F

Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: F69322

A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-440 <KLE>
A;Cross-references: UNIPROT:O29673; UNIPARC:UPI0000057054; GB:AE001064; GB:AE000782; NID

Query Match 87.5%; Score 35; DB 2; Length 440;
Best Local Similarity 83.3%; Pred. No. 49;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGYLWN 6
||| ||
DB 218 GGYWN 223

RESULT 13
A38598
mannose-6-phosphate isomerase (EC 5.3.1.8) / mannose-1-phosphate guanylyltransferase (GD
N;Alternate names: phosphomannose isomerase
C;Species: Pseudomonas aeruginosa
C;Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 09-Jul-2004
C;Accession: A38598; A25638
R;Shinabarger, D.; Berry, A.; May, T.B.; Rothmel, R.; Fialho, A.; Chakrabarty, A.M.
J. Biol. Chem. 266, 2080-2088, 1991
A;Title: Purification and characterization of phosphomannose isomerase-guanosine diphosph
inosa.

A;Reference number: A38598; MUID:91115815; PMID:1846611
A;Accession: A38598
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-481 <SHI>
A;Cross-references: UNIPROT:P07874; UNIPARC:UPI000016PCF0; GB:M14037; NID:g151503; PIDN:
R;Darling, A.; Frantz, B.; Vanags, R.I.; Chakrabarty, A.M.

Gene 42, 293-302, 1986
A;Title: Nucleotide sequence analysis of the phosphomannose isomerase gene (pmi) of Pseud
A;Reference number: A25638; MUID:86276004; PMID:3089876
A;Accession: A25638
A;Molecule type: DNA
A;Residues: 1-25, 'FL', 28-39, 'L', 41-57, 'A', 59-106, 108-114, 'I', 116-358, 'EV', 361-478, 'A', 48
A;Cross-references: UNIPARC:UPI0000176197
A;Note: the nucleotide sequence given predicts 26-Leu, 27-Val, 115-Leu, 359-Asp, and 360
C;Superfamily: Helicobacter mannose-6-phosphate isomerase
C;Keywords: intramolecular oxidoreductase; isomerase; nucleotidyltransferase

Query Match 87.5%; Score 35; DB 2; Length 481;
Best Local Similarity 83.3%; Pred. No. 49;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGYLWN 6
||| ||
DB 188 GGYWN 193

RESULT 14
B83201
phosphomannose isomerase / guanosine 5'-diphospho-D-mannose pyrophosphorylase PA3551 [im
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: B83201
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: B83201
A;Status: preliminary

A;Molecule type: DNA
A;Residues: 1-481 <STO>
A;Cross-references: UNIPROT:P07874; UNIPARC:UPI0000125847; GB:AE004776; GB:AE004091; NID
A;Experimental source: strain PA01

C;Genetics:
A;Gene: algA; PA3551
C;Superfamily: Helicobacter mannose-6-phosphate isomerase

Query Match 87.5%; Score 35; DB 2; Length 481;
Best Local Similarity 83.3%; Pred. No. 49;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGYLWN 6
||| ||
DB 188 GGYWN 193

RESULT 15
AG1979
hypothetical protein alr1386 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AG1979
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AG1979
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-1001 <KUR>
A;Cross-references: UNIPROT:Q8YX32; UNIPARC:UPI000000CE0A1; GB:BA000019; PIDN:BAE73343.1.
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr1386

Query Match 87.5%; Score 35; DB 2; Length 1001;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6
||| ||
DB 667 GGYLWD 672

Search completed: December 30, 2005, 13:34:55
Job time : 9.51613 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:11:26 ; Search time 54 Seconds
(without alignments)
78.392 Million cell updates/sec

Title: US-10-735-916A-8
Perfect score: 40
Sequence: 1 GGYLWN 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	100.0	467	Q9EXY5	Escherichia coli
2	40	100.0	492	Q31278	Acetobacter
3	40	100.0	492	Q8RR87	Acetobacter
4	40	100.0	560	Q55V27	Cryptococcus
5	40	100.0	560	Q55K79	Cryptococcus
6	37	92.5	368	Q4PIK9	Ustilago ma
7	37	92.5	425	Q6EVV9	Yersinia ps
8	37	92.5	1097	Q9VA99	Drosophila
9	37	92.5	1109	Q8IM19	Drosophila
10	37	92.5	1199	Q6NP40	Drosophila
11	37	92.5	1279	Q522J8	Magnaporthe
12	36	90.0	277	Q522J8	Magnaporthe
13	36	90.0	281	Q4K774	Pseudomonas
14	36	90.0	370	Q4IPC3	Gibberella
15	36	90.0	430	Q6WN42	Pseudomonas
16	36	90.0	479	Q8T266	Pseudomonas
17	36	90.0	479	Q9HTB7	Pseudomonas
18	36	90.0	483	ALGA_PSEFL	Alga
19	36	90.0	483	Q4KH79	Pseudomonas
20	36	90.0	485	ALGA_PSEPK	Alga
21	36	90.0	530	LH18_EUGGR	Euglena gra
22	36	90.0	798	Q4UPI7	Xanthomonas
23	36	90.0	798	Q8P3J4	Xanthomonas
24	36	90.0	801	Q5H632	Xanthomonas
25	36	90.0	814	Q52DW1	Magnaporthe
26	35	87.5	70	Q8YKP7	Anabaena sp
27	35	87.5	83	Q7ULK5	Mycobacteri
28	35	87.5	83	Q8VRH3	Mycobacteri
29	35	87.5	86	Q5BD31	Aspergillus
30	35	87.5	87	Q5WGf8	Bacillus cl
31	35	87.5	111	Q70IV0	Clostridium

32	35	87.5	111	2	Q70IV1	CLODI
33	35	87.5	121	2	Q5FN84	GLUOX
34	35	87.5	147	2	Q4IVK8	AZOVI
35	35	87.5	148	2	Q4KAB9	PSEPS
36	35	87.5	148	2	Q880D2	PSESM
37	35	87.5	209	2	Q8A573	BACTN
38	35	87.5	221	2	Q5YMI3	NOCPA
39	35	87.5	223	2	Q7NWT8	CHRCVO
40	35	87.5	258	2	Q57R07	SALCH
41	35	87.5	258	2	Q5PGF7	SALPA
42	35	87.5	258	2	Q8Z7Z8	SALTI
43	35	87.5	258	2	Q8ZQB8	SALTY
44	35	87.5	259	1	YCBC	ECOLI
45	35	87.5	259	2	Q8FJA7	ECOL6

ALIGNMENTS

RESULT 1
Q9EXY5_ECOLI
ID Q9EXY5_ECOLI PRELIMINARY; PRT; 467 AA.
AC Q9EXY5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE GDP-mannose pyrophosphorylase.
GN Name=manC;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21135136; PubMed=11238967;
RA Jensen S.O., Reeves P.R.;
RT "Molecular evolution of the GDP-mannose pathway genes (manB and manC) in Salmonella enterica."
RL Microbiology 147:599-610(2001).
DR EMBL; AY012189; AAC41753.1; -, Genomic_DNA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0008928; F:mannose-1-phosphate guanylyltransferase (GD. .; IEA.
DR GO; GO:0016779; F:nucleotidyltransferase activity; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
DR GO; GO:0009103; P:lipopolysaccharide biosynthesis; IEA.
DR GO; GO:0005976; P:polysaccharide metabolism; IEA.
DR InterPro; IPR007113; Cupin region.
DR InterPro; IPR006375; GMP PMI.
DR InterPro; IPR001538; Man6P isomerase.
DR Pfam; PF01050; MannoseP_Isomerase; 1.
DR Pfam; PF00483; NTP_transferase; 1.
DR ProDom; PD002664; Man6P isomerase; 1.
DR TIGRFAMs; TIGR01479; GMP PMI; 1.
SQ SEQUENCE 467 AA; 52570 MW; 41359274844CDAD3 CRC64;

Query Match 100.0%; Score 40; DB 2; Length 467;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGYLWN 6
Db 187 GGYLWN 192

RESULT 2
Q31278_ACXY
ID Q31278_ACXY PRELIMINARY; PRT; 492 AA.
AC Q31278;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Mannose-6-phosphate isomerase (EC 5.3.1.8).
GN Name:aceF;
OS Acetobacter xylinus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Acetobacteraceae; Gluconacetobacter.
OX NCBI_TaxID=28448;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C1;
RX MEDLINE=97457201; PubMed=9311139; DOI=10.1016/S0378-1097(97)00358-3;
RA Griffin A.M., Poelwick E., Morris V.J., Gasson M.J.;
RT "Cloning of the aceF gene encoding the phosphomannose isomerase and
GDP-mannose pyrophosphorylase activities involved in acetan
biosynthesis in Acetobacter xylinum.";
RT FEMS Microbiol. Lett. 154:389-396(1997).
RL EMBL, Y11554; CAA72316.1; -; Genomic DNA.
DR GO; GO:0016853; F:isomerase activity; IEA.
DR GO; GO:0008928; F:mannose-1-phosphate isomerase activity; IEA.
DR GO; GO:0004476; F:mannose-6-phosphate isomerase activity; IEA.
DR GO; GO:0016779; F:nucleotidyltransferase activity; IEA.
DR GO; GO:0009058; P:lipopolysaccharide biosynthesis; IEA.
DR GO; GO:0009103; P:lipopolysaccharide metabolism; IEA.
DR GO; GO:0005976; P:polysaccharide metabolism; IEA.
DR InterPro; IPR007113; Cupin_region.
DR InterPro; IPR006375; GMP_PMI.
DR InterPro; IPR001538; Man6P_isomerII.
DR InterPro; IPR005835; NTP_transferase.
DR Pfam; PF01050; Mannosep_isomer; 1.
DR Pfam; PF00483; NTP_transferase; 1.
DR ProDom; PD002664; Man6P_isomerII; 1.
DR TIGRFAMs; TIGR01479; GMP_PMI; 1.
KW Isomerase.
SQ SEQUENCE 492 AA; 54811 MW; 9FBA45F1F0257A5F CRC64;
Query Match 100.0%; Score 40; DB 2; Length 492;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGYLWN 6
|||||
DB 211 GGYLWN 216
RESULT 3
Q8RR87 ACXY PRELIMINARY; PRT; 492 AA.
AC Q8RR87;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Mannose-6-phosphate isomerase.
GN Name:aceF;
OS Acetobacter xylinus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Acetobacteraceae; Gluconacetobacter.
OX NCBI_TaxID=28448;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BPR2001;
RX MEDLINE=22145717; PubMed=12150936; DOI=10.1016/S0006-291X(02)00663-0;
RA Ishida T., Sugano Y., Shoda M.;
RT "Novel glycosyltransferase genes involved in the acetan biosynthesis
of Acetobacter xylinum.";
RL Biochem. Biophys. Res. Commun. 295:230-235(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BPR2001;
RX MEDLINE=2240619; PubMed=12353627; DOI=10.1271/bbb.66.1677;
RA Ishida T., Sugano Y., Nakai T., Shoda M.;
RT "Effects of acetan on production of bacterial cellulose by Acetobacter
xylinum.";
RL Biosci. Biotechnol. Biochem. 66:1677-1681(2002).
DR EMBL; AB059427; BAB88842.1; -; Genomic DNA.

DR GO; GO:0016853; F:isomerase activity; IEA.
DR GO; GO:0008928; F:mannose-1-phosphate guanylyltransferase (GD. . .; IEA.
DR GO; GO:0016779; F:nucleotidyltransferase activity; IEA.
DR GO; GO:0009058; P:lipopolysaccharide biosynthesis; IEA.
DR GO; GO:0009103; P:lipopolysaccharide metabolism; IEA.
DR GO; GO:0005976; P:polysaccharide metabolism; IEA.
DR InterPro; IPR007113; Cupin_region.
DR InterPro; IPR006375; GMP_PMI.
DR InterPro; IPR001538; Man6P_isomerII.
DR InterPro; IPR005835; NTP_transferase.
DR Pfam; PF01050; Mannosep_isomer; 1.
DR Pfam; PF00483; NTP_transferase; 1.
DR ProDom; PD002664; Man6P_isomerII; 1.
DR TIGRFAMs; TIGR01479; GMP_PMI; 1.
KW Isomerase.
SQ SEQUENCE 492 AA; 54684 MW; 3ACCC80CBEF4317C CRC64;
Query Match 100.0%; Score 40; DB 2; Length 492;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGYLWN 6
|||||
DB 211 GGYLWN 216
RESULT 4
Q55VE7 CRYNE PRELIMINARY; PRT; 560 AA.
AC Q55VE7;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=CNB5380;
OS Cryptococcus neoformans var. neoformans B-3501A.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX NCBI_TaxID=283643;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B-3501A;
RA Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,
Wickes B.L., Fu J., Davis R.W.;
RT "Cryptococcus neoformans serotype D sequencing.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL; AA00100015; EAL21837.1; -; Genomic DNA.
DR EMBL; AA00100015; EAL21837.1; -; Genomic DNA.
KW Hypothetical protein.
SQ SEQUENCE 560 AA; 62193 MW; 9BD25DC23AE3B652 CRC64;
Query Match 100.0%; Score 40; DB 2; Length 560;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGYLWN 6
|||||
DB 498 GGYLWN 503
RESULT 5
Q5KKT9 CRYNE PRELIMINARY; PRT; 560 AA.
AC Q5KKT9;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Eukaryotic translation initiation factor 3 62 kDa subunit,
putative.
GN ORFNames=CNB01870;
OS Cryptococcus neoformans var. neoformans JEC21.

OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
 OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
 OX NCBI_TaxID=214684;
 [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=JEC21;
 RA Loftus B., Amedeo P., Roncaglia P., Vamathevan J., Utterback T.,
 RA Van Aken S., Fraser C.;
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=JEC21;
 RX PubMed=15653466; DOI=10.1126/science.1103773;
 RA Loftus B.J., Fung E., Roncaglia P., Rowley D., Amedeo P., Bruno D.,
 RA Vamathevan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E.,
 RA Boedet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J.,
 RA D'Souza C.A., Fox D.S., Grinberg V., Fu J., Fukushima M., Haas B.J.,
 RA Huang J.C., Janbon G., Jones S.J.M., Koo H.L., Krzywinski M.I.,
 RA Kwon-Chung K.J., Lengeler K.B., Maiti R., Marra M.A., Marra R.E.,
 RA Mathewson C.A., Mitchell T.G., Pertea R., Riggs F.R., Salzberg S.L.,
 RA Schein J.E., Shvartsbeyn A., Shin H., Shumway M., Specht C.A.,
 RA Suh B.B., Tenney A., Utterback T.R., Wickes B.L., Wortman J.R.,
 RA Wye N.H., Kronstad J.W., Lodge J.K., Heitman J., Davis R.W.,
 RA Fraser C.M., Hyman R.W.;
 RT "The genome of the basidiomycetous yeast and human pathogen
 RT Cryptococcus neoformans";
 RL Science 307:1321-1324(2005).
 DR EMBL; AE017343; AAM42248.1; -; Genomic DNA.
 DR GO; GO:0003743; P:translation initiation factor activity; IEA.
 DR GO; GO:0006446; P:regulation of translational initiation; IEA.
 DR InterPro; IPR007316; EIF3_gamma.
 DR Pfam; PF04189; Gcd10p; 1.
 KW Complete proteome; Initiation factor.
 SQ SEQUENCE 560 AA; 62193 MW; 9BD25DC23AE3B652 CRC64;

Query Match 100.0%; Score 40; DB 2; Length 560;
 Best Local Similarity 100.0%; Pred. No. 74;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6
 Db 498 GGYLWN 503
 |||||

RESULT 6
 Q4PIK9_USTMA PRELIMINARY; PRT; 368 AA.
 AC Q4PIK9;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=UM00054.1;
 OS Ustilago maydis 521.
 OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
 OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
 OX NCBI_TaxID=237631;
 [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=521;
 RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
 RA Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
 RA Arachchi H., Armbruster J., Bachantsang P., Baldwin J., Barry A.,
 RA Bayul T., Blitshteyn B., Bloom T., Blye J., Boguslavskiy L.,
 RA Borowsky M., Boukhgalter B., Brunache A., Butler J., Calixte N.,
 RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
 RA Collamore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
 RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
 RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
 RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
 RA Fitzgerald M., Foley K., Gage D., Galagan J., Garin G., Gnerre S.,
 RA Gnirke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
 RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,

RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
 RA Jaffe D., Jones C., Kamal M., Katat A., Kanvasselis M., Karlsson E.,
 RA Kells C., Kieu A., Kisner P., Kodira C., Kulbokas E., Labutti K.,
 RA Lana D., Landers T., Leger J., Levine S., Lewis D., Lewis T., O.,
 RA Lindblad-toh K., Liu X., Lokitsang T., Lokitsang Y., Lucien O.,
 RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
 RA Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,
 RA McCarthy M., McDonough S., Mcghee T., Meldrim J., Meneus L.,
 RA Mesirov J., Mihalev A., Mihova T., Mikkelson T., Mlenga V., Moru K.,
 RA Mozes J., Mulrain L., Munson G., Naylor J., Neves C., Nguyen C.,
 RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
 RA Norbu N., O'donnell P., Okoawo O., O'leary S., Omotosho B.,
 RA O'neil K., Osman S., Parker S., Perrin D., Phunkhang P., Piquani B.,
 RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
 RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
 RA Rutman M., Schubach R., Seaman C., Settipalli S., Sharpe T.,
 RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,
 RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
 RA Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,
 RA Tenzing P., Tesfaye S., Theodore J., Thoultsang Y., Topham K.,
 RA Towey S., Teamla T., Tsomo N., Vallee D., Vassiliev H.,
 RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
 RA Wangdi T., Whitaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
 RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
 RA Zimmer A., Zody M., Lander E.;
 RT "The genome sequence of Ustilago maydis";
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AACP01000002; EAK81439.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 368 AA; 40022 MW; 2B992BDCFA44362 CRC64;

Query Match 92.5%; Score 37; DB 2; Length 368;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6
 Db 177 GGYLWN 182
 |||||

RESULT 7
 Q6EVV9_YERPS PRELIMINARY; PRT; 425 AA.
 ID Q6EVV9_YERPS PRELIMINARY;
 AC Q6EVV9;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Secondary type IV prepilin.
 GN Name=piLV;
 OS Yersinia pseudotuberculosis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 OX NCBI_TaxID=633;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=32777;
 RX MEDLINE=22267116; PubMed=12379698;
 RX DOI=10.1128/IAI.70.11.6196-6205.2002;
 RA Marceau M.,
 RA "Yersinia pseudotuberculosis harbors a type IV pilus gene cluster that
 RT contributes to pathogenicity";
 RN Infect. Immun. 70:6196-6205(2002).
 [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=32777;
 RA Collin F., Billault A., Mullet C., Simonet M., Marceau M.;
 RT "YAPI, a new Yersinia pseudotuberculosis pathogenicity island";
 RL Infect. Immun. 72:4784-4790(2004).
 DR EMBL; AJ627388; CAP28494.1; -; Genomic_DNA.
 DR InterPro; IPR007001; Shufflon_N.

DR Pfam: PF04917; Shufflon N; 1.
SQ SEQUENCE 425 AA; 45880 MW; 74021D2C2807F57B CRC64;

Query Match 92.5%; Score 37; DB 2; Length 425;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6
|||:|
Db 148 GGYVWN 153

RESULT 8
Q9VA99 DROME
ID Q9VA99_DROME PRELIMINARY; PRT; 1097 AA.
AC Q9VA99;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CG31028-PA, isoform A.
GN Names=CG31028; ORFNames=CG31028;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananidis P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.B., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Frannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Fertaz C., Ferrera S., Fleischmann W.,
RA Foelel K., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.C., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler P., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,

RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
RT a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RX Berkeley *Drosophila* Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacle J., Park S., Svirskas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE.
RX FlyBase;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; A8003772; AAF57015.4; -; Genomic_DNA.
DR HSSP; P07505; ISR.D.
DR Ensembl; CG31028; *Drosophila melanogaster*.
DR FlyBase; Fggn0051028; CG31028.
DR FlyBase; Fggn0051030; CG31030.
DR GO; GO:0014209; F-antioxidant activity; IEA.
DR GO; GO:0004785; F-copper, zinc superoxide dismutase activity; IEA.
DR GO; GO:0046872; F-metal ion binding; IEA.
DR GO; GO:0016491; F-oxidoreductase activity; IEA.
DR GO; GO:0006801; P-superoxide metabolism; IEA.
DR InterPro; IPR001424; SOD_CU_ZN.
DR Pfam; PF00080; Sod_Cu; 1.
DR SEQUENCE 1097 AA; 123028 MW; 66A6B5BD00E9C667 CRC64;
SQ

Query Match 92.5%; Score 37; DB 2; Length 1097;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6
|||:|
Db 917 GGYVWN 922

RESULT 9
Q8IM19 DROME
ID Q8IM19_DROME PRELIMINARY; PRT; 1109 AA.
AC Q8IM19;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CG31028-PB, isoform B.
DE Names=CG31028; ORFNames=CG31028;
GN *Drosophila melanogaster* (Fruit fly).
OS

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
RA Ballev R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieria S., Fleischmann W.,
RA Foeller C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasako P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mikhlov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclele J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler P., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasearman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*."
RT Science 287:2185-2195(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celnikier S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan R., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Paclele J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskaas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
RT melanogaster euchromatic genome sequence."
RT Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskaas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celnikier S.E.;
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
RT a genomics perspective."
RT Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celnikier S.E., de Grey A.D.N.J., Drysdale R.A.,

RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
RT systematic review."
RT Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RX Berkeley *Drosophila* Genome Project;
RA Celnikier S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Paclele J., Park S., Svirskaas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence."
RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE.
RX FlyBase;
RA Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB003772; AAN14221.1; -; Genomic_DNA.
DR HSP; P07505; ISRD.
DR Ensembl; CG31028; *Drosophila melanogaster*.
DR FlyBase; FBgn0051028; CG31028.
DR GO; GO:0016209; F:antioxidant activity; IEA.
DR GO; GO:0004785; F:copper, zinc superoxide dismutase activity; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006801; P:superoxide metabolism; IEA.
DR InterPro; IPR001424; SOD_CU_ZN.
DR Pfam; PF00080; SOD_Cu; 1.
SQ SEQUENCE 1109 AA; 124552 MW; 5D020EF2910000A6 CRC64;
Query Match 92.5%; Score 37; DB 2; Length 1109;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGYLWN 6
Db 929 GGYVMN 934
RESULT 10
QID QGNP40_DROME PRELIMINARY; PRT; 1199 AA.
AC QGNP40;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE R50384p (Fragment).
GN Names:CG31028;
OS *Drosophila melanogaster* (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; *Drosophila*.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe R., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Paclele J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celnikier S.;
RT Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BT011091; AAR82757.1; -; mRNA.
DR HSP; P00445; 1B4L.
DR GO; GO:0004785; F:copper, zinc superoxide dismutase activity; IEA.
DR GO; GO:0020037; F:heme binding; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0006801; P:superoxide metabolism; IEA.
DR InterPro; IPR012282; Cytochrome_c_r.
DR InterPro; IPR001424; SOD_CU_ZN.

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DR Pfam: PF00080; Sod_Cu; 1.
FT NON_TER 1
SQ SEQUENCE 1199 AA; 134574 MW; 55E0A00A85DA0FCB CRC64;

Query Match 92.5%; Score 37; DB 2; Length 1199;
Best Local Similarity 83.3%; Pred. No. 5.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6
Db 962 GGYVWN 967
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RESULT 11
Q522J8_MAGGR PRELIMINARY; PRT; 1279 AA.
AC Q522J8_MAGGR
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=MG04852.4;
OS Magnaporthe grisea 70-15.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthae.
OX NCBI_TaxID=242507;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Birren B., Nussbaum C., Abebe A., Abouelleil A., Adekoya E.,
RA Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
RA Arachi H., Armbruster J., Bachantsang P., Baldwin J., Barry A.,
RA Bayul T., Blitshstein B., Bloom T., Blye J., Boguslavskiy L.,
RA Borowsky M., Boukgalter B., Brunache A., Butler J., Calixte N.,
RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
RA Collimore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,
RA Gnikre A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
RA Jaffe D., Jones C., Kamal M., Kamat A., Kamysseleis M., Karlsson E.,
RA Kells C., Kieu A., Klenner P., Kodira C., Kulbokas E., Labutti K.,
RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
RA Lindblad-toh K., Liu X., Lokyitsang T., Lokyitsang Y., Lucien O.,
RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
RA Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,
RA McCarthy M., McDonough S., Mcghee T., Meldrim J., Meneus L.,
RA Mesirov J., Mihalev A., Mihova T., Mikkelsen T., Mienga V., Moru K.,
RA Mozes J., Multain L., Munson G., Naylor J., Neues C., Nguyen C.,
RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
RA Norbu N., O'donnell P., Okoawo O., O'leary S., Omotosho B.,
RA O'Neill K., Osman S., Parker S., Perrin D., Phunkhang P., Pignani B.,
RA Purcell S., Rachupka T., Ramasany U., Rameau R., Ray V., Raymond C.,
RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
RA Rutnan M., Schupbach R., Seaman C., Settipalli S., Sharpe T.,
RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,
RA Spencer B., Stalker C., Stange-thomann N., Stavropoulos S.,
RA Stenson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,
RA Tensing P., Tesfaye S., Theodore J., Thoulutsang Y., Topham K.,
RA Towey S., Tsamila T., Tsomo N., Vallee D., Vassiliev H.,
RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
RA Wangdi T., Whitaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
RA Zimmer A., Zody M., Lander E.;
RT "The genome sequence of Magnaporthe grisea."
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
[2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=70-15;
RC Dean R., Mitchell T., Brown D., Pan H., Thon M.;

Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
[3]
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Zhu H., Blackmon B.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the cation transport ATPase (P-type)
family.
CC EMBL; AACU01000757; EAA52160.1; -; Genomic_DNA.
DR InterPro; IPR001757; ATPase_E1-E2.
DR InterPro; IPR005834; Dehal_like_hydro.
DR InterPro; IPR006539; Flippase.
DR Pfam; PF00702; Hydrolase; 1.
DR PRINTS; PR00119; CATATPASE.
DR TIGRPFAMs; TIGR01652; ATPase-Plipid; 1.
DR TIGRPFAMs; TIGR01494; ATPase_P-type; 2.
DR PROSITE; PS00154; ATPASE_E1_E2; UNKNOWN 1.
KW ATP-binding; Hydrolase; Hypothetical protein; Nucleotide-binding;
Transmembrane.
SQ SEQUENCE 1279 AA; 143438 MW; 1A3E021D4AA1E99C CRC64;

Query Match 92.5%; Score 37; DB 2; Length 1279;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6
Db 536 GGYVWN 541
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RESULT 12
MSGM_STRMU
ID MSGM_STRMU STANDARD; PRT; 277 AA.
AC Q00751;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Multiple sugar-binding transport system permease protein msgm.
GN Name=msgm; OrderedLocNames=SMO.880;
OS Streptococcus mutans.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1309;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ingbritt;
RX MEDLINE=92165821; PubMed=1537846;
RA Russell R.R.B., Aduse-Opoku J., Sutcliffe I.C., Tao L., Ferretti J.J.;
RT "A binding protein-dependent transport system in Streptococcus mutans
responsible for multiple sugar metabolism."
RL J. Biol. Chem. 267:4631-4637(1992).
[2]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=UA159 / ATCC 700610 / Serotype C;
RX MEDLINE=2295063; PubMed=12397186; DOI=10.1073/pnas.172501299;
RA Ajdic D.J., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
RA Carson M.B., Primeaux C., Tian R., Kenton S., Jia H.G., Lin S.P.,
RA Qian Y., Li S., Zhu H., Najjar F.Z., Lai H., White J., Roe B.A.,
RA Ferretti J.J.;
RT "Genome sequence of Streptococcus mutans UA159, a cariogenic dental
pathogen."
RL Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).
CC -!- FUNCTION: Involved in a binding protein-dependent transport system
responsible for the uptake of melibiose, raffinose and
isomaltotriose.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: Belongs to the binding-protein-dependent transport
system permease family. MalFG subfamily.
CC -!- SIMILARITY: Contains 1 ABC transmembrane type-1 domain.
```

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 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.

EMBL; M77351; AAA26936.1; -; Genomic DNA.
 EMBL; AE014929; AAN58595.1; -; Genomic DNA.

PIR; D42400; D42400.

InterPro; IPR000515; BPD transp.

Pfam; PF00528; BPD_transp_1; 1.

PROSITE; PS0928; ABC_TM1; 1.

Complete proteome; Membrane; Sugar transport; Transmembrane;

Transmembrane

TRANSMEM 13 33 Potential.

TRANSMEM 74 94 Potential.

TRANSMEM 110 130 Potential.

TRANSMEM 141 161 Potential.

TRANSMEM 198 218 Potential.

TRANSMEM 243 263 Potential.

DOMAIN 69 263 ABC transmembrane type-1.

SEQUENCE 277 AA; 31654 MW; C6B6D5C2F805B61A CRC64;

Query Match 90.0%; Score 36; DB 1; Length 277;

Best Local Similarity 83.3%; Pred. No. 2e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGYLWN 6

DB 66 GGYFWN 71

RESULT 13

Q4K7T4_PSEF5

ID Q4K7T4_PSEF5 PRELIMINARY; PRT; 281 AA.

AC Q4K7T4;

DT 13-SEP-2005 (TrEMBLrel. 31, Created)

DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)

DE Sugar ABC transporter, permease protein.

GN ORFNames=PFL_4615;

OS Pseudomonas fluorescens (strain Pf-5).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

OC Pseudomonadaceae; Pseudomonas.

OX NCBI_TaxID=220664;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=PF-5;

RX PubMed=15980861; DOI=10.1038/nbt1110;

RA Paulsen I.T., Press C., Ravel J., Kobayashi D., Myers G.S.,

Mavrodi D., DeBoy R.T., Seshadri R., Ren Q., Madupu R., Dodson R.J.,

Durkin S., Brinkac L.M., Daugherty S.C., Sullivan S.A., Rosovitz M.,

RA Gwinn M.L., Zhou L., Nelson W.C., Weidman J., Watkins K., Tran K.,

RA Khouri H.M., Pierson E., Pierson L. III, Thomasow L., Loper J.,

RT "Complete genome sequence of the plant commensal Pseudomonas

fluorescens Pf-5."

RL Nat. Biotechnol. 23:873-878 (2005).

DR EMBL; CP000076; AAY93862.1; -; Genomic DNA.

SQ SEQUENCE 281 AA; 30668 MW; B2EF2A87BA2E4D5D CRC64;

Query Match 90.0%; Score 36; DB 2; Length 281;

Best Local Similarity 83.3%; Pred. No. 2e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGYLWN 6

DB 71 GGYFWN 76

RESULT 14

Q4IPC3_GIBZE

ID Q4IPC3_GIBZE PRELIMINARY; PRT; 370 AA.

Q4IPC3;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=FG00935.1;
 OS Gibberella zeae PH-1.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
 OX NCBI_TaxID=229533;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PH-1;
 RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
 RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,
 RA Boukhalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
 RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArelano K.,
 RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
 RA Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,
 RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
 RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
 RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
 RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
 RA Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,
 RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
 RA Mihova T., Menga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
 RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
 RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
 RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
 RA Roman J., Schauer S., Schuback R., Seaman S., Severy P., Smirnov S.,
 RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
 RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
 RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
 RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
 RA Lander E.;
 RT "Fusarium graminearum genome sequence."
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AACM01000045; EAA67712.1; -; Genomic DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 370 AA; 41068 MW; 32B07413C046F7D4 CRC64;
 Query Match 90.0%; Score 36; DB 2; Length 370;
 Best Local Similarity 83.3%; Pred. No. 2.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGYLWN 6
 DB 269 GGFLWN 274
 RESULT 15
 Q6WN42_9PSED
 ID Q6WN42_9PSED PRELIMINARY; PRT; 430 AA.
 AC Q6WN42;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Mannose-1-phosphate guanylyltransferase/mannose-6-phosphate isomerase
 DE (fragment).
 GN Name=algA;
 OS Pseudomonas sp. QDA.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=211594;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Han W.J., Yu W.G.;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY279078; AAO84559.1; -; Genomic DNA.
 DR GO; GO:0016853; F1somerase activity; IEA.

DR GO; GO:0008928; F:mannose-1-phosphate guanylyltransferase (GD. . .; IEA.
 DR GO; GO:0016779; F:nucleotidyltransferase activity; IEA.
 DR GO; GO:0016740; P:transferase activity; IEA.
 DR GO; GO:0009058; P:biosynthesis; IEA.
 DR GO; GO:0009103; P:lipopolysaccharide biosynthesis; IEA.
 DR GO; GO:0005976; P:polysaccharide metabolism; IEA.
 DR InterPro; IPR006375; GMP_FMI.
 DR InterPro; IPR001538; Man6P_isomerase.
 DR InterPro; IPR005835; NTP transferase.
 DR Pfam; PF01050; Mannosep_isomerase; 1.
 DR Pfam; PF00483; NTP transferase; 1.
 DR ProDom; PD02864; Man6P_isomerase; 1.
 DR TIGRfams; TIGR01479; GMP_FMI; 1.
 KW Isomerase; Nucleotidyltransferase; Transferase.
 FT NON_TER 430 430
 SQ SEQUENCE 430 AA; 47847 MW; 249A1E894633E807 CRC64;

Query Match 90.0%; Score 36; DB 2; Length 430;
 Best Local Similarity 83.3%; Pred. No. 3.1e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGYLWN 6
 Db 189 GGYFWN 194

Search completed: December 30, 2005, 13:33:29
 Job time : 57 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:14:26 ; Search time 13.4516 Seconds
(without alignments)
36.877 Million cell updates/sec

Title: US-10-735-916A-8
Perfect score: 40
Sequence: 1 GGYLWN 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*
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2: /cgn2_6/ptodata/1/iaa/6 COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCUTS COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	90.0	480	2	US-09-252-991A-19202
2	35	87.5	275	2	US-09-489-039A-12128
3	35	87.5	277	2	US-09-583-110-2944
4	35	87.5	278	2	US-09-769-787-19
5	35	87.5	290	2	US-09-107-433-4262
6	35	87.5	550	2	US-09-252-991A-17547
7	35	87.5	739	2	US-09-540-236-3594
8	34	85.0	144	1	US-09-108-051-2
9	34	85.0	144	2	US-09-440-833-2
10	34	85.0	180	2	US-08-913-159-13
11	34	85.0	301	2	US-09-328-352-7439
12	34	85.0	326	2	US-09-489-039A-9700
13	34	85.0	349	2	US-09-270-767-45401
14	34	85.0	516	2	US-09-489-039A-12893
15	34	85.0	609	2	US-09-949-016-6846
16	34	85.0	984	2	US-09-171-461-14
17	34	85.0	984	2	US-09-970-711-14
18	34	85.0	1091	2	US-09-328-352-5758
19	33	82.5	324	2	US-09-549-848B-34
20	33	82.5	324	2	US-09-688-069-34
21	33	82.5	347	2	US-09-902-540-13914
22	33	82.5	601	2	US-09-902-540-12462
23	32	80.0	114	1	US-08-741-437-3
24	32	80.0	114	1	US-09-134-593-3
25	32	80.0	143	1	US-09-270-767-33503
26	32	80.0	143	2	US-09-270-767-48720
27	32	80.0	289	1	US-08-741-437-1

28	32	80.0	289	1	US-08-741-437-4	Sequence 4, Appli
29	32	80.0	289	1	US-09-134-593-1	Sequence 1, Appli
30	32	80.0	289	1	US-09-134-593-4	Sequence 4, Appli
31	32	80.0	289	2	US-09-538-092-1335	Sequence 1335, Ap
32	32	80.0	339	2	US-09-583-110-3067	Sequence 3067, Ap
33	32	80.0	348	2	US-09-107-433-2966	Sequence 2966, Ap
34	32	80.0	411	2	US-09-540-236-3549	Sequence 3549, Ap
35	32	80.0	533	2	US-09-252-991A-25841	Sequence 25841, A
36	32	80.0	545	2	US-08-976-063E-10	Sequence 10, Appl
37	32	80.0	613	1	US-08-484-101B-46	Sequence 46, Appl
38	32	80.0	613	1	US-08-484-101B-48	Sequence 48, Appl
39	32	80.0	613	2	US-08-714-524D-46	Sequence 46, Appl
40	32	80.0	613	2	US-08-714-524D-48	Sequence 48, Appl
41	32	80.0	738	2	US-09-328-352-4315	Sequence 4315, Ap
42	32	80.0	886	2	US-09-769-787-126	Sequence 126, App
43	32	80.0	2504	2	US-09-328-352-5821	Sequence 5821, Ap
44	31	77.5	94	2	US-09-543-681A-7919	Sequence 7919, Ap
45	31	77.5	120	2	US-09-991-181-199	Sequence 199, App

ALIGNMENTS

RESULT 1
US-09-252-991A-19202
; Sequence 19202, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19202
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19202

Query Match 90.0%; Score 36; DB 2; Length 480;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6
Db 194 GGYLWN 199

RESULT 2
US-09-489-039A-12128
; Sequence 12128, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12128
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12128

Query Match 87.5%; Score 35; DB 2; Length 275;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGYLWN 6
||| ||

Db 103 GGYTWN 108

RESULT 3
US-09-583-110-2944
; Sequence 2944, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 2944
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-2944

Query Match 87.5%; Score 35; DB 2; Length 277;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGYLWN 6
||| ||

Db 66 GGYTWN 71

RESULT 4
US-09-769-787-19
; Sequence 19, Application US/09769787
; Patent No. 6936252
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics Limited
; APPLICANT: Gilbert, Christophe FG
; APPLICANT: Hansbro, Philip M
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: FWC/F21129WO
; CURRENT APPLICATION NUMBER: US/09/769,787
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: GB 9816337.1
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/125164
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-769-787-19

Query Match 87.5%; Score 35; DB 2; Length 278;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGYLWN 6
||| ||

Db 67 GGYTWN 72

RESULT 5
US-09-107-433-4262
; Sequence 4262, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 4262:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 290 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...290
; SEQUENCE DESCRIPTION: SEQ ID NO: 4262:
US-09-107-433-4262

Query Match 87.5%; Score 35; DB 2; Length 290;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGYLWN 6
||| ||

Db 79 GGYTWN 84

RESULT 6
US-09-252-991A-17547
; Sequence 17547, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136

/ CURRENT APPLICATION NUMBER: US/09/252,991A
/ CURRENT FILING DATE: 1999-02-18
/ PRIOR APPLICATION NUMBER: US 60/074,788
/ PRIOR FILING DATE: 1998-02-18
/ PRIOR APPLICATION NUMBER: US 60/094,190
/ PRIOR FILING DATE: 1998-07-27
/ NUMBER OF SEQ ID NOS: 33142
/ SEQ ID NO 17547
/ LENGTH: 550
/ TYPE: PRT
/ ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17547

Query Match 87.5%; Score 35; DB 2; Length 550;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGYLWN 6
Db 257 GGYWN 262
|||||

RESULT 7
US-09-540-236-3594
/ Sequence 3594, Application US/09540236
/ Patent No. 6673910
/ GENERAL INFORMATION:
/ APPLICANT: Gary L. Breton et al.
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS
/ FILE REFERENCE: 2709.2005-001
/ CURRENT APPLICATION NUMBER: US/09/540,236
/ CURRENT FILING DATE: 2000-04-04
/ NUMBER OF SEQ ID NOS: 3840
/ SEQ ID NO 3594
/ LENGTH: 739
/ TYPE: PRT
/ ORGANISM: M.catarrhalis
US-09-540-236-3594

Query Match 87.5%; Score 35; DB 2; Length 739;
Best Local Similarity 83.3%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6
Db 339 GGYLWN 344
|||||

RESULT 8
US-09-108-051-2
/ Sequence 2, Application US/09108051
/ Patent No. 5985576
/ GENERAL INFORMATION:
/ APPLICANT: Ellingson, Jay L.E.
/ APPLICANT: Stabel, Judith R.
/ TITLE OF INVENTION: Species-Specific Genetic Identification
/ TITLE OF INVENTION: of Mycobacterium Paratuberculosis
/ NUMBER OF SEQUENCES: 16
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Curtis P. Ribando
/ STREET: 1815 N. University Street
/ CITY: Peoria
/ STATE: IL
/ COUNTRY: US
/ ZIP: 61604
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/108,051

/ FILING DATE:
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Ribando, Curtis P.
/ REGISTRATION NUMBER: 27,976
/ REFERENCE/DOCKET NUMBER: 0229.97
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 309/681-6513
/ TELEFAX: 309/681-6688
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 144 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-09-108-051-2

Query Match 85.0%; Score 34; DB 1; Length 144;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYLWN 6
Db 30 GYLWN 34
|||||

RESULT 9
US-09-440-833-2
/ Sequence 2, Application US/09440833
/ Patent No. 6277580
/ GENERAL INFORMATION:
/ APPLICANT: Ellingson, Jay L.E.
/ APPLICANT: Stabel, Judith R.
/ TITLE OF INVENTION: Species-Specific Genetic Identification
/ TITLE OF INVENTION: of Mycobacterium Paratuberculosis
/ NUMBER OF SEQUENCES: 16
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Curtis P. Ribando
/ STREET: 1815 N. University Street
/ CITY: Peoria
/ STATE: IL
/ COUNTRY: US
/ ZIP: 61604
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/440,833
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/108,051
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Ribando, Curtis P.
/ REGISTRATION NUMBER: 27,976
/ REFERENCE/DOCKET NUMBER: 0229.97
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 309/681-6513
/ TELEFAX: 309/681-6688
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 144 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-09-440-833-2

Query Match 85.0%; Score 34; DB 2; Length 144;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 9700
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9700

Query Match      85.0%; Score 34; DB 2; Length 326;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GYLWN 6
      |||||
Db      240 GYLWN 244

RESULT 13
US-09-270-767-45401
; Sequence 45401, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45401
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-45401

Query Match      85.0%; Score 34; DB 2; Length 349;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGYLW 5
      |||||
Db      57 GGYLW 61

RESULT 14
US-09-489-039A-12893
; Sequence 12893, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12893
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12893

; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 9700
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9700

Query Match      85.0%; Score 34; DB 2; Length 301;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GYLWN 6
      |||||
Db      215 GYLWN 219

RESULT 12
US-09-489-039A-9700
; Sequence 9700, Application US/09489039A
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Query Match 85.0%; Score 34; DB 2; Length 516;
Best Local Similarity 100.0%; Pred.No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYLW 5
Db 491 GYLW 495

RESULT 15
US-09-949-016-6846
; Sequence 6846, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6846
; LENGTH: 609
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(609)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-949-016-6846

Query Match 85.0%; Score 34; DB 2; Length 609;
Best Local Similarity 100.0%; Pred.No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYLW 6
Db 294 GYLW 298

Search completed: December 30, 2005, 13:37:18
Job time : 14.4516 secs

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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:33:42 ; Search time 44.6129 Seconds
(without alignments)
56.194 Million cell updates/sec

Title: US-10-735-916A-8

Perfect score: 40

Sequence: 1 GGYLWN 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	6	5	US-10-735-916A-8
2	40	100.0	87	4	US-10-425-115-201562
3	40	100.0	117	5	US-10-735-916A-69
4	40	100.0	117	5	US-10-735-916A-75
5	40	100.0	117	5	US-10-735-916A-79
6	40	100.0	117	5	US-10-735-916A-83
7	40	100.0	127	5	US-10-735-916A-52
8	40	100.0	135	5	US-10-735-916A-77
9	40	100.0	135	5	US-10-735-916A-81
10	40	100.0	135	5	US-10-735-916A-85
11	40	100.0	544	4	US-10-320-797-3242
12	37	92.5	1471	6	US-11-097-143-3009
13	35	87.5	75	4	US-10-424-599-232932
14	35	87.5	83	4	US-10-080-170-414
15	35	87.5	83	4	US-10-080-170-414
16	35	87.5	83	4	US-10-468-356-414
17	35	87.5	86	4	US-10-425-115-192203
18	35	87.5	121	4	US-10-308-817-137
19	35	87.5	121	4	US-10-453-698-137
20	35	87.5	125	4	US-10-309-762-8
21	35	87.5	125	4	US-10-309-762-16
22	35	87.5	256	4	US-10-424-599-151457
23	35	87.5	278	3	US-09-769-787-19
24	35	87.5	285	5	US-10-472-928-3940
25	35	87.5	290	5	US-10-617-320-4262
26	35	87.5	400	4	US-10-017-161-2290
27	35	87.5	400	4	US-10-292-798-1936

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28 34 85.0 50 4 US-10-424-599-232749 Sequence 232749,
29 34 85.0 58 4 US-10-425-115-336772 Sequence 336772,
30 34 85.0 72 4 US-10-106-698-4772 Sequence 4772, Ap
31 34 85.0 73 4 US-10-425-115-328910 Sequence 328910,
32 34 85.0 74 4 US-10-424-599-270959 Sequence 270959,
33 34 85.0 79 4 US-10-437-963-141746 Sequence 141746,
34 34 85.0 84 4 US-10-437-963-152064 Sequence 152064,
35 34 85.0 109 4 US-10-074-024-293 Sequence 293, App
36 34 85.0 115 4 US-10-425-115-364926 Sequence 364926,
37 34 85.0 117 4 US-10-424-599-259100 Sequence 259100,
38 34 85.0 137 6 US-11-097-143-3858 Sequence 3858, Ap
39 34 85.0 139 3 US-09-864-408A-7378 Sequence 7378, Ap
40 34 85.0 159 4 US-10-424-599-257904 Sequence 257904,
41 34 85.0 168 4 US-10-767-701-32069 Sequence 32069, A
42 34 85.0 170 4 US-10-424-599-163133 Sequence 163133,
43 34 85.0 228 4 US-10-425-115-284834 Sequence 284834,
44 34 85.0 230 4 US-10-767-701-51631 Sequence 51631, A
45 34 85.0 240 6 US-11-097-143-22905 Sequence 22905, A

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ALIGNMENTS

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RESULT 1
US-10-735-916A-8
; Sequence 8, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOSTSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFIOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10735,916A
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-735-916A-8

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Query Match 100.0%; Score 40; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GGYLWN 6
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Db 1 GGYLWN 6

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RESULT 2
US-10-425-115-201562
; Sequence 201562, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua

```

; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 201562
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MR74577_115409C.1.pcp
US-10-425-115-201562

Query Match 100.0%; Score 40; DB 4; Length 87;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6
| | | | |
Db 62 GGYLWN 67

RESULT 3
US-10-735-916A-69
; Sequence 69, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10/735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 69
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-735-916A-69

Query Match 100.0%; Score 40; DB 5; Length 117;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6
| | | | |
Db 31 GGYLWN 36

RESULT 4
US-10-735-916A-75
; Sequence 75, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie

; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10/735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 75
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-735-916A-75

Query Match 100.0%; Score 40; DB 5; Length 117;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6
| | | | |
Db 31 GGYLWN 36

RESULT 5
US-10-735-916A-79
; Sequence 79, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10/735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-735-916A-79

Query Match 100.0%; Score 40; DB 5; Length 117;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6


```
Db          31 GGYLWN 36
|||||
RESULT 6
US-10-735-916A-83
; Sequence 83, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 83
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-735-916A-83

Query Match          100.0%; Score 40; DB 5; Length 117;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGYLWN 6
      |||||
Db      31 GGYLWN 36

RESULT 7
US-10-735-916A-52
; Sequence 52, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 83
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-735-916A-83

Query Match          100.0%; Score 40; DB 5; Length 117;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGYLWN 6
      |||||
Db      31 GGYLWN 36

RESULT 8
US-10-735-916A-77
; Sequence 77, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 77
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-735-916A-77

Query Match          100.0%; Score 40; DB 5; Length 135;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGYLWN 6
      |||||
Db      49 GGYLWN 54

RESULT 9
US-10-735-916A-81
; Sequence 81, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
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; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-735-916A-81
```

```
Query Match      100.0%; Score 40; DB 5; Length 135;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GGYLWN 6
        |||||
DB      49 GGYLWN 54
```

```
RESULT 10
US-10-735-916A-85
; Sequence 85, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10/735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 85
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-735-916A-85
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Query Match      100.0%; Score 40; DB 5; Length 135;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 GGYLWN 6
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DB      49 GGYLWN 54
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RESULT 11
US-10-320-797-3242
; Sequence 3242, Application US/10320797
; Publication No. US20040014955A1
; GENERAL INFORMATION:
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; APPLICANT: Eroshkin, Alexey M.
; APPLICANT: Zamudio, Carlos
; TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF CRYPTOCOCCUS NEOFORMANS AND
; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: 10182-021-999
; CURRENT APPLICATION NUMBER: US/10/320,797
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,261
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 3361
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3242
; LENGTH: 544
; TYPE: PRT
; ORGANISM: Cryptococcus neoformans
US-10-320-797-3242
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Query Match      100.0%; Score 40; DB 4; Length 544;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 GGYLWN 6
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DB      467 GGYLWN 472
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RESULT 12
US-11-097-143-3009
; Sequence 3009, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3009
; LENGTH: 1471
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-3009
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Query Match      92.5%; Score 37; DB 6; Length 1471;
Best Local Similarity 83.3%; Pred. No. 7.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 GGYLWN 6
        |||||
DB      871 GGYVWN 876
```

RESULT 13

US-10-424-599-232932
; Sequence 232932, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 232932
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_52362C.1.pep
US-10-424-599-232932

Query Match 87.5%; Score 35; DB 4; Length 75;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGYLWN 6
Db 69 GGYLWS 74
|||||:

RESULT 14
US-10-080-170-414
; Sequence 414, Application US/10080170
; Publication No. US20030129601A1
; GENERAL INFORMATION:
; APPLICANT: COLE, S.T.
; TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
; TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
; TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES
; FILE REFERENCE: 03495.0218
; CURRENT APPLICATION NUMBER: US/10/080,170
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/270,123
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 652
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 414
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-080-170-414

Query Match 87.5%; Score 35; DB 4; Length 83;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGYLWN 6
Db 8 GGYLWS 13
|||||:

RESULT 15
US-10-080-170-414
; Sequence 414, Application US/10080170
; Publication No. US20040121322A9
; GENERAL INFORMATION:
; APPLICANT: COLE, S.T.
; TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
; TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
; TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES
; FILE REFERENCE: 03495.0218
; CURRENT APPLICATION NUMBER: US/10/080,170

; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/270,123
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 652
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 414
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-080-170-414
Query Match 87.5%; Score 35; DB 4; Length 83;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGYLWN 6
Db 8 GGYLWS 13
|||||:
Search completed: December 30, 2005, 14:14:53
Job time : 45.6129 secs

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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:35:07 ; Search time 2.22581 Seconds
(without alignments)
20.187 Million cell updates/sec

Title: US-10-735-916A-8

Perfect score: 40

Sequence: 1 GGYLWN 6

Scoring table: BLOSUM62

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Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 57103

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA_New:*
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8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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2	40	100.0	117	7 US-11-012-353-69	Sequence 69, Appli
3	40	100.0	117	7 US-11-012-353-75	Sequence 75, Appli
4	40	100.0	117	7 US-11-012-353-79	Sequence 79, Appli
5	40	100.0	117	7 US-11-012-353-83	Sequence 83, Appli
6	40	100.0	127	7 US-11-012-353-52	Sequence 52, Appli
7	40	100.0	135	7 US-11-012-353-77	Sequence 77, Appli
8	40	100.0	135	7 US-11-012-353-81	Sequence 81, Appli
9	40	100.0	135	7 US-11-012-353-85	Sequence 85, Appli
10	35	87.5	278	6 US-10-873-528-19	Sequence 19, Appli
11	33	82.5	324	7 US-11-092-140-34	Sequence 34, Appli
12	32	80.0	289	6 US-10-821-234-1289	Sequence 1289, Ap
13	32	80.0	886	6 US-10-873-528-126	Sequence 126, App
14	32	80.0	1029	6 US-10-821-234-908	Sequence 908, App
15	32	80.0	1032	6 US-10-467-657-3278	Sequence 3278, Ap
16	31	77.5	120	6 US-10-131-826A-434	Sequence 434, App
17	30	75.0	99	7 US-11-054-669-36	Sequence 36, Appli
18	30	75.0	99	7 US-11-054-669-39	Sequence 39, Appli
19	30	75.0	99	7 US-11-084-554-50	Sequence 50, Appli
20	30	75.0	99	7 US-11-084-554-55	Sequence 55, Appli
21	30	75.0	253	7 US-11-054-515-1619	Sequence 1619, Ap
22	29	72.5	6	7 US-11-009-939-23	Sequence 23, Appli
23	29	72.5	90	6 US-10-467-657-3624	Sequence 3624, Ap
24	29	72.5	99	7 US-11-054-669-37	Sequence 37, Appli
25	29	72.5	118	7 US-11-012-353-70	Sequence 70, Appli

ALIGNMENTS

RESULT 1

US-11-012-353-8
; Sequence 8, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFILOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-012-353-8

Query Match 100.0%; Score 40; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.4e+04;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6
|||||
DB 1 GGYLWN 6

RESULT 2

US-11-012-353-69
; Sequence 69, Application US/11012353

; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; PRIOR FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 69
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-012-353-69

Query Match 100.0%; Score 40; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.67; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

QY 1 GGYLWN 6
Db 31 GGYLWN 36

RESULT 3
US-11-012-353-75
; Sequence 75, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 75

; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-012-353-75

Query Match 100.0%; Score 40; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.67; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

QY 1 GGYLWN 6
Db 31 GGYLWN 36

RESULT 4
US-11-012-353-79
; Sequence 79, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 79
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-012-353-79

Query Match 100.0%; Score 40; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.67; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

QY 1 GGYLWN 6
Db 31 GGYLWN 36

RESULT 5
US-11-012-353-83
; Sequence 83, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-198

; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 83
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-012-353-83

Query Match 100.0%; Score 40; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGYLWN 6
|||||
Db 31 GGYLWN 36

RESULT 6

US-11-012-353-52
; Sequence 52, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 52
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-012-353-52

Query Match 100.0%; Score 40; DB 7; Length 127;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGYLWN 6
|||||

Db 41 GGYLWN 46

RESULT 7

US-11-012-353-77
; Sequence 77, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 77
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-012-353-77

Query Match 100.0%; Score 40; DB 7; Length 135;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGYLWN 6
|||||
Db 49 GGYLWN 54

RESULT 8

US-11-012-353-81
; Sequence 81, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
US-11-012-353-81

Query Match 100.0%; Score 40; DB 7; Length 127;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGYLWN 6
|||||

; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 81
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-012-353-81

Query Match 100.0%; Score 40; DB 7; Length 135;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6
|||
Db 49 GGYLWN 54

RESULT 9
US-11-012-353-85
; Sequence 85, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 85
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-012-353-85

Query Match 100.0%; Score 40; DB 7; Length 135;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6
|||
Db 49 GGYLWN 54

RESULT 10
US-10-873-528-19
; Sequence 19, Application US/10873528
; Publication No. US20050276814A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics Limited
; APPLICANT: Gilbert, Christophe FG
; APPLICANT: Hansbro, Philip M

; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21129WO
; CURRENT APPLICATION NUMBER: US/10/873,528
; CURRENT FILING DATE: 2004-06-23
; PRIOR APPLICATION NUMBER: US/09/769,787
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: GB 9816337.1
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/125164
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-873-528-19

Query Match 87.5%; Score 35; DB 6; Length 278;
Best Local Similarity 83.3%; Pred. No. 10;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGYLWN 6
|||
Db 67 GGYLWN 72

RESULT 11
US-11-092-140-34
; Sequence 34, Application US/11092140
; Publication No. US20050262590A1
; GENERAL INFORMATION:
; APPLICANT: Subramaniam, S.; Slater, S.; Karberg, K.; Chen, R.; Valentin, H.; Wong, Y
; TITLE OF INVENTION: Nucleic Acid Sequences to Proteins Involved in Tocopherol Synthe
; FILE REFERENCE: 16515.054
; CURRENT APPLICATION NUMBER: US/11/092,140
; CURRENT FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: US/09/688,069
; PRIOR FILING DATE: 2000-10-14
; NUMBER OF SEQ ID NOS: 114
; SEQ ID NO 34
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Synechocystis sp.
US-11-092-140-34

Query Match 82.5%; Score 33; DB 7; Length 324;
Best Local Similarity 66.7%; Pred. No. 25;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6
|||
Db 58 GGYLWN 63

RESULT 12
US-10-821-234-1289
; Sequence 1289, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: Pt SEQ_genes Version 1.0
; SEQ ID NO 1289

; LENGTH: 289
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1289

Query Match 80.0%; Score 32; DB 6; Length 289;
Best Local Similarity 80.0%; Pred. No. 34;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GYLWN 6
||:|
Db 89 GYIWN 93

RESULT 13

US-10-873-528-126
; Sequence 126, Application US/10873528
; Publication No. US20050276814A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics Limited
; APPLICANT: Gilbert, Christophe FG
; APPLICANT: Hansbro, Philip M
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21129WO
; CURRENT APPLICATION NUMBER: US/10/873,528
; CURRENT FILING DATE: 2004-06-23
; PRIOR APPLICATION NUMBER: US/09/769,787
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: GB 9816337.1
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/125164
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 398
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 126
; LENGTH: 886
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-873-528-126

Query Match 80.0%; Score 32; DB 6; Length 886;
Best Local Similarity 80.0%; Pred. No. 86;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGYLW 5
|||:|
Db 482 GGYIW 486

RESULT 14

US-10-821-234-908
; Sequence 908, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 908
; LENGTH: 1029
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-908

Query Match 80.0%; Score 32; DB 6; Length 1029;

Best Local Similarity 80.0%; Pred. No. 97;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GYLWN 6
||:|
Db 124 GYIWN 128

RESULT 15

US-10-467-657-3278
; Sequence 3278, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3278
; LENGTH: 1032
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3278

Query Match 80.0%; Score 32; DB 6; Length 1032;
Best Local Similarity 66.7%; Pred. No. 97;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGYLWN 6
|||:|
Db 302 GGYVWH 307

Search completed: December 30, 2005, 14:15:21
Job time : 2.22581 secs

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OM protein - protein search, using sw model

Run on: December 30, 2005, 15:23:43 ; Search time 181 Seconds
(without alignments)
14.565 Million cell updates/sec

Title: US-10-735-916A-8

Perfect score: 40

Sequence: 1 GGYLWN 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 41471

Minimum DB seq length: 6

Maximum DB seq length: 6

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_21:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	40	100.0	6	7	ADJ76842 CDR seque
2	40	100.0	6	9	ADZ67012 Murine in
3	32	80.0	6	2	AAR05974 Somatic i
4	30	75.0	6	9	AAR40139 TNF resis
5	29	72.5	6	9	ADZ45406 Murine fa
6	29	72.5	6	9	ABE70898 Toll-like
7	27	67.5	6	8	ADP05843 Trp-conta
8	27	67.5	6	8	ADP07180 Trp-conta
9	26	65.0	6	8	ADP05839 Trp-conta
10	26	65.0	6	8	ADP07176 Trp-conta
11	26	65.0	6	8	ADP05872 Trp-conta
12	23	57.5	6	2	AAR24717 Sequence
13	23	57.5	6	2	AAR01150 Mab 1.4 h
14	23	57.5	6	2	AAR98564 N-terminu
15	23	57.5	6	2	AAR98564 Heavy cha
16	23	57.5	6	2	AAR44173 Monoclonal
17	23	57.5	6	2	AAR87989 Type I re
18	23	57.5	6	7	ADM83262 Hepatitis
19	23	57.5	6	8	ADL26967 Murine de
20	23	57.5	6	8	ADS82610 Anti-IL-2
21	23	57.5	6	9	ADZ45518 Murine fa
22	23	57.5	6	9	ADZ45310 Murine fa
23	23	57.5	6	9	ADZ45342 Murine fa
24	23	57.5	6	9	ADZ51223 Amino aci

25	23	57.5	6	9	ADZ51255 Amino aci
26	23	57.5	6	9	ADZ42129 Mouse ant
27	23	57.5	6	9	ADZ42097 Mouse ant
28	23	57.5	6	9	AEA88995 Hepatitis
29	23	57.5	6	9	AEC20779 M-CSF spe
30	22	55.0	6	2	AAR66826 Hexapepti
31	22	55.0	6	2	AAY33848 G30 sub d
32	22	55.0	6	3	AAY90100 Enhancer
33	22	55.0	6	3	AAY50634 Alphasal-pr
34	22	55.0	6	3	AAY85089 HBV surfa
35	22	55.0	6	4	AAY06272 Anti-HIV
36	22	55.0	6	4	AAB77005 Retrovira
37	22	55.0	6	4	ABB03059 Viral cor
38	22	55.0	6	5	ABP67968 Human CD6
39	22	55.0	6	5	ABP67966 Human CD6
40	22	55.0	6	5	ABP67967 Human CD6
41	22	55.0	6	5	ABP67965 Human CD6
42	22	55.0	6	5	ABP67361 Human CD6
43	22	55.0	6	5	AAM48304 Human CD4
44	22	55.0	6	5	ADE03081 Hybrid po
45	22	55.0	6	6	ADA19581 Carcinoem

ALIGNMENTS

RESULT 1

ADJ76842
ID ADJ76842 standard; peptide; 6 AA.

XX AC ADJ76842;

XX DT 06-MAY-2004 (first entry)

XX DE CDR sequence for anti-IGF-1R antibody.

XX KW cytotatic; antipsoriatic; antibody;

XX KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;
or epidermal growth factor receptor; EGFR; signal transduction pathway;

XX KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;
CDR.

XX OS Mus musculus.

XX PN WO2003059951-A2.

XX PD 24-JUL-2003.

XX PF 20-JAN-2003; 2003WO-FR000178.

XX PR 18-JAN-2002; 2002FR-00000653.

XX PR 18-JAN-2002; 2002FR-00000654.

XX PR 07-MAY-2002; 2002FR-00005753.

XX PA (FABR) FABRE MEDICAMENT SA PIERRE.

XX PI Goetsch L, Corvaia N, Leger O;

XX DR WPI; 2003-569653/53.

XX DR N-PSDB; ADJ76841.

XX PT New antibodies that bind to human insulin-like growth factor receptor,
useful for treatment, prevention and diagnosis of cancers.

XX PT Claim 1; SEQ ID NO 8; 164pp; French.

XX CC The invention relates to an isolated antibody (Ab), and its functional
fragments, that bind to human insulin-like growth factor-1 receptor (IGF-
1R) and optionally; (i) inhibit natural binding of insulin-like growth
factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine
kinase activity of IGF-1R. Ab and its fragments are used to prevent or
treat diseases associated with overexpression and/or abnormal activity of
IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with

CC hyperactivity of signal transduction pathways mediated by interaction of
 CC these receptors with their ligands. Especially they inhibit
 CC transformation of normal cells to tumor cells, inhibit growth and/or
 CC proliferation of tumor cells, so are useful against cancers of the
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused
 CC by abnormal expression of IGF-IR and/or EGFR. This sequence represents an
 CC CDR sequence used to generate the Ab of the invention.

XX Sequence 6 AA;

Query Match 100.0%; Score 40; DB 7; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6
 |||||
 Db 1 GGYLWN 6

RESULT 2

ID ADZ67012 standard; peptide; 6 AA.

XX ADZ67012;

DT 30-JUN-2005 (first entry)

DE Murine insulin-like growth factor T receptor IGF-IR CDR SEQ ID NO:8.

XX Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
 KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;
 KW musculoskeletal disease; respiratory disease; lung tumor;
 KW endocrine disease; gynecology and obstetrics; breast tumor;
 KW endometroid carcinoma; gastrointestinal disease; colon tumor;
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder.

XX Mus musculus.

XX US2005084906-A1.

XX 21-APR-2005.

XX 16-DEC-2003; 2003US-00735916.

XX 18-JAN-2002; 2002FR-0000653.

XX 18-JAN-2002; 2002FR-0000654.

XX 07-MAY-2002; 2002FR-00005753.

XX 20-JAN-2003; 2003WO-FR000178.

XX 11-JUL-2003; 2003FR-00008538.

XX (GOET/) GOETSCH L.

XX (CORV/) CORVAIA N.

XX (LEGE/) LEGER O.

XX (DUFL/) DUFLOS A.

XX (HAEU/) HAEUW J.

XX (BECK/) BECK A.

XX Goetech L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;

XX WPI; 2005-321968/33.

XX N-PSDB; ADZ67011.

XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)
 PT antibody or its functional fragment, being capable of binding human IGF-
 PT IR and specifically inhibiting tyrosine kinase activity of receptor,
 PT useful for treating cancer.

XX Claim 1; SEQ ID NO 8; 125pp; English.

XX The invention relates to a novel isolated anti-insulin-like growth factor
 CC I receptor (IGF-IR) antibody (I) or its functional fragment, being
 CC capable of binding to human IGF-IR and, if necessary, capable of

CC specifically inhibiting tyrosine kinase activity of the receptor,
 CC comprising a light or heavy chain having at least one complementary
 CC determining region (CDR) consisting of one of two fully defined 16 amino
 CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in
 CC the preparation of a medicament intended for the prevention or treatment
 CC of an illness connected with an overexpression and/or an abnormal
 CC activation of the IGF-IR and/or EGFR, and/or connected with a
 CC hyperactivation of the transduction pathway of the signal mediated by the
 CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where
 CC the administration of the medicament does not induce or only slightly
 CC induces secondary effects connected with inhibition of the insulin
 CC receptor. The antibody is useful for preparation of a medicament intended
 CC to inhibit the transformation of normal cells into cells with tumoral
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is
 CC useful for preparation of a medicament intended to inhibit the growth
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a
 CC medicament intended for prevention or for the treatment of cancer, where
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the
 CC preparation of a medicament intended for the prevention or for the
 CC treatment of psoriasis. (I) is useful in preparation of a medicament
 CC intended for the specific targeting of a biologically active compound to
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)
 CC is useful for in vitro diagnosis of illnesses induced by an
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor
 CC starting from a biological sample in which the abnormal presence of IGF-
 CC IR and/or EGFR receptor is suspected, which involves contacting the
 CC biological sample with (I), which is optionally labeled. The present
 CC sequence is used in the exemplification of the invention.

SQ Sequence 6 AA;

Query Match 100.0%; Score 40; DB 9; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6
 |||||
 Db 1 GGYLWN 6

RESULT 3

AAR05974

ID AAR05974 standard; protein; 6 AA.

XX AAR05974;

AC AAR05974;

XX 16-NOV-1990 (first entry)

XX Somatic immunoglobulin DH fragment DOB.

XX Immunoglobulin DH; cancer; lymphoid tumour; leukaemia; ds.

XX Homo sapiens.

XX WO9006998-A.

XX 28-JUN-1990.

XX 19-DEC-1988; 88JP-00319809.

XX 19-DEC-1988; 88JP-00319809.

XX (MITK) MITSUI TOATSU CHEM INC.

XX (EDUC-) EDUCATIONAL FOUND FUJITA.

XX Kurosawa Y, Ichihara Y, Awaya K, Ishizuka Y;

XX WPI; 1990-224526/29.

PT DNA fragments related to human immunoglobulin genes - in which are
 PT markers for diagnosis of lymphoid tumours by detection of B- and T-type
 PT tumour cells.

XX Disclosure; Page ?; -pp; Japanese.

XX DH immunoglobulin encoding sequences may be extracted as fragments and
 CC used in diagnosis of lymphoid tumours and leukaemias, detecting marker
 CC sequences from the VhDhJh gene cluster

XX Sequence 6 AA;

Query Match 80.0%; Score 32; DB 2; Length 6;
 Best Local Similarity 80.0%; Pred. No. 2e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GYLNW 6
 ||:||
 Db 1 GYIWN 5

RESULT 4
 AEA40139
 ID AEA40139 standard; peptide; 6 AA.

XX AEA40139;

XX 28-JUL-2005 (first entry)

XX TNF resistant monoclonal antibody VH region, F6VH CDR1.

XX tumor necrosis factor; TNF; monoclonal antibody; F6 mAb;
 XX light chain variable region; heavy chain variable region; F6VH.

XX Unidentified.

XX CN1544466-A.

XX 10-NOV-2004.

XX 13-NOV-2003; 2003CN-01105919.

XX 13-NOV-2003; 2003CN-01105919.

XX (UYFO-) UNIV FOURTH MILITARY MEDICAL.

XX Jin B, Liu X, Zhu C;

XX WPI; 2005-153078/17.

XX N-PSDB; AEA40138.

XX Variable region gene of high affinity monoclonal antibody of tumor
 PT necrosis factor and its preparation.

XX Claim 1; Page 3; 20pp; Chinese.

XX The invention relates to a method for preparing variable region genes of
 CC high affinity tumor necrosis factor (TNF) resistant monoclonal antibody
 CC (F6 mAb). The method comprises using recombinant human TNF immune BALB/c
 CC mouse to prepare mouse anti-TNF monoclonal antibody, screening high
 CC affinity F6 mAb using an indirect enzyme linked immunosorbent assay
 CC (ELISA). By cloning the monoclonal antibody light chain and heavy chain
 CC variable region (VL and VH respectively) genes, the monoclonal antibody
 CC light chain and heavy chain variable region gene sequence and amino acid
 CC sequence can be obtained, and the identity of the gene sequence and
 CC protein sequence can be confirmed. This sequence represents
 CC complementarity determining region, CDR1 of F6VH.

XX Sequence 6 AA;

Query Match 75.0%; Score 30; DB 9; Length 6;
 Best Local Similarity 80.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GYLNW 6
 ||:||
 Db 2 GYFWN 6

RESULT 5

ADZ45406

ID ADZ45406 standard; peptide; 6 AA.

XX ADZ45406;

XX 30-JUN-2005 (first entry)

XX Murine factor IX directed antibody CDR1 SEQ ID NO 110.

XX bispecific antibody; blood coagulation factor VIII; bleeding;
 KW fibrinolysis; blood coagulation factor X; blood-coagulation factor IX;
 KW factor VIII deficiency; von Willebrand disease; hemostatic;
 KW immunostimulator; antibody engineering.

XX Mus musculus.

XX WO2005035756-A1.

XX 21-APR-2005.

XX 08-OCT-2004; 2004WO-JP014911.

XX 10-OCT-2003; 2003WO-JP013062.

XX 14-OCT-2003; 2003WO-JP013123.

XX (CHUS) CHUGAI SEIYAKU KK.

XX Hattori K, Kojima T, Miyazaki T, Soeda T;

XX WPI; 2005-315563/32.

XX Novel bispecific antibody substituting for function of cofactor that
 PT enhances enzyme reaction, and recognizing both enzyme and substrates of
 PT enzyme, useful for treating hemophilia A.

XX Disclosure; SEQ ID NO 110; 69pp; Japanese.

XX This invention describes a novel bispecific antibody which can act as a
 CC cofactor to enhance an enzyme reaction and can recognize the enzyme and
 CC the enzyme substrate. The antibody specifically binds to blood
 CC coagulation factor VIII. The invention also describes a composition
 CC comprising the antibody and a carrier, a kit useful in preventing and/or
 CC treating bleeding associated with a disorder or from a disease caused by
 CC bleeding. The composition includes blood coagulation factor VIII. The
 CC antibody of the invention can be a blood-coagulation fibrinolysis related
 CC factor including blood-coagulation factor VIII, blood coagulation factor
 CC X, or blood-coagulation factor IX. The antibody comprises a complementary
 CC determining region (CDR) of anti-blood-coagulation factor IX/IXa factor
 CC antibody. The novel antibody or composition is useful for preventing
 CC and/or treating a disease accompanying bleeding, or the disease resulting
 CC from bleeding, where the disease accompanying bleeding or the disease
 CC resulting from bleeding develops and/or progresses by an active reduction
 CC or deletion of the blood coagulation factor VIII. The disease the
 CC develops and/or progresses by an active reduction or deletion of the
 CC blood coagulation factor VIII and/or activation blood coagulation factor
 CC VIII, is hemophilia A or von Willebrand disease, where the hemophilia is
 CC an acquired hemophilia A. This sequence represents a fragment of the
 CC antibody described in the method of the invention. Note: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 6 AA;

Query Match 72.5%; Score 29; DB 9; Length 6;
 Best Local Similarity 80.0%; Pred. No. 2e+06;

Qy	2 GYLWN 6 :	Matches	3; Conservative	2; Mismatches	0; Indels	0; Gaps	0;
Db	1 GWMWN 5						
RESULT 8							
ID	ADP07180						
AC	ADP07180 standard; peptide; 6 AA.						
XX	ADP07180;						
DT	26-AUG-2004 (first entry)						
XX	XX						
DE	XX						
XX	XX						
KW	cell adhesion modulating agent;						
KW	desmosomal cadherin-mediated cell adhesion;						
KW	Trp-containing cell adhesion recognition sequence; CAR sequence;						
KW	desmosomal cadherin molecule; cancer metastasis; angiogenesis;						
KW	demyelinating neurological disorder; immune system modulation;						
KW	pregnancy prevention; vasopermeability; synaptic stability;						
KW	blood vessel regression; neurite outgrowth; spinal cord injury;						
KW	angiogenesis; neovascularisation; psoriasis; diabetic retinopathy;						
KW	dermatitis.						
OS	Unidentified.						
XX	XX						
PN	WO2004048411-A2.						
XX	XX						
PD	10-JUN-2004.						
XX	XX						
PF	14-NOV-2003; 2003WO-IB006208.						
XX	XX						
PR	14-NOV-2002; 2002US-0426551P.						
PR	14-NOV-2002; 2002US-0426689P.						
XX	XX						
PA	(ADHE-) ADHEREX TECHNOLOGIES INC.						
XX	XX						
PI	Blaschuk OW, Michaud SD;						
XX	XX						
DR	WPI; 2004-450349/42.						
XX	XX						
PT	Cell adhesion modulating agent that modulates desmosomal cadherin-						
PT	mediated cell adhesion, useful for inhibiting cancer metastasis,						
PT	comprises Trp-containing cell adhesion recognition sequence of desmosomal						
PT	cadherin molecule.						
XX	XX						
PS	Claim 51; SEQ ID NO 1357; 507pp; English.						
XX	XX						
CC	The invention comprises a cell adhesion modulating agent that modulates						
CC	desmosomal cadherin-mediated cell adhesion. The cell adhesion modulating						
CC	agent comprises a Trp-containing cell adhesion recognition (CAR) sequence						
CC	of a desmosomal cadherin molecule. The cell adhesion modulating agent of						
CC	the invention is useful for: inhibiting cancer metastasis, inhibiting						
CC	angiogenesis in a mammal, ameliorating a demyelinating neurological						
CC	disorder in a mammal, modulating immune system of a mammal, preventing						
CC	pregnancy in a mammal, increasing vasopermeability in a mammal,						
CC	inhibiting synaptic stability in a mammal, stimulating blood vessel						
CC	regression, increasing blood flow to a tumour in a mammal, disrupting						
CC	neovascularisation in a mammal, inhibiting endometriosis in a mammal,						
CC	enhancing inhaled compound delivery in a mammal, enhancing adhesion of a						
CC	foreign tissue implanted within a mammal, for enhancing/directing neurite						
CC	outgrowth, and for ameliorating a spinal cord injury in a mammal. The						
CC	cell adhesion modulating agent of the invention is useful for treating						
CC	disease conditions that are dependent on angiogenesis and						
CC	neovascularisation (e.g. psoriasis, diabetic retinopathy or dermatitis).						
CC	The present amino acid sequence represents a Trp-containing CAR sequence						
CC	of the invention.						
XX	XX						
SQ	Sequence 6 AA;						
Query Match	67.5%; Score 27; DB 8; Length 6;						
Best Local Similarity	60.0%; Pred. No. 2e+06;						
Qy	2 GYLWN 6 :	Matches	3; Conservative	2; Mismatches	0; Indels	0; Gaps	0;
Db	1 GWMWN 5						
RESULT 9							
ID	ADP05839						
AC	ADP05839 standard; peptide; 6 AA.						
XX	ADP05839;						
DT	26-AUG-2004 (first entry)						
XX	XX						
DE	XX						
XX	XX						
KW	cell adhesion modulating agent;						
KW	desmosomal cadherin-mediated cell adhesion;						
KW	Trp-containing cell adhesion recognition sequence; CAR sequence;						
KW	desmosomal cadherin molecule; cancer metastasis; angiogenesis;						
KW	demyelinating neurological disorder; immune system modulation;						
KW	pregnancy prevention; vasopermeability; synaptic stability;						
KW	blood vessel regression; neurite outgrowth; spinal cord injury;						
KW	angiogenesis; neovascularisation; psoriasis; diabetic retinopathy;						
KW	dermatitis.						
OS	Unidentified.						
XX	XX						
PN	WO2004048411-A2.						
XX	XX						
PD	10-JUN-2004.						
XX	XX						
PF	14-NOV-2003; 2003WO-IB006208.						
XX	XX						
PR	14-NOV-2002; 2002US-0426551P.						
PR	14-NOV-2002; 2002US-0426689P.						
XX	XX						
PA	(ADHE-) ADHEREX TECHNOLOGIES INC.						
XX	XX						
PI	Blaschuk OW, Michaud SD;						
XX	XX						
DR	WPI; 2004-450349/42.						
XX	XX						
PT	Cell adhesion modulating agent that modulates desmosomal cadherin-						
PT	mediated cell adhesion, useful for inhibiting cancer metastasis,						
PT	comprises Trp-containing cell adhesion recognition sequence of desmosomal						
PT	cadherin molecule.						
XX	XX						
PS	Claim 51; SEQ ID NO 16; 507pp; English.						
XX	XX						
CC	The invention comprises a cell adhesion modulating agent that modulates						
CC	desmosomal cadherin-mediated cell adhesion. The cell adhesion modulating						
CC	agent comprises a Trp-containing cell adhesion recognition (CAR) sequence						
CC	of a desmosomal cadherin molecule. The cell adhesion modulating agent of						
CC	the invention is useful for: inhibiting cancer metastasis, inhibiting						
CC	angiogenesis in a mammal, ameliorating a demyelinating neurological						
CC	disorder in a mammal, modulating immune system of a mammal, preventing						
CC	pregnancy in a mammal, increasing vasopermeability in a mammal,						
CC	inhibiting synaptic stability in a mammal, stimulating blood vessel						
CC	regression, increasing blood flow to a tumour in a mammal, disrupting						
CC	neovascularisation in a mammal, inhibiting endometriosis in a mammal,						
CC	enhancing inhaled compound delivery in a mammal, enhancing adhesion of a						
CC	foreign tissue implanted within a mammal, for enhancing/directing neurite						
CC	outgrowth, and for ameliorating a spinal cord injury in a mammal. The						
CC	cell adhesion modulating agent of the invention is useful for treating						
CC	disease conditions that are dependent on angiogenesis and						
CC	neovascularisation (e.g. psoriasis, diabetic retinopathy or dermatitis).						
CC	The present amino acid sequence represents a Trp-containing CAR sequence						
CC	of the invention.						
XX	XX						
SQ	Sequence 6 AA;						

Query Match 65.0%; Score 26; DB 8; Length 6;
Best Local Similarity 60.0%; Pred. No. 2e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYLWN 6
|::||
Db 1 GWVWN 5

RESULT 10
ID ADP07176 standard; peptide; 6 AA.
XX AC ADP07176;
XX 26-AUG-2004 (first entry)
XX Trp-containing cell adhesion recognition (CAR) sequence #211.
XX cell adhesion modulating agent;
KW desmosomal cadherin-mediated cell adhesion;
KW Trp-containing cell adhesion recognition sequence; CAR sequence;
KW desmosomal cadherin molecule; cancer metastasis; angiogenesis;
KW demyelinating neurological disorder; immune system modulation;
KW pregnancy prevention; vasopermeability; synaptic stability;
KW blood vessel regression; neurite outgrowth; spinal cord injury;
KW angiogenesis; neovascularisation; psoriasis; diabetic retinopathy;
KW dermatitis.
XX Unidentified.
OS WO2004048411-A2.
XX PN 10-JUN-2004.
XX PD 14-NOV-2003; 2003WO-IB006208.
XX PF 14-NOV-2002; 2002US-0426551P.
XX PR 14-NOV-2002; 2002US-0426689P.
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX PA Blaschuk OW, Michaud SD;
XX PI WPI; 2004-450349/42.
XX DR Cell adhesion modulating agent that modulates desmosomal cadherin-mediated cell adhesion, useful for inhibiting cancer metastasis, comprises Trp-containing cell adhesion recognition sequence of desmosomal cadherin molecule.
XX PT Claim 51; SEQ ID NO 1353; 507pp; English.
XX PS The invention comprises a cell adhesion modulating agent that modulates desmosomal cadherin-mediated cell adhesion. The cell adhesion modulating agent comprises a Trp-containing cell adhesion recognition (CAR) sequence of a desmosomal cadherin molecule. The cell adhesion modulating agent of the invention is useful for: inhibiting cancer metastasis, inhibiting angiogenesis in a mammal, ameliorating a demyelinating neurological disorder in a mammal, modulating immune system of a mammal, preventing pregnancy in a mammal, increasing vasopermeability in a mammal, inhibiting synaptic stability in a mammal, stimulating blood vessel regression, increasing blood flow to a tumour in a mammal, disrupting neovasculature in a mammal, inhibiting endometriosis in a mammal, enhancing inhaled compound delivery in a mammal, enhancing adhesion of a foreign tissue implanted within a mammal, for enhancing/directing neurite outgrowth, and for ameliorating a spinal cord injury in a mammal. The cell adhesion modulating agent of the invention is useful for treating disease conditions that are dependent on angiogenesis and neovascularisation (e.g. psoriasis, diabetic retinopathy or dermatitis). The present amino acid sequence represents a Trp-containing CAR sequence of the invention.

QY 2 GYLWN 6
|::||
Db 1 GWVWN 5

RESULT 11
ID ADP05872 standard; peptide; 6 AA.
XX AC ADP05872;
XX 26-AUG-2004 (first entry)
XX Trp-containing cell adhesion recognition (CAR) sequence #37.
XX cell adhesion modulating agent;
KW desmosomal cadherin-mediated cell adhesion;
KW Trp-containing cell adhesion recognition sequence; CAR sequence;
KW desmosomal cadherin molecule; cancer metastasis; angiogenesis;
KW demyelinating neurological disorder; immune system modulation;
KW pregnancy prevention; vasopermeability; synaptic stability;
KW blood vessel regression; neurite outgrowth; spinal cord injury;
KW angiogenesis; neovascularisation; psoriasis; diabetic retinopathy;
KW dermatitis.
XX Unidentified.
OS WO2004048411-A2.
XX PN 10-JUN-2004.
XX PD 14-NOV-2003; 2003WO-IB006208.
XX PF 14-NOV-2002; 2002US-0426551P.
XX PR 14-NOV-2002; 2002US-0426689P.
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX PA Blaschuk OW, Michaud SD;
XX PI WPI; 2004-450349/42.
XX DR Cell adhesion modulating agent that modulates desmosomal cadherin-mediated cell adhesion, useful for inhibiting cancer metastasis, comprises Trp-containing cell adhesion recognition sequence of desmosomal cadherin molecule.
XX PT Disclosure; SEQ ID NO 49; 507pp; English.
XX PS The invention comprises a cell adhesion modulating agent that modulates desmosomal cadherin-mediated cell adhesion. The cell adhesion modulating agent comprises a Trp-containing cell adhesion recognition (CAR) sequence of a desmosomal cadherin molecule. The cell adhesion modulating agent of the invention is useful for: inhibiting cancer metastasis, inhibiting angiogenesis in a mammal, ameliorating a demyelinating neurological disorder in a mammal, modulating immune system of a mammal, preventing pregnancy in a mammal, increasing vasopermeability in a mammal, inhibiting synaptic stability in a mammal, stimulating blood vessel regression, increasing blood flow to a tumour in a mammal, disrupting neovasculature in a mammal, inhibiting endometriosis in a mammal, enhancing inhaled compound delivery in a mammal, enhancing adhesion of a foreign tissue implanted within a mammal, for enhancing/directing neurite outgrowth, and for ameliorating a spinal cord injury in a mammal. The cell adhesion modulating agent of the invention is useful for treating disease conditions that are dependent on angiogenesis and neovascularisation (e.g. psoriasis, diabetic retinopathy or dermatitis). The present amino acid sequence represents a Trp-containing CAR sequence of the invention.

CC of the invention.
XX
SQ Sequence 6 AA;

Query Match 65.0%; Score 26; DB 8; Length 6;
Best Local Similarity 60.0%; Pred. No. 2e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYLWN 6
|:|
Db 2 GWVWN 6

RESULT 12

AAR24717
ID AAR24717 standard; protein; 6 AA.

XX
AC AAR24717;

XX 25-MAR-2003 (revised)
DT 28-DEC-1992 (first entry)

XX Sequence of an anti-urokinase antibody heavy chain variable region chain
DE designated 'J'.

XX Chimeric monoclonal antibody; anti-urokinase antibody;
KW antithrombotic agent; myocardial infarction therapy.

XX Mus musculus.

XX EP491351-A2.

XX 24-JUN-1992.

XX 17-DEC-1991; 91EP-00121591.

XX 18-DEC-1990; 90JP-00413829.

XX 11-NOV-1991; 91JP-00294464.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Iwasa S, Tada H, Watanabe T;

XX WPI; 1992-209528/26.

XX Chimeric monoclonal antibodies - contain anti-human fibrin antibody light
PT and heavy chain variable and constant for treating thrombotic conditions
PT e.g. myocardial infarction.

XX Claim 21; Page 50; 87pp; English.

XX The inventors claim a chimeric monoclonal antibody which contains a
CC urokinase-recognising antibody heavy chain variable region contg. at least
CC one of the polypeptide chains G, H and I (AAR24717, R24718, AAR24719) and a
CC human antibody heavy chain constant region. The chimeric Abs can be used
CC both in vivo and in vitro and, since they have very low immunogenicity as
CC compared with mouse Abs, they can be administered to humans for
CC diagnostic and therapeutic purposes. They are also more stable and show a
CC longer half-life in the blood as compared with the original mouse Abs.
CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 6 AA;

Query Match 57.5%; Score 23; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 2e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YLWN 6
|:|
Db 3 YAWN 6

RESULT 13

AAW01150

ID AAW01150 standard; peptide; 6 AA.

XX
AC AAW01150;

XX 10-FEB-1997 (first entry)

XX MAb 1.4 heavy chain CDR (Mab binds type II phospholipase A2).

XX Monoclonal antibody; phospholipase; myocardial infarction; pancreatitis;
KW cerebral infarction; acute kidney failure; colitis; chronic rheumatism;
KW adult respiratory distress syndrome; cardiac shock; treatment;
KW preclinical testing; disease; hybridoma.

XX Mus musculus.

XX WO9620959-A1.

XX 11-JUL-1996.

XX 27-DEC-1995; 95WO-00340006.

XX 29-DEC-1994; 94JP-00340006.

XX (YAMA) YAMANOUCHI PHARM CO LTD.

XX Kawauchi Y, Takasaki J, Yasunaga T, Masuho Y;

XX WPI; 1996-333946/33.

XX Monoclonal antibody inhibiting type II phospholipase A2 activity - for
PT treatment of myocardial and cerebral infarction.

XX Claim 7; Page 42; 69pp; Japanese.

XX Monoclonal antibodies which inhibit type II phospholipase A2 are useful
CC in the treatment of myocardial infarction, cerebral infarction, acute
CC kidney failure, chronic rheumatism, cardiac shock, pancreatitis, adult
CC respiratory distress syndrome and colitis. The antibodies were generated
CC by immunising Balb/C mice with recombinant human type II phospholipase
CC A2. Spleen cells from the mice were fused with mouse myeloma P3U1
CC (P3x63Ag8.U1) and the hybridomas obtained were screened for phospholipase
CC A2 inhibitory activity. Active clones were isolated including 12H5, 1.4
CC and 10.1. These were cultured and the antibody isolated from the culture
CC supernatant by precipitation with ammonium sulphate and purification on a
CC column of protein A-Sepharose CL4B. Because the antibody acts on the
CC primate and mouse forms of enzyme as well as human it is particularly
CC suitable for preclinical testing. This peptide sequence corresponds to
CC the first complementary determining region of the heavy chain of the
CC monoclonal antibody isolated from the clone designated 1.4

XX Sequence 6 AA;

Query Match 57.5%; Score 23; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 2e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YLWN 6
|:|
Db 3 YAWN 6

RESULT 14

AAR98564

ID AAR98564 standard; peptide; 6 AA.

XX
AC AAR98564;

XX 25-MAR-2003 (revised)

DT 06-NOV-1996 (first entry)

XX N-terminus of 6-SFT 49 kDa subunit.

XX

```

KW Oligosaccharide production; sucrose-sucrose-fructosyl transferase;
KW sucrose-fructan-6-fructosyl transferase; SST; 6-SFT; barley; onion;
XX Hordeum vulgare; transgenic plant.
XX
OS Hordeum vulgare.
XX
PN WO9601904-A1.
XX
PD 25-JAN-1996.
XX
PF 07-JUL-1995; 95WO-NL000241.
XX
PR 08-JUL-1994; 94NL-00001140.
XX
PR 05-APR-1995; 95NL-01000064.
XX
XX (SCHE-) STICHTING SCHEIKUNDIG ONDERZOEK IN NEDER.
XX
XX Smeekens JCM, Ebekamp MJM, Geerts HAM, Weisbeek PJ;
XX
XX WPI; 1996-097634/10.
XX
XX Prodn. of oligo-saccharide(s) by transgenic plants - for use as sugar
XX substitutes, nutritional fibre and bifidogenic agents in food prods. and
XX animal feeds.
XX
XX Example 4; Fig 7; 64pp; English.
XX
XX Sucrose-fructan 6-fructosyl transferase, isolated from barley (Hordeum
XX vulgare), is a key enzyme for the biosynthesis of fructed fructans which
XX are typical for grasses. 6-SFT comprises 2 subunits/isoforms of 49 and 23
XX kDa resp. . The enzyme forms kestose from sucrose and bifurcose from
XX sucrose and isokestose. Transgenic plants contg. the cDNA can be used for
XX the prodn. of oligosaccharides that have more desirable properties
XX compared with the oligosaccharides prepared by known industrial
XX processes. An advantage of the method is that the chain length
XX distribution is narrower, with no or few free sugars occurring in the end
XX product. This means lower cariogenicity and lower energy value. The
XX present sequence is that of the N-terminal of the 6-SFT 49 kDa subunit.
XX (Updated on 25-MAR-2003 to correct PR field.)
XX
XX Sequence 6 AA;

Query Match 57.5%; Score 23; DB 2; Length 6;
Best Local Similarity 60.0%; Pred. No. 2e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGYLW 5
DB 2 GGFPW 6

RESULT 15
AAW39848
ID AAW39848 standard; peptide; 6 AA.
XX
XX AAW39848;
XX
XX 16-JUN-1998 (first entry)
XX
XX Heavy chain CDR1 of catalytic antibody 2A10.
XX
XX Variable domain; lambda light chain; catalytic antibody; degradation;
XX cocaine; cocaine transition state analogue; TSA; benzoic acid;
XX phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
XX overdose; addiction.
XX
XX Mus sp.
XX
XX WO9749800-A1.
XX
XX 31-DEC-1997.
XX
XX 25-JUN-1997; 97WO-US010965.

XX 25-JUN-1996; 96US-00672345.
XX (UYCO ) UNIV COLUMBIA NEW YORK.
XX
XX Landry DW;
XX
XX WPI; 1998-077166/07.
XX
XX New catalytic antibodies able to decompose cocaine, single-chain
XX analogues - used to treat cocaine overdose and addiction, required in far
XX smaller doses than antibodies that antagonise cocaine by simply binding.
XX
XX Claim 15; Page 89; 147pp; English.
XX
XX AAW39848-50 represent the sequences of the heavy chain complementarity
XX determining regions (CDRs) of the catalytic antibody 2A10, which is able
XX to degrade cocaine. A series of cocaine transition state analogues (TSAs)
XX were prepared and used to immunise mice for production of hybridomas.
XX Catalytic antibodies were identified by their capacity to release 3H-
XX benzoic acid from 3H-phenyl cocaine. The 2A10 antibody was identified
XX using TSA1, which is an immunogenic conjugate of a phosphate monoester
XX transition state analogue. Antibody 2A10 has a per minute Kcat of 0.011.
XX The antibodies reduce the concentration of cocaine in a subject, and are
XX used particularly for the treatment of an overdose. They are also used
XX for treating addiction (by reducing the in vivo concentration that can be
XX achieved)
XX
XX Sequence 6 AA;

Query Match 57.5%; Score 23; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 2e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YLWN 6
DB 3 YAWN 6

Search completed: December 30, 2005, 15:34:05
Job time : 183 secs

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2005, 15:24:08 ; Search time 37 Seconds
(without alignments)
15.603 Million cell updates/sec

Title: US-10-735-916A-8

Perfect score: 40

Sequence: 1 GGYLWN 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 110

Minimum DB seq length: 6

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	40.0	6	2 PT0519	T-cell receptor be
2	15	37.5	6	2 B34835	dnaA protein - Pse
3	13	32.5	6	2 A61411	ameletin - rat
4	12	30.0	6	2 JU0355	lipopeptide WS1279
5	12	30.0	6	2 PT0514	T-cell receptor be
6	12	30.0	6	2 PT0512	T-cell receptor be
7	12	30.0	6	2 PT0720	T-cell receptor be
8	12	30.0	6	2 PT0560	T-cell receptor be
9	12	30.0	6	2 PT0723	T-cell receptor be
10	12	30.0	6	2 PT0727	T-cell receptor be
11	12	30.0	6	2 PT0730	T-cell receptor be
12	12	30.0	6	2 P41946	T-cell receptor ga
13	12	30.0	6	2 PT0605	T-cell receptor be
14	11	27.5	6	2 S66195	alcohol dehydrogen
15	11	27.5	6	2 B44510	hypothetical prote
16	11	27.5	6	2 A31263	dihydrofolate redu
17	11	27.5	6	2 B31263	dihydrofolate redu
18	11	27.5	6	2 B35640	carebollar degener
19	11	27.5	6	2 PT0629	T-cell receptor be
20	11	27.5	6	2 PT0532	T-cell receptor be
21	11	27.5	6	2 PT0637	T-cell receptor be
22	11	27.5	6	2 PT0641	T-cell receptor be
23	11	27.5	6	2 PT0726	T-cell receptor be
24	11	27.5	6	2 PD0028	pev-kinin 2 - pena
25	11	27.5	6	2 A61068	locustakinin - mig
26	11	27.5	6	4 I79564	hypothetical TCU3
27	10	25.0	6	2 JN0861	peptidyl-dipeptida
28	9	22.5	6	2 A41946	T-cell receptor ga
29	9	22.5	6	2 A43129	neuropeptide GNPFR

ALIGNMENTS

RESULT 1

PT0519

T-cell receptor beta chain V-D-J region (100-4C) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0519

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0519

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-6 <PEE>

A;Cross-references: UNIPARC:UPI000017C7BE

A;Experimental source: adult thymus, strain BALB/c

C;Keywords: T-cell receptor

Query Match 40.0%; Score 16; DB 2; Length 6;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LWN 6

Db 4 LWD 6

RESULT 2

B34835

dnaA protein - Pseudomonas aeruginosa (fragment)

C:Species: Pseudomonas aeruginosa

C>Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 08-Oct-1999

C:Accession: B34835

R;Yee, T.W.; Smith, D.W.

Proc. Natl. Acad. Sci. U.S.A. 87, 1278-1282, 1990

A;Title: Pseudomonas chromosomal replication origins: a bacterial class distinct from

A;Reference number: A34835; MUID:90160310; PMID:2106132

A;Accession: B34835

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-6 <YEE>

A;Cross-references: UNIPARC:UPI000011EAEC; GB:M30125; NID:G151419; PIDN:AAA25916.1; PIC

C;Keywords: DNA binding

Query Match 37.5%; Score 15; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5

Db 5 LW 6

sarcosine dehydrog
collagen alpha 1(I
hydrogensulfite re
protamine P1 - gor
laminin B1 - weste
RNA-directed DNA p
halo-toxin - Pseud
phosphoglycerate t
hydrogensulfite re
mesquitecoidal toxi
parasporal crystal
jacalin beta-II ch
angiotensin-conver
variant surface gly
antineoplastic gly
H4 histone - Afric

30 8 20.0 6 2 A61419
31 8 20.0 6 2 B56979
32 7 17.5 6 2 S11556
33 7 17.5 6 2 I37027
34 7 17.5 6 2 I49421
35 6 15.0 6 2 A35890
36 6 15.0 6 2 A61049
37 6 15.0 6 2 T11779
38 6 15.0 6 2 S11024
39 6 15.0 6 2 A44916
40 6 15.0 6 2 S14159
41 6 15.0 6 2 S29637
42 6 15.0 6 2 PQ0008
43 6 15.0 6 2 B61512
44 6 15.0 6 2 A60494
45 6 15.0 6 2 I51434

```

RESULT 3
A61411
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 05-Oct-2004
C;Accession: A61411
R;Burzynski, S.R.
Anal. Biochem. 70, 359-365, 1976
A;Title: Sequential analysis in subnanomolar amounts of peptides. Determination of the
A;Reference number: A61411; MUID:76182447; PMID:1267130
A;Accession: A61411
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-6 <BUR>
A;Cross-references: UNIPARC:UPI000017A501
C;Keywords: pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 32.5%; Score 13; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GY 3
   ||
Db 3 GY 4

RESULT 4
JU0355
C;Species: Streptomyces willmorei
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: JU0355
R;Iwada, Y.; Okada, Y.; Tanaka, M.; Shigematsu, N.; Hori, Y.; Goto, T.; Hashimoto, M.
Chem. Pharm. Bull. 39, 607-611, 1991
A;Title: Structure and synthesis of an immunoactive lipopeptide, WS1279, of microbial or
A;Reference number: JU0355; MUID:91300586; PMID:2070441
A;Accession: JU0355
A;Molecule type: protein
A;Residues: 1-6 <TSU>
A;Cross-references: UNIPARC:UPI000017AB43
A;Note: the structure was confirmed by synthesis
C;Keywords: blocked amino end; lipopeptide
F;1/Binding site: sn-2,3-diacylglycerol (Cys) (covalent) #status experimental
F;1/Modified site: fatty acylated amino end (Cys) #status experimental

Query Match 30.0%; Score 12; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GG 2
   ||
Db 4 GG 5

RESULT 5
PT0514
T-cell receptor beta chain V-D-J region (100-4AC) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0514
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0514
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-6 <FEE>
A;Cross-references: UNIPARC:UPI000017C7B4
A;Experimental source: adult thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 30.0%; Score 12; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GG 2
   ||
Db 5 GG 6

RESULT 6
PT0512
T-cell receptor beta chain V-D-J region (100-4D) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0512
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0512
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-6 <FEE>
A;Cross-references: UNIPARC:UPI000017C7BF
A;Experimental source: adult thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 30.0%; Score 12; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GG 2
   ||
Db 3 GG 4

RESULT 7
PT0720
T-cell receptor beta chain V-D-J region (126-1BB) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0548; PT0720
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0548
A;Accession: PT0548
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-6 <FEE>
A;Cross-references: UNIPARC:UPI000017C809
A;Experimental source: day 18 fetal thymus, strain BALB/c, clone 126-1BB
A;Accession: PT0720
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-6 <FE2>
A;Cross-references: UNIPARC:UPI000017C809
A;Experimental source: newborn thymus, strain BALB/c, clone 140-2J
C;Keywords: T-cell receptor

Query Match 30.0%; Score 12; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GG 2
   ||
Db 5 GG 6

RESULT 8
PT0560
T-cell receptor beta chain V-D-J region (126-1CE) - mouse (fragment)

```

```

Query Match 30.0%; Score 12; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GG 2
   ||
Db 3 GG 4

RESULT 6
PT0512
T-cell receptor beta chain V-D-J region (100-4D) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0512
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0512
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-6 <FEE>
A;Cross-references: UNIPARC:UPI000017C7BF
A;Experimental source: adult thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 30.0%; Score 12; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GG 2
   ||
Db 3 GG 4

RESULT 7
PT0720
T-cell receptor beta chain V-D-J region (126-1BB) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0548; PT0720
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0548
A;Accession: PT0548
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-6 <FEE>
A;Cross-references: UNIPARC:UPI000017C809
A;Experimental source: day 18 fetal thymus, strain BALB/c, clone 126-1BB
A;Accession: PT0720
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-6 <FE2>
A;Cross-references: UNIPARC:UPI000017C809
A;Experimental source: newborn thymus, strain BALB/c, clone 140-2J
C;Keywords: T-cell receptor

Query Match 30.0%; Score 12; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GG 2
   ||
Db 5 GG 6

RESULT 8
PT0560
T-cell receptor beta chain V-D-J region (126-1CE) - mouse (fragment)

```

C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0560
R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0560
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-6 <PEE>
A;Cross-references: UNIPARC:UPI000017C811
A;Experimental source: day 18 fetal thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 30.0%; Score 12; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GG 2
||
Db 5 GG 6

RESULT 9

PT0723
T-cell receptor beta chain V-D-J region (135-1AF) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0723
R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0723

A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-6 <PEE>
A;Cross-references: UNIPARC:UPI000017C819
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 30.0%; Score 12; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GG 2
||
Db 5 GG 6

RESULT 10

PT0727
T-cell receptor beta chain V-D-J region (161-2F) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0727
R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0727

A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-6 <PEE>
A;Cross-references: UNIPARC:UPI000017C844
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 30.0%; Score 12; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GG 2
||
Db 3 GG 4

RESULT 11

PT0730
T-cell receptor beta chain V-D-J region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0730; PT0594; PT0731
R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0730

A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-6 <PEE>
A;Cross-references: UNIPARC:UPI000017C850
A;Experimental source: newborn thymus, strain BALB/c (clone 163-2C)
A;Accession: PT0594

A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-6 <PE2>
A;Cross-references: UNIPARC:UPI000017C850
A;Experimental source: day 19 fetal thymus, strain BALB/c (clone 159-2F)
A;Accession: PT0731
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-6 <PE3>
A;Cross-references: UNIPARC:UPI000017C850
A;Experimental source: newborn thymus, strain BALB/c (clone 165-3E)
C;Keywords: T-cell receptor

Query Match 30.0%; Score 12; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GG 2
||
Db 5 GG 6

RESULT 12

F41946
T-cell receptor gamma chain (1a.27) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: F41946
R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991

A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma
A;Reference number: A41946; MUID:92049316; PMID:1658619
A;Accession: F41946
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-6 <WHE>
A;Cross-references: UNIPARC:UPI000017C862
C;Keywords: T-cell receptor

Query Match 30.0%; Score 12; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
:|
Db 4 VW 5

RESULT 13

PT0605
T-cell receptor beta chain V-D-J region (120-1L) - mouse (fragment)

C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C;Accession: PT0605
R;Feeney, A.J.
J;Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0605
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-6 <FEE>
A;Cross-references: UNIPROT:O70566; UNIPARC:UPI000017C7DD
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 30.0%; Score 12; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GG 2
||
Db 5 GG 6

RESULT 14
S66195
alcohol dehydrogenase (EC 1.1.1.1) class III low affinity form - cod (Gadus sp.) (fragment)
C;Species: Gadus sp. (cod)
C;Date: 13-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 12-Jun-1998
C;Accession: S66195
R;Hjelmqvist, L.; Hackett, M.; Shafqat, J.; Danielsson, O.; Iida, J.; Hendrickson, R.C.; FEBS Lett. 367, 237-240, 1995
A;Title: Multiplicity of N-terminal structures of medium-chain alcohol dehydrogenases. M nzyme
A;Reference number: S66191; MUID:95331382; PMID:7607314
A;Accession: S66195
A;Molecule type: protein
A;Residues: 1-6 <HJE>
A;Cross-references: UNIPARC:UPI0000171EA5
C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C;Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 27.5%; Score 11; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
|
Db 5 W 5

RESULT 15
B44510
hypothetical protein C (mler 3' region) - Lactococcus lactis (fragment)
C;Species: Lactococcus lactis
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 30-Sep-1993
C;Accession: B44510
R;Renault, P.; Gaillardin, C.; Heslot, H.
J. Bacteriol. 171, 3108-3114, 1989
A;Title: Product of the Lactococcus lactis gene required for malolactic fermentation is
A;Reference number: A44510; MUID:89255069; PMID:2498286
A;Accession: B44510
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-6 <REN>
A;Cross-references: UNIPARC:UPI000017AC46; EMBL:M90762

Query Match 27.5%; Score 11; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YL 4
||

Db 5 YL 6

Search completed: December 30, 2005, 15:34:47
Job time : 38 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2005, 15:14:23 ; Search time 229 Seconds
(without alignments)
18.485 Million cell updates/sec

Title: US-10-735-916A-8
Perfect score: 40
Sequence: 1 GGYLWN 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 19

Minimum DB seq length: 6
Maximum DB seq length: 6

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13	32.5	6	E101_LITRU	P82096 litoria rub
2	11	27.5	6	L0K1_LOCMI	P41491 locusta mig
3	9	22.5	6	FARP_MONEX	P41966 moniezia ex
4	8	20.0	6	ASP2_LACSN	P82655 lactobacill
5	7	17.5	6	QVM_LEPDE	P42985 leptinotars
6	6	15.0	6	CIP1_MYTED	P13736 mytilus edu
7	6	15.0	6	CIP2_MYTED	P13737 mytilus edu
8	6	15.0	6	SNAP_SEPOF	P83569 sepiia offic
9	6	15.0	6	TMOF_SARBU	P41495 sarcophaga
10	6	15.0	6	UN06_CLOPA	P81351 clostridium
11	6	15.0	6	VP19_HHV1K	P23210 human herpe
12	6	15.0	6	P83533_LACSN	P83533 lactobacill
13	4	10.0	6	ACPH_RABIT	P25154 oryctolagus
14	4	10.0	6	TRP1_PSEPU	P36414 pseudomonas
15	4	10.0	6	P82541_SPIOL	P82541 spinacia ol
16	3	7.5	6	PYF1_PENMO	P84005 penaeus mon
17	2	5.0	6	MAF_SCHWA	P84575 schistosoma
18	2	5.0	6	P82181_SPIOL	P82181 spinacia ol
19	2	5.0	6	P82182_SPIOL	P82182 spinacia ol

ALIGNMENTS

RESULT 1
E101_LITRU
ID E101_LITRU STANDARD; PRT; 6 AA.
AC P82096;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Electrin-1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
Litoria electrica. Comparison with the skin peptides from Litoria
rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the skin glands.
CC -----
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CC removed.
CC -----
CC Amidation; Amphibian defense peptide; Direct protein sequencing.
KW MOD_RES 6
FT MTHIONINE AMIDE.
SQ SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;

Query Match 32.5%; Score 13; DB 1; Length 6;
Best Local Similarity 50.0%; Pred. No. 2.2e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
DB 4 IW 5

RESULT 2
L0K1_LOCMI
ID L0K1_LOCMI STANDARD; PRT; 6 AA.
AC P41491;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
OS Locustakinin I.
OC Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=92262851; PubMed=1585017; DOI=10.1016/0167-0115(92)90063-2;
RA Schoofs L., Holman G.M., Proost P., van Damme J., Hayes T.K.,
de Loof A.;
RT "Locustakinin, a novel myotropic peptide from Locusta migratoria,
isolation, primary structure and synthesis.";
Regul. Pept. 37:49-57(1992).
CC -1- FUNCTION: Myotropic peptide. May be important in the stimulation
CC of ion transport and inhibition of diuretic activity in Malpighian
CC tubules.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -----
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CC removed.
CC -----
DR PIR; A61068; A61068.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 6
SQ SEQUENCE 6 AA; 654 MW; 686365A5B9CDB000 CRC64;

```

Query Match      27.5%; Score 11; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 W 5
DB      5 W 5

RESULT 3
FARP_MONEX
ID FARP_MONEX STANDARD; PRT; 6 AA.
AC P41966;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE FMRamide-like neuropeptide GNFRF-amide.
OS Moniezia expansa (Sheep tapeworm).
OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
OC Cyclophyllidae; Anoplocephalidae; Moniezia.
OX NCBI_TaxID=28841;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=93312289; PubMed=8323531;
RA Maule A.G., Shaw C., Halton D.W., Thim L.;
RT "GNFRFamide: a novel FMRamide-immunoreactive peptide isolated from
RL Biochem. Biophys. Res. Commun. 193:1054-1060(1993).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
family.
CC -----
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CC removed.
CC -----
CC PIR; A43129; A43129.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD RES 6 6 Phenylalanine amide.
SQ SEQUENCE 6 AA; 787 MW; 69D409C9C4481000 CRC64;

Query Match      22.5%; Score 9; DB 1; Length 6;
Best Local Similarity 33.3%; Pred. No. 2.2e+06;
Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGY 3
DB      1 GNF 3

RESULT 4
ASP2_LACSN
ID ASP2_LACSN STANDARD; PRT; 6 AA.
AC P82655;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Acid shock protein 2 (Fragment).
OS Lactobacillus sanfranciscensis [Lactobacillus sanfrancisco].
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1625;
RN [1]
RP PROTEIN SEQUENCE.
RX STRAIN=CB1;
RX MEDLINE=21322712; PubMed=11429463;
RA De Angelis M., Bini L., Pallini V., Cocconcelli P.S., Gobetti M.;
RT "The acid-stress response in Lactobacillus sanfranciscensis CB1."
RL Microbiology 147:1863-1873(2001).
CC -!- INDUCTION: Overexpressed in acid environments.

Query Match      20.0%; Score 8; DB 1; Length 6;
Best Local Similarity 50.0%; Pred. No. 2.2e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      5 WN 6
DB      4 YN 5

RESULT 5
OVM_LPDDE
ID OVM_LPDDE STANDARD; PRT; 6 AA.
AC P42385;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Oviductal motility stimulating peptide (LeD-OVM).
OS Leptinotarsa decemlineata (Colorado potato beetle).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
OC Chrysomeloidea; Chrysomelidae; Chrysomelinae; Doryphorini;
OC Leptinotarsa.
OX NCBI_TaxID=7539;
RN [1]
RP PROTEIN SEQUENCE, AND SYNTHESIS.
RX TISSUS=Head;
RX MEDLINE=91271080; PubMed=2052497; DOI=10.1016/0196-9781(91)90162-I;
RA Spittaels K., Schoofs L., Grauwels L., Smet H., van Damme J.,
RA Proost P., Torrekens S., de Loof A.;
RT "Isolation, identification and synthesis of novel oviductal motility
RT stimulating head peptide in the Colorado potato beetle, Leptinotarsa
RT decemlineata."
RL Peptides 12:31-36(1991).
CC -!- FUNCTION: Myotropic peptide. Stimulates the contractions of the
oviduct.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD RES 6 6 Glutamic acid 1-amide.
SQ SEQUENCE 6 AA; 720 MW; 6B07632B5DD03000 CRC64;

Query Match      17.5%; Score 7; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 Y 3
DB      3 Y 3

RESULT 6
CIP1_MYTED
ID CIP1_MYTED STANDARD; PRT; 6 AA.
AC P13736;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-FEB-2005 (Rel. 46, Last annotation update)

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DE Contraction-inhibiting peptide I (MIP I).
 OS Mytilus edulis (Blue mussel).
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
 OC Mytiloidea; Mytilidae; Mytilinae; Mytilus.
 OX NCBI_TaxID=6550;
 RN [1]
 RP PROTEIN SEQUENCE.
 RC TISSUE=Pedal ganglion;
 RX MEDLINE=88240357; PubMed=3377776;
 RA Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;
 RT "Structures and actions of Mytilus inhibitory peptides."
 RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
 CC -1- FUNCTION: Inhibitory action on contractions in several molluscan
 CC muscles.
 CC -1- SIMILARITY: To M. edulis MIP II.
 CC -----
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 CC -----
 CC PIR; A27696; A27696.
 KW Amidation; Direct protein sequencing; Hormone.
 FT MOD RES 6 6 Valine amide.
 SQ SEQUENCE 6 AA; 637 MW; 72C9C68775B81000 CRC64;
 Query Match 15.0%; Score 6; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 G 1
 DB 1 G 1
 RESULT 7
 CIP2_MYTED
 ID CIP2_MYTED STANDARD; PRT; 6 AA.
 AC P13737;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-FEB-2005 (Rel. 46, Last annotation update)
 DE Contraction-inhibiting peptide II (MIP II).
 OS Mytilus edulis (Blue mussel).
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
 OC Mytiloidea; Mytilidae; Mytilinae; Mytilus.
 OX NCBI_TaxID=6550;
 RN [1]
 RP PROTEIN SEQUENCE.
 RC TISSUE=Pedal ganglion;
 RX MEDLINE=88240357; PubMed=3377776;
 RA Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;
 RT "Structures and actions of Mytilus inhibitory peptides."
 RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
 CC -1- FUNCTION: Inhibitory action on contractions in several molluscan
 CC muscles.
 CC -1- SIMILARITY: To M. edulis MIP I.
 CC -----
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 CC -----
 CC PIR; B27696; B27696.
 KW Amidation; Direct protein sequencing; Hormone.
 FT MOD RES 6 6 Valine amide.
 SQ SEQUENCE 6 AA; 621 MW; 72C9C6876DD81000 CRC64;
 Query Match 15.0%; Score 6; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 G 1
 DB 1 G 1
 RESULT 8
 SAPP_SEPOF
 ID SAPP_SEPOF STANDARD; PRT; 6 AA.
 AC P83569;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Sperm attracting peptide SepSAP.
 OS Sepia officinalis (Common cuttlefish).
 OC Eukaryota; Metazoa; Cephalopoda; Coleoidea; Neocoleoidea;
 OC Decapodiformes; Sepioidae; Sepiidae; Sepia.
 OX NCBI_TaxID=6610;
 RN [1]
 RP PROTEIN SEQUENCE, FUNCTION, DEVELOPMENTAL STAGE, MASS SPECTROMETRY,
 RP AND AMIDATION.
 RC TISSUE=Egg;
 RX MEDLINE=22197108; PubMed=12207899; DOI=10.1016/S0006-291X(02)02036-3;
 RA Zatylny C., Marvin L., Gagnon J., Henry J.;
 RT "Fertilization in Sepia officinalis: the first mollusk sperm-
 RT attracting peptide."
 RL Biochem. Biophys. Res. Commun. 296:1186-1193(2002).
 CC -1- FUNCTION: Attracts sperm increasing the chances of gamete
 CC collision.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DEVELOPMENTAL STAGE: First appears in the ovarian follicles during
 CC vitellogenesis. Accumulates in the oocytes before being secreted
 CC during fertilization. Expression continues in the embedded oocyte.
 CC Accumulates in the egg capsule after fertilization.
 CC -1- MASS SPECTROMETRY: MW=596.6; METHOD=MALDI; RANGE=1-6; NOTE=Ref. 1.
 CC -----
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 CC -----
 KW Amidation; Direct protein sequencing.
 FT MOD RES 6 6 Valine amide.
 SQ SEQUENCE 6 AA; 597 MW; 72C8676AA0470000 CRC64;
 Query Match 15.0%; Score 6; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 G 1
 DB 5 G 5
 RESULT 9
 TMOP_SARBU
 ID TMOP_SARBU STANDARD; PRT; 6 AA.
 AC P41495;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Trypsin-modulating oostatic factor (TMOF)
 OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Sarcophagidae; Sarcophaga; Neobellieria.
 OX NCBI_TaxID=7385;
 RN [1]
 RP PROTEIN SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Ovary;
 RX MEDLINE=94211930; PubMed=8159807; DOI=10.1016/0167-0115(94)90192-9;
 RA Bylemans D., Borovsky D., Hunt D.F., Shabanowitz J., Grauwels L.,

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RA de Loof A.;
RT "Sequencing and characterization of trypsin modulating oostatic factor
RT (TMOF) from the ovaries of the grey fleshfly, Neobellieria
RT (Sarcophaga) bullata.";
RL Regul. Pept. 50:61-72(1994).
CC -!- FUNCTION: Has an oostatic activity. Inhibits trypsin biosynthesis
CC in the midgut which indirectly reduces the vitellogenin
CC concentration in the hemolymph resulting in inhibition of oocyte
CC development.
CC -!- DEVELOPMENTAL STAGE: Synthesized and released from follicular
CC epithelium after a blood meal.
CC -----
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CC -----
KW Direct protein sequencing; Hormone.
SQ SEQUENCE 6 AA; 695 MW; 61E72451B7642000 CRC64;

Query Match 15.0%; Score 6; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 N 6
Db 1 N 1

RESULT 10
UN06_CLOPA STANDARD; PRT; 6 AA.
AC P81351;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE Unknown protein CP 6 from 2D-PAGE (Fragment).
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP STRAIN=W5;
RC PROTEIN SEQUENCE.
RX Flengsrud R., Skjeldal L.;
RX MEDLINE=98291870; PubMed=9629918;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 5.0, its MW is: 75.9 kDa.
CC -----
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CC -----
KW Direct protein sequencing.
FT NON_TER 6
SQ SEQUENCE 6 AA; 658 MW; 605B1DC1A45A8000 CRC64;

Query Match 15.0%; Score 6; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 N 6
Db 2 N 2

RESULT 11

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VPI9_HHV1K
ID VPI9_HHV1K STANDARD; PRT; 6 AA.
AC P23210;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Capsid assembly and DNA maturation protein (Viron protein UL38)
DE (Capsid protein VPI9C) (Fragment).
GN Name=UL38;
OS Human herpesvirus 1 (strain KOS) (HHV-1) (Human herpes simplex virus
1).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10306;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=91101287; PubMed=1846198;
RX Flanagan W.M., Papavassiliou A.G., Rice M., Hecht L.B.,
RA Silverstein S., Wagner E.K.;
RT "Analysis of the herpes simplex virus type 1 promoter controlling the
RT expression of UL38, a true late gene involved in capsid assembly.";
RL J. Virol. 65:769-786(1991).
CC -!- FUNCTION: Component of the basal layer in which the capsids are
CC embedded. Binds DNA.
CC -!- SIMILARITY: Belongs to the herpesviruses VPI9C family.
CC -----
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CC -----
DR EMBL; M57646; AAA45830.1; -; Genomic DNA.
KW Capsid protein; DNA packaging; DNA-binding; Structural protein.
FT NON_TER 6
SQ SEQUENCE 6 AA; 703 MW; 67376451A336F000 CRC64;

Query Match 15.0%; Score 6; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 N 6
Db 4 N 4

RESULT 12
P83533_LACSN
ID P83533_LACSN PRELIMINARY; PRT; 6 AA.
AC P83533;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Unknown protein from 2D-page (Fragment).
OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1625;
RN [1]
RP PROTEIN SEQUENCE.
RX STRAIN=DSM 20451;
RX PubMed=12112860;
RX DOI=10.1002/1615-9861(200206)216:7655::AID-PROT76553.0.CO;2-V;
RA Drews O., Weiss W., Reil G., Parlar H., Wait R., Goerg A.;
RT "High pressure effects step-wise altered protein expression in
RT Lactobacillus sanfranciscensis.";
RL Proteomics 2:765-774(2002).
CC -!- MISCELLANEOUS: On the 2D-gel the determined MW of this unknown
CC protein is: 15 kDa.
CC NON_TER 1
FT NON_TER 1
SQ SEQUENCE 6 AA; 590 MW; 6DDDD452D1AAC000 CRC64;

```

Query Match 15.0%; Score 6; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 N 6
DB 4 N 4

RESULT 13

ACPH_RABIT STANDARD; PRT; 6 AA.
ID P25154;
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-FEB-2005 (Rel. 46, Last annotation update)
DE Acylamino-acid-releasing enzyme (EC 3.4.19.1) (AARE) (Acyl-peptide
hydrolase) (APH) (Acylaminoacyl-peptidase) (Fragment).
GN Names=APRH;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]

PROTEIN SEQUENCE.

TISSUE=Muscle;
MEDLINE=92222120; PubMed=1807161;
RA Krishna R.G., Chin C.C.Q., Wolf F.;
RT "N-terminal sequence analysis of N alpha-acetylated proteins after
unblocking with N-acetylaminoacyl-peptide hydrolase.";
RL Anal. Biochem. 199;45:50(1991).
CC -1- FUNCTION: This enzyme catalyzes the hydrolysis of the N-terminal
peptide bond of an N-acetylated peptide to generate an N-
acetylated amino acid and a peptide with a free N-terminus. It
preferentially cleaves off Ac-Ala, Ac-Met and Ac-Ser.
CC -1- CATALYTIC ACTIVITY: Cleavage of an N-acetyl or N-formyl amino acid
from the N-terminus of a polypeptide.
CC -1- SUBUNIT: Homotetramer.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the peptidase S9C family.

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removed.

PIR; A49792; A49792.
InterPro; IPR002471; Pept S9 AS.
DR PROSITE; PS00708; PRO_ENDOPEP_SER; PARTIAL.
KW Acetylation; Direct protein sequencing; Hydrolase.
FT MOD_RES 1 1 N-acetylmethionine.
FT NON_TER 6 6
SQ SEQUENCE 6 AA; 775 MW; 6732D6C40B16F000 CRC64;

Query Match 10.0%; Score 4; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4
DB 6 L 6

RESULT 14

TRPI_PSEPU STANDARD; PRT; 6 AA.
ID P36414;
AC P36414;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE HTH-type transcriptional regulator trpi (TrpBA operon transcriptional

activator) (Fragment).
DE Name=trpi;
GN Pseudomonas putida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=303;
RN [1]
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=PPG1 C18;
RX MEDLINE=89335826; PubMed=2503057; DOI=10.1016/0300-9084(89)90183-1;
RA Eberly L., Crawford I.P.;
RT "DNA sequence of the tryptophan synthase genes of Pseudomonas
putida.";
RL Biochimie 71:521-531(1989).
CC -1- FUNCTION: Activates the expression of the trpBA genes encoding the
two tryptophan synthase subunits. In the absence of the inducer
(indoleglycerol phosphate), trpi binds upstream of the trpAB
operon, overlapping its own promoter region.
CC -1- SIMILARITY: Contains 1 HTH lyseR-type DNA-binding domain.

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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.

EMBL; X13299; CAA31660.1; -; Genomic_DNA.
InterPro; IPR000847; HTH_LyseR.
DR PROSITE; PS00931; HTH_LyseR; PARTIAL.
KW Activator; Amino-acid biosynthesis; Aromatic amino acid biosynthesis;
KW DNA-binding; Transcription; Transcription regulation;
KW Tryptophan biosynthesis.
FT NON_TER 6 6
SQ SEQUENCE 6 AA; 683 MW; 77672AA1EDD6F000 CRC64;

Query Match 10.0%; Score 4; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4
DB 5 L 5

RESULT 15

P82541_SPIOL PRELIMINARY; PRT; 6 AA.
ID P82541_SPIOL PRELIMINARY; PRT; 6 AA.
AC P82541;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Chloroplast 30S ribosomal protein S19 beta (Fragment).
OS Spinacia oleracea (Spinach).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Caryophyllales; Amaranthaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]

PROTEIN SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC STRAIN=cv. ALWARO; TISSUE=Leaf;
RX MEDLINE=20435797; PubMed=10874039; DOI=10.1074/jbc.M004350200;
RA Yamaguchi K., von Knoblauch K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in
the 30S subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 275:28455-28465(2000).

CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -1- MASS SPECTROMETRY: MW=10477.0; METHOD=ELECTROSPRAY.
CC -1- MASS SPECTROMETRY: MW=10495; METHOD=WALDI.
CC -1- MISCELLANEOUS: S19 ALPHA AND BETA FORMS DIFFER IN P1. S19 BETA
FORM IS THE MINOR BASIC FORM.

CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 12 kDa.
CC -!- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0019843; F:rRNA binding; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR InterPro; IPR002222; Ribosomal_S19.
DR PROSITE; PS00323; RIBOSOMAL_S19; PARTIAL.
KW Chloroplast; Ribosomal protein; rRNA-binding.
FT NON_TER 6
SQ SEQUENCE 6 AA; 732 MW; 63333735A411C000 CRC64;

Query Match 10.0%; Score 4; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4
Db 4 L 4

Search completed: December 30, 2005, 15:30:57
Job time : 230 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2005, 15:26:49 ; Search time 45 Seconds
(without alignments)
11.023 Million cell updates/sec

Title: US-10-735-916A-8
Perfect score: 40
Sequence: 1 GGYLWN 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 19666

Minimum DB seq length: 6
Maximum DB seq length: 6

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5 COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6 COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PTUS COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES						
Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	23	57.5	6	1	US-08-672-345C-52	Sequence 52, Appl
2	23	57.5	6	2	US-09-214-095D-52	Sequence 52, Appl
3	23	57.5	6	2	US-09-940-727B-52	Sequence 52, Appl
4	22	55.0	6	1	US-08-089-994A-2	Sequence 2, Appli
5	22	55.0	6	1	US-09-127-574-14	Sequence 14, Appl
6	22	55.0	6	2	US-09-315-304B-1588	Sequence 1588, Ap
7	22	55.0	6	2	US-09-350-325-48	Sequence 48, Appl
8	22	55.0	6	2	US-09-350-641C-1588	Sequence 1588, Ap
9	22	55.0	6	4	PCT-US94-07605-2	Sequence 2, Appli
10	21	52.5	6	1	US-08-073-028-45	Sequence 45, Appl
11	21	52.5	6	1	US-08-785-571-9	Sequence 9, Appli
12	21	52.5	6	2	US-08-336-553A-32	Sequence 32, Appl
13	21	52.5	6	2	US-08-554-616-45	Sequence 45, Appl
14	21	52.5	6	2	US-08-439-157-32	Sequence 32, Appl
15	21	52.5	6	2	US-09-437-895-32	Sequence 32, Appl
16	21	52.5	6	2	US-09-515-965A-1658	Sequence 1658, Ap
17	21	52.5	6	2	US-09-350-841A-1688	Sequence 1688, Ap
18	21	52.5	6	2	US-09-211-715-99	Sequence 99, Appl
19	21	52.5	6	2	US-09-211-715-155	Sequence 155, App
20	21	52.5	6	2	US-09-578-063-65	Sequence 65, Appl
21	21	52.5	6	2	US-10-005-305-37	Sequence 37, Appl
22	21	52.5	6	2	US-10-005-305-94	Sequence 94, Appl
23	21	52.5	6	4	PCT-US93-06734-9	Sequence 9, Appli
24	20	50.0	6	1	US-08-024-253-11	Sequence 11, Appl
25	20	50.0	6	1	US-08-482-228-186	Sequence 186, App
26	20	50.0	6	2	US-08-482-528-186	Sequence 186, App
27	20	50.0	6	2	US-09-620-091-470	Sequence 470, App

28	20	50.0	6	2	US-09-620-091-471	Sequence 471, App
29	19	47.5	6	1	US-07-822-924-9	Sequence 9, Appli
30	19	47.5	6	1	US-07-805-727-3	Sequence 3, Appli
31	19	47.5	6	1	US-07-805-727-7	Sequence 7, Appli
32	19	47.5	6	1	US-07-718-577-5	Sequence 5, Appli
33	19	47.5	6	1	US-07-969-307A-11	Sequence 11, Appli
34	19	47.5	6	1	US-08-390-272-7	Sequence 7, Appli
35	19	47.5	6	1	US-07-973-235A-10	Sequence 10, Appl
36	19	47.5	6	1	US-07-802-667-33	Sequence 33, Appl
37	19	47.5	6	1	US-08-351-058A-9	Sequence 9, Appli
38	19	47.5	6	1	US-07-943-709-11	Sequence 11, Appl
39	19	47.5	6	1	US-07-943-709-12	Sequence 12, Appl
40	19	47.5	6	1	US-07-943-709-17	Sequence 17, Appl
41	19	47.5	6	1	US-08-227-184A-4	Sequence 4, Appli
42	19	47.5	6	1	US-08-487-890A-82	Sequence 82, Appl
43	19	47.5	6	1	US-08-209-747-56	Sequence 56, Appl
44	19	47.5	6	1	US-08-388-321-7	Sequence 7, Appli
45	19	47.5	6	1	US-08-466-632-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-08-672-345C-52
; Sequence 52, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-52

Query Match 57.5%; Score 23; DB 1; Length 6;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YLWN 6
| | |
Db 3 YAWN 6

RESULT 2

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US-09-214-095D-52
; Sequence 52, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 52
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-52
Query Match 57.5%; Score 23; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YLWN 6
| | |
Db 3 YAWN 6

RESULT 3
US-09-940-727B-52
; Sequence 52, Application US/09940727B
; Patent No. 6913917
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 6
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-52
Query Match 57.5%; Score 23; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YLWN 6
| | |
Db 3 YAWN 6

RESULT 4
US-08-089-994A-2
; Sequence 2, Application US/0808994A
; Patent No. 5380668
; GENERAL INFORMATION:
; APPLICANT: Herron, James N.
; TITLE OF INVENTION: Compounds Having the Antigenicity of
; FILE REFERENCE: hCG
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: University of Utah Technology
; ADDRESSEE: Transfer Office
; STREET: 421 Wakara Way, Suite 170
; CITY: Salt Lake City

US-09-127-574-14
; Sequence 14, Application US/09127574
; Patent No. 5985836
; GENERAL INFORMATION:
; APPLICANT: Bastek, Patrick
; APPLICANT: Lang, John M.
; APPLICANT: Baumbach, George A.
; APPLICANT: Carbonell, Ruben G.
; TITLE OF INVENTION: Alpha-1 Proteinase Inhibitor Binding Peptides
; FILE REFERENCE: MSB-7248
; CURRENT APPLICATION NUMBER: US/09/127,574
; CURRENT FILING DATE: 1998-07-31
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-127-574-14
Query Match 55.0%; Score 22; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLW 5
| | |
Db 4 YLW 6

RESULT 5
US-09-127-574-14
; Sequence 14, Application US/09127574
; Patent No. 5985836
; GENERAL INFORMATION:
; APPLICANT: Bastek, Patrick
; APPLICANT: Lang, John M.
; APPLICANT: Baumbach, George A.
; APPLICANT: Carbonell, Ruben G.
; TITLE OF INVENTION: Alpha-1 Proteinase Inhibitor Binding Peptides
; FILE REFERENCE: MSB-7248
; CURRENT APPLICATION NUMBER: US/09/127,574
; CURRENT FILING DATE: 1998-07-31
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-127-574-14
Query Match 55.0%; Score 22; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLW 5
| | |
Db 4 YLW 6

RESULT 6
US-09-315-304B-1588
```

; Sequence 1588, Application US/09315304B
; Patent No. 6348568
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.

; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-052
; CURRENT APPLICATION NUMBER: US/09/315,304B
; CURRENT FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1667

; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1588
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide

US-09-315-304B-1588

Query Match 55.0%; Score 22; DB 2; Length 6;
Best Local Similarity 60.0%; Pred. No. 4.6e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGYLW 5
||:|
Db 1 GGWNW 5

RESULT 7

US-09-350-325-48

; Sequence 48, Application US/09350325
; Patent No. 6541020
; GENERAL INFORMATION:
; APPLICANT: Ding, S.
; APPLICANT: Kang, M.
; APPLICANT: Venetta, T.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ADMINISTRATION OF
; TITLE OF INVENTION: THERAPEUTIC REAGENTS
; FILE REFERENCE: 7872-062
; CURRENT APPLICATION NUMBER: US/09/350,325
; CURRENT FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 48
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: enhancer peptide

US-09-350-325-48

Query Match 55.0%; Score 22; DB 2; Length 6;
Best Local Similarity 60.0%; Pred. No. 4.6e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGYLW 5
||:|
Db 1 GGWNW 5

RESULT 8

US-09-350-641C-1588

; Sequence 1588, Application US/09350641C
; Patent No. 6656906
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.

; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-067
; CURRENT APPLICATION NUMBER: US/09/350,641C
; CURRENT FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757

; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1588
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide

US-09-350-641C-1588

Query Match 55.0%; Score 22; DB 2; Length 6;
Best Local Similarity 60.0%; Pred. No. 4.6e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGYLW 5
||:|
Db 1 GGWNW 5

RESULT 9

PCT-US94-07605-2

; Sequence 2, Application PC/TUS9407605
; GENERAL INFORMATION:
; APPLICANT: Herron, James N.
; TITLE OF INVENTION: Compounds Having the Antigenicity of
; TITLE OF INVENTION: hCG
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: University of Utah Technology
; ADDRESSEE: Transfer Office
; STREET: 421 Wakara Way, Suite 170
; CITY: Salt Lake City
; STATE: UT
; COUNTRY: USA
; ZIP: 84108

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORD PERFECT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07605
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/089,994
; FILING DATE: 6 Jul 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Turner, Allen C.
; REGISTRATION NUMBER: 33,041
; REFERENCE/DOCKET NUMBER: 2224
; TELEPHONE: 801/532-1922
; TELEFAX: 801/531-9168
; TELEX: 388961 1PM04UT

; INFORMATION FOR SEQ ID NO: 2:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

PCT-US94-07605-2

Query Match 55.0%; Score 22; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLW 5
DB 4 YLW 6

RESULT 10
US-08-073-028-45
; Sequence 45, Application US/08073028
; Patent No. 5464933
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/073,028
; FILING DATE: 07-JUN-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-073-028-45

Query Match 52.5%; Score 21; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LWN 6
DB 2 LWN 4

RESULT 11
US-08-785-571-9
; Sequence 9, Application US/08785571
; Patent No. 5854070
; GENERAL INFORMATION:
; APPLICANT: Rose, Lynn M.
; TITLE OF INVENTION: Alleviation of Symptoms Associated with
; TITLE OF INVENTION: Inflammatory Disease States
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/785,571
; FILING DATE: 21-JAN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/396,089
; FILING DATE:
; APPLICATION NUMBER: US/08/094,535
; FILING DATE:
; APPLICATION NUMBER: US 08/060,699
; FILING DATE: 10-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/915,068
; FILING DATE: 16-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 31574
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-785-571-9

Query Match 52.5%; Score 21; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LWN 6
DB 4 LWN 6

RESULT 12
US-08-336-553A-32
; Sequence 32, Application US/08336553A
; Patent No. 6054264
; GENERAL INFORMATION:
; APPLICANT: CHIEN, DAVID Y.
; APPLICANT: KOO, GEORGE
; TITLE OF INVENTION: METHODS OF TYPING HEPATITIS C VIRUS AND
; TITLE OF INVENTION: REAGENTS FOR USE THEREIN
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,553A

GENERAL INFORMATION:
APPLICANT: CHIEN, DAVID Y.
 KUO, GEORGE
TITLE OF INVENTION: METHODS OF TYPING HEPATITIS C VIRUS AND
 REAGENTS FOR USE THEREIN
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/437,895
FILING DATE: 09-No. 6416946-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/336,553
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/060,400
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 22300-20947.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-437-895-32

Query Match 52.5%; Score 21; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYLW 5
 |||
Db 2 GYPW 5

Search completed: December 30, 2005, 15:35:38
Job time : 46 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2005, 15:34:14 ; Search time 161 Seconds
(without alignments)
15.571 Million cell updates/sec

Title: US-10-735-916A-8
Perfect score: 40
Sequence: 1 GGYLWN 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 20794

Minimum DB seq length: 6
Maximum DB seq length: 6

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	6	5	US-10-735-916A-8
2	29	72.5	6	3	US-09-791-551-77
3	27	67.5	6	4	US-10-714-564A-20
4	27	67.5	6	4	US-10-714-564A-1357
5	26	65.0	6	4	US-10-714-564A-16
6	26	65.0	6	4	US-10-714-564A-49
7	26	65.0	6	4	US-10-714-564A-1353
8	24	60.0	6	4	US-10-024-652-844
9	23	57.5	6	3	US-09-940-727B-52
10	23	57.5	6	5	US-10-798-380-68
11	22	55.0	6	4	US-10-347-562-48
12	22	55.0	6	4	US-10-351-641-1588
13	22	55.0	6	4	US-10-714-564A-413
14	22	55.0	6	6	US-11-041-199-1
15	22	55.0	6	6	US-11-041-199-9
16	22	55.0	6	6	US-11-041-199-10
17	22	55.0	6	6	US-11-041-199-11
18	21	52.5	6	3	US-09-759-1308-435
19	21	52.5	6	4	US-10-074-547-6
20	21	52.5	6	4	US-10-042-431-65
21	21	52.5	6	4	US-10-005-305-37
22	21	52.5	6	4	US-10-005-305-94
23	21	52.5	6	4	US-10-741-790-435
24	21	52.5	6	4	US-10-714-564A-17
25	21	52.5	6	4	US-10-714-564A-18
26	21	52.5	6	4	US-10-714-564A-65
27	21	52.5	6	4	US-10-714-564A-70

ALIGNMENTS

RESULT 1
US-10-735-916A-8
; Sequence 8, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10/735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-735-916A-8

Query Match 100.0%; Score 40; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6
|||
Db 1 GGYLWN 6

RESULT 2
US-09-791-551-77
; Sequence 77, Application US/09791551
; Publication No. US20030235584A1
; GENERAL INFORMATION:
; APPLICANT: KLOETZER, WILLIAM S.
; APPLICANT: HANNA, NABIL
; TITLE OF INVENTION: METHOD FOR PREPARING ANTI-MIF ANTIBODIES

Sequence 86, Appl
Sequence 91, Appl
Sequence 229, App
Sequence 236, App
Sequence 243, App
Sequence 388, App
Sequence 399, App
Sequence 406, App
Sequence 552, App
Sequence 555, App
Sequence 562, App
Sequence 569, App
Sequence 707, App
Sequence 714, App
Sequence 721, App
Sequence 873, App
Sequence 880, App
Sequence 1354, Ap

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; FILE REFERENCE: 037003/0277869
; CURRENT APPLICATION NUMBER: US/09/791,551
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/185,390
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/233,625
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 77
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-791-551-77

Query Match          72.5%; Score 29; DB 3; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GYLMN 6
      |||||
Db      2 GYWN 6

RESULT 3
US-10-714-564A-20
; Sequence 20, Application US/10714564A
; Publication No. US20040175361A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Michaud, Stephanie D.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; TITLE OF INVENTION: FUNCTIONS OF NONCLASSICAL CADHERINS
; FILE REFERENCE: 100086.418
; CURRENT APPLICATION NUMBER: US/10/714,564A
; CURRENT FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 1402
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative atypical cadherin Trp-containing
; OTHER INFORMATION: CAR sequence
US-10-714-564A-20

Query Match          67.5%; Score 27; DB 4; Length 6;
Best Local Similarity 60.0%; Pred. No. 1.7e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 GYLMN 6
      |||||
Db      1 GWMWN 5

RESULT 4
US-10-714-564A-1357
; Sequence 1357, Application US/10714564A
; Publication No. US20040175361A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Michaud, Stephanie D.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; TITLE OF INVENTION: FUNCTIONS OF NONCLASSICAL CADHERINS
; FILE REFERENCE: 100086.418
; CURRENT APPLICATION NUMBER: US/10/714,564A
; CURRENT FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 1402
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1357
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Exemplary Trp-containing CAR sequences for
; OTHER INFORMATION: atypical cadherins
US-10-714-564A-49

Query Match          65.0%; Score 26; DB 4; Length 6;
Best Local Similarity 60.0%; Pred. No. 1.7e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 GYLMN 6
      |||||
Db      1 GWMWN 5

RESULT 5
US-10-714-564A-16
; Sequence 16, Application US/10714564A
; Publication No. US20040175361A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Michaud, Stephanie D.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; TITLE OF INVENTION: FUNCTIONS OF NONCLASSICAL CADHERINS
; FILE REFERENCE: 100086.418
; CURRENT APPLICATION NUMBER: US/10/714,564A
; CURRENT FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 1402
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative atypical cadherin Trp-containing
; OTHER INFORMATION: CAR sequence
US-10-714-564A-16

Query Match          65.0%; Score 26; DB 4; Length 6;
Best Local Similarity 60.0%; Pred. No. 1.7e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 GYLMN 6
      |||||
Db      1 GWMWN 5

RESULT 6
US-10-714-564A-49
; Sequence 49, Application US/10714564A
; Publication No. US20040175361A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Michaud, Stephanie D.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; TITLE OF INVENTION: FUNCTIONS OF NONCLASSICAL CADHERINS
; FILE REFERENCE: 100086.418
; CURRENT APPLICATION NUMBER: US/10/714,564A
; CURRENT FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 1402
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Exemplary Trp-containing CAR sequences for
; OTHER INFORMATION: atypical cadherins
US-10-714-564A-49

Query Match          65.0%; Score 26; DB 4; Length 6;
Best Local Similarity 60.0%; Pred. No. 1.7e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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Qy 2 GYLWN 6
|:|
Db 2 GWVWN 6

RESULT 7

US-10-714-564A-1353
; Sequence 1353, Application US/10714564A
; Publication No. US20040175361A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; TITLE OF INVENTION: FUNCTIONS OF NONCLASSICAL CADHERINS
; FILE REFERENCE: 100086.418
; CURRENT APPLICATION NUMBER: US/10/714.564A
; CURRENT FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 1402
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1353
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Trp-containing cell adhesion recognition sequence
US-10-714-564A-1353

Query Match 65.0%; Score 26; DB 4; Length 6;
Best Local Similarity 60.0%; Pred. No. 1.7e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GYLWN 6
|:|
Db 1 GWVWN 5

RESULT 8

US-10-024-652-844
; Sequence 844, Application US/10024652
; Publication No. US20030219738A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Faris, Mary
; APPLICANT: Afar, Daniel E.H.
; APPLICANT: Hubert, Rene S.
; APPLICANT: Mitchell, Steve Chappell
; APPLICANT: Levin, Elana
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Encoded Zinc
; TITLE OF INVENTION: Transporter Protein Entitled 108P5H8 Useful in Treatment and
; TITLE OF INVENTION: Detection of Cancer
; FILE REFERENCE: 51158-20025.00
; CURRENT APPLICATION NUMBER: US/10/024.652
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/256,210
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 2598
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 844
; LENGTH: 6
; TYPE: PRT
; ORGANISM: homo sapien
US-10-024-652-844

Query Match 60.0%; Score 24; DB 4; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGYLWN 6
|:|:|

Db 1 GGYIAN 6

RESULT 9

US-09-940-727B-52
; Sequence 52, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940.727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 6
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-52

Query Match 57.5%; Score 23; DB 3; Length 6;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YLWN 6
|:|
Db 3 YAWN 6

RESULT 10

US-10-798-380-68
; Sequence 68, Application US/10798380
; Publication No. US20040265960A1
; GENERAL INFORMATION:
; APPLICANT: YOUNG, DEBORAH A.
; APPLICANT: WHITTERS, MATTHEW J.
; APPLICANT: VALGE-ARCHER, VIIA
; APPLICANT: COLLINS, MARY
; APPLICANT: WILLIAMS, ANDREW JAMES
; APPLICANT: WITEK, JOANNE
; TITLE OF INVENTION: ANTIBODIES AGAINST HUMAN IL-21 RECEPTOR AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 08702.0137-00000
; CURRENT APPLICATION NUMBER: US/10/798,380
; CURRENT FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: 60/454,336
; PRIOR FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 68
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-798-380-68

Query Match 57.5%; Score 23; DB 5; Length 6;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GYLW 5
|:|
Db 2 GYTW 5

RESULT 11
US-10-347-562-48

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; Sequence 48, Application US/10347562
; Publication No. US2003016555A1
; GENERAL INFORMATION:
; APPLICANT: Ding, S.
; APPLICANT: Kang, M.
; APPLICANT: Venetta, T.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ADMINISTRATION OF
; TITLE OF INVENTION: THERAPEUTIC REAGENTS
; FILE REFERENCE: 7872-104
; CURRENT APPLICATION NUMBER: US/10/347,562
; CURRENT FILING DATE: 2003-01-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 48
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: enhancer peptide
US-10-347-562-48

Query Match          55.0%; Score 22; DB 4; Length 6;
Best Local Similarity 60.0%; Pred. No. 1.7e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGYLW 5
      ||: |
Db      1 GGWNW 5

RESULT 12
US-10-351-641-1588
; Sequence 1588, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1588
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-1588

Query Match          55.0%; Score 22; DB 4; Length 6;
Best Local Similarity 60.0%; Pred. No. 1.7e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGYLW 5
      ||: |
Db      1 GGWNW 5

RESULT 13
US-10-714-564A-413
; Sequence 413, Application US/10714564A
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; Publication No. US20040175361A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Michaud, Stephanie D.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; TITLE OF INVENTION: FUNCTIONS OF NONCLASSICAL CADHERINS
; FILE REFERENCE: 10086.418
; CURRENT APPLICATION NUMBER: US/10/714,564A
; CURRENT FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 1402
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 413
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Exemplary cyclic peptide
US-10-714-564A-413

Query Match          55.0%; Score 22; DB 4; Length 6;
Best Local Similarity 40.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      2 GYLWN 6
      ||: |
Db      2 GNMWD 6

RESULT 14
US-11-041-199-1
; Sequence 1, Application US/11041199
; Publication No. US20050153375A1
; GENERAL INFORMATION:
; APPLICANT: STANNERS, Clifford P.
; APPLICANT: ILANTZIS, Christian
; APPLICANT: ORDONEZ-GARCIA, Cosme
; APPLICANT: TAHERI, Maryam
; APPLICANT: SCREATON, Robert A.
; APPLICANT: FUKS, Abraham
; APPLICANT: SARAGOVIT, H. Uri
; TITLE OF INVENTION: CEA/NCA-BASED DIFFERENTIATION CANCER THERAPY
; FILE REFERENCE: 14952
; CURRENT APPLICATION NUMBER: US/11/041,199
; CURRENT FILING DATE: 2005-01-25
; PRIOR APPLICATION NUMBER: 09/637,530
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: CA99/00119
; PRIOR FILING DATE: 1999-02-11
; PRIOR APPLICATION NUMBER: CA 2,224,129
; PRIOR FILING DATE: 1998-02-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-041-199-1

Query Match          55.0%; Score 22; DB 6; Length 6;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GYLW 5
      ||: |
Db      1 GYSW 4

RESULT 15
US-11-041-199-9
; Sequence 9, Application US/11041199
; Publication No. US20050153375A1
; GENERAL INFORMATION:
; APPLICANT: STANNERS, Clifford P.
```

; APPLICANT: ILANTZIS, Christian
; APPLICANT: ORDONEZ-GARCIA, Cosme
; APPLICANT: TAHERI, Marviam
; APPLICANT: SREANTON, Robert A.
; APPLICANT: FUKS, Abraham
; APPLICANT: SARAGOV, H. Uri
; TITLE OF INVENTION: CEA/NCA-BASED DIFFERENTIATION CANCER THERAPY
; FILE REFERENCE: 14952
; CURRENT APPLICATION NUMBER: US/11/041,199
; PRIOR FILING DATE: 2005-01-25
; PRIOR APPLICATION NUMBER: 09/637,530
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: CA99/00119
; PRIOR FILING DATE: 1999-02-11
; PRIOR APPLICATION NUMBER: CA 2,224,129
; PRIOR FILING DATE: 1998-02-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-041-199-9

Query Match 55.0%; Score 22; DB 6; Length 6;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GYLW 5
| |
Db 1 GYSW 4

Search completed: December 30, 2005, 15:48:02
Job time : 162 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2005, 15:34:55 ; Search time 12 Seconds
(without alignments)

3.744 Million cell updates/sec

Title: US-10-735-916A-8

Perfect score: 40

Sequence: 1 GGYLWN 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 568

Minimum DB seq length: 6

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA New:
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB_PEP.*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB_PEP.*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB_PEP.*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB_PEP.*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB_PEP.*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB_PEP.*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB_PEP.*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB_PEP.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	40	100.0	6	7	US-11-012-353-8
2	29	72.5	6	7	US-11-009-939-23
3	20	50.0	6	6	US-10-929-988-470
4	20	50.0	6	6	US-10-929-988-471
5	18	45.0	6	7	US-11-054-515-3210
6	15	37.5	6	6	US-10-929-988-122
7	15	37.5	6	6	US-10-485-788A-288
8	15	37.5	6	7	US-11-090-497-18
9	14	35.0	6	6	US-10-485-788A-243
10	14	35.0	6	7	US-11-119-098-9
11	13	32.5	6	6	US-10-494-781-13
12	13	32.5	6	6	US-10-494-781-15
13	13	32.5	6	6	US-10-613-744-15
14	13	32.5	6	6	US-10-485-788A-138
15	13	32.5	6	7	US-11-079-969-1
16	13	32.5	6	7	US-11-113-224-58
17	13	32.5	6	7	US-11-113-224-60
18	13	32.5	6	7	US-11-108-185-64
19	13	32.5	6	7	US-11-022-341-63
20	13	32.5	6	7	US-11-102-743-8
21	12	32.5	6	7	US-11-195-197-1
22	12	30.0	6	6	US-10-966-648-19
23	12	30.0	6	6	US-10-467-657-9110
24	12	30.0	6	6	US-10-846-188C-7
25	12	30.0	6	6	US-10-522-398-2

Sequence 88, Appl
Sequence 228, App
Sequence 448, App
Sequence 3, Appli
Sequence 41, Appl
Sequence 2193, Ap
Sequence 78, Appl
Sequence 737, App
Sequence 737, App
Sequence 160, App
Sequence 3, Appli
Sequence 5, Appli
Sequence 43, Appl
Sequence 94, Appl
Sequence 7, Appli
Sequence 8, Appli
Sequence 9, Appli
Sequence 18, Appl
Sequence 958, App
Sequence 1, Appli

US-11-012-353-8
; Sequence 8, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUM, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-012-353-8

ALIGNMENTS

RESULT 1

US-11-012-353-8
; Sequence 8, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUM, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-012-353-8

Query Match 100.0%; Score 40; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.4e+04;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6
|||||
Db 1 GGYLWN 6

RESULT 2
US-11-009-939-23
; Sequence 23, Application US/11009939

```
/ Publication No. US20050265998A1
/ GENERAL INFORMATION:
/ APPLICANT: Elson, Greg Christopher Andrew
/ TITLE OF INVENTION: Neutralizing Antibodies and Methods of Use Thereof
/ FILE REFERENCE: 23135-402
/ CURRENT APPLICATION NUMBER: US/11/009,939
/ PRIOR FILING DATE: 2005-12-10
/ PRIOR APPLICATION NUMBER: 60/528,811
/ PRIOR FILING DATE: 2003-12-10
/ PRIOR APPLICATION NUMBER: 60/528,812
/ PRIOR FILING DATE: 2003-12-10
/ PRIOR APPLICATION NUMBER: 60/528,962
/ PRIOR FILING DATE: 2003-12-10
/ NUMBER OF SEQ ID NOS: 44
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 23
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-11-009-939-23

Query Match 72.5%; Score 29; DB 7; Length 6;
Best Local Similarity 66.7%; Pred. No. 4.4e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYLWN 6
Db 1 GGYSWH 6

RESULT 3
US-10-929-988-470
/ Sequence 470, Application US/10929988
/ Publication No. US2005027558A1
/ GENERAL INFORMATION:
/ APPLICANT: CWIRLA, STEVEN E.
/ APPLICANT: BALU, PALANI
/ APPLICANT: DUFFIN, DAVID J.
/ APPLICANT: PIPLANI, SUNILA
/ APPLICANT: MERRILL, BARBARA MCEOWEN
/ APPLICANT: SCHATZ, PETER JOSEPH
/ TITLE OF INVENTION: COMPOUNDS HAVING AFFINITY FOR THE GRANULOCYTE-COLONY
/ TITLE OF INVENTION: STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED
/ FILE REFERENCE: 0300-0014
/ CURRENT APPLICATION NUMBER: US/10/929,988
/ CURRENT FILING DATE: 2004-08-30
/ PRIOR APPLICATION NUMBER: US/09/620,091
/ PRIOR FILING DATE: 2000-07-20
/ NUMBER OF SEQ ID NOS: 491
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 470
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-929-988-470

Query Match 50.0%; Score 20; DB 6; Length 6;
Best Local Similarity 50.0%; Pred. No. 4.4e+04;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYLW 5
Db 3 GWVW 6

RESULT 4
US-10-929-988-471
/ Sequence 471, Application US/10929988
/ Publication No. US2005027558A1
```

```
/ GENERAL INFORMATION:
/ APPLICANT: CWIRLA, STEVEN E.
/ APPLICANT: BALU, PALANI
/ APPLICANT: DUFFIN, DAVID J.
/ APPLICANT: PIPLANI, SUNILA
/ APPLICANT: MERRILL, BARBARA MCEOWEN
/ APPLICANT: SCHATZ, PETER JOSEPH
/ TITLE OF INVENTION: COMPOUNDS HAVING AFFINITY FOR THE GRANULOCYTE-COLONY
/ TITLE OF INVENTION: STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED
/ FILE REFERENCE: 0300-0014
/ CURRENT APPLICATION NUMBER: US/10/929,988
/ CURRENT FILING DATE: 2004-08-30
/ PRIOR APPLICATION NUMBER: US/09/620,091
/ PRIOR FILING DATE: 2000-07-20
/ NUMBER OF SEQ ID NOS: 491
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 471
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-929-988-471

Query Match 50.0%; Score 20; DB 6; Length 6;
Best Local Similarity 50.0%; Pred. No. 4.4e+04;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYLW 5
Db 3 GWVW 6

RESULT 5
US-11-054-515-3210
/ Sequence 3210, Application US/11054515
/ Publication No. US2005025532A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PFS23P3
/ CURRENT APPLICATION NUMBER: US/11/054,515
/ CURRENT FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: 60/543,296
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/580,347
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 3210
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-054-515-3210
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Query Match 45.0%; Score 18; DB 7; Length 6;
Best Local Similarity 75.0%; Pred. No. 4.4e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGYL 4
|||
Db 1 GGWL 4

RESULT 6

US-10-929-988-122
; Sequence 122, Application US/10929988
; Publication No. US20050277588A1
; GENERAL INFORMATION:
; APPLICANT: CWRILA, STEVEN E.
; APPLICANT: BALU, PALANI
; APPLICANT: DUFFIN, DAVID J.
; APPLICANT: PIPLANI, SUNILA
; APPLICANT: MERRILL, BARBARA MCEOWEN
; APPLICANT: SCHATZ, PETER JOSEPH
; TITLE OF INVENTION: COMPOUNDS HAVING AFFINITY FOR THE GRANULOCYTE-COLONY
; TITLE OF INVENTION: STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED
; TITLE OF INVENTION: USES
; FILE REFERENCE: 0300-0014
; CURRENT APPLICATION NUMBER: US/10/929,988
; CURRENT FILING DATE: 2004-08-30
; PRIOR APPLICATION NUMBER: US/09/620,091
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 491
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 122
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-929-988-122

Query Match 37.5%; Score 15; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
|||
Db 3 LW 4

RESULT 7

US-10-485-788A-288
; Sequence 288, Application US/10485788A
; Publication No. US20050282743A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Rabinowitz, Joshua D.
; APPLICANT: Schweizer, Johannes
; APPLICANT: Carrick, Deanna Marie
; APPLICANT: Carrick, Deanna Marie
; APPLICANT: Arbor Vita Corporation
; TITLE OF INVENTION: Molecular Interactions in Cells
; FILE REFERENCE: 20054-003320US
; CURRENT APPLICATION NUMBER: US/10/485,788A
; CURRENT FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: US 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: WO PCT/US02/24655
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 841
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 288
; LENGTH: 6
; TYPE: PRT

; ORGANISM: Homo sapiens
US-10-485-788A-288

Query Match 37.5%; Score 15; DB 6; Length 6;
Best Local Similarity 50.0%; Pred. No. 4.4e+04;
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GYLW 5
|||
Db 2 GQYW 5

RESULT 8

US-11-090-497-18
; Sequence 18, Application US/11090497
; Publication No. US20050282263A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology Corporation
; TITLE OF INVENTION: FLEXIBLE VACCINE ASSEMBLY AND VACCINE DELIVERY PLATFORM
; FILE REFERENCE: N8630
; CURRENT APPLICATION NUMBER: US/11/090,497
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: 60/386,921
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/407,795
; PRIOR FILING DATE: 2002-09-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 18
; LENGTH: 6
; TYPE: PRT
; ORGANISM: human laminin
US-11-090-497-18

Query Match 37.5%; Score 15; DB 7; Length 6;
Best Local Similarity 66.7%; Pred. No. 4.4e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYL 4
|||
Db 1 GYI 3

RESULT 9

US-10-485-788A-243
; Sequence 243, Application US/10485788A
; Publication No. US20050282743A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Rabinowitz, Joshua D.
; APPLICANT: Schweizer, Johannes
; APPLICANT: Carrick, Deanna Marie
; APPLICANT: Arbor Vita Corporation
; TITLE OF INVENTION: Molecular Interactions in Cells
; FILE REFERENCE: 20054-003320US
; CURRENT APPLICATION NUMBER: US/10/485,788A
; CURRENT FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: US 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: WO PCT/US02/24655
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 841
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 243
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-485-788A-243

Query Match 35.0%; Score 14; DB 6; Length 6;
Best Local Similarity 66.7%; Pred. No. 4.4e+04;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYL 4
Db 4 GIV 6

RESULT 10
US-11-119-098-9
; Sequence 9, Application US/11119098
; Publication No. US20050267030A1
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; TITLE OF INVENTION: Use of deltapKC Peptides for Modulation of Reactive Oxygen Species
; FILE REFERENCE: 58600-8213 US00
; CURRENT APPLICATION NUMBER: US/11/119,098
; CURRENT FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/567,315
; PRIOR FILING DATE: 2004-04-30
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: beta-PKC-selective activator peptide
US-11-119-098-9

Query Match 35.0%; Score 14; DB 7; Length 6;
Best Local Similarity 33.3%; Pred. No. 4.4e+04;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 LWN 6
Db 4 IWD 6

RESULT 11
US-10-494-781-13
; Sequence 13, Application US/10494781
; Publication No. US20050244895A1
; GENERAL INFORMATION:
; APPLICANT: King's College London
; TITLE OF INVENTION: Diagnosis of Demyelinating or Spongiform Disease
; FILE REFERENCE: IT/KE/N13246
; CURRENT APPLICATION NUMBER: US/10/494,781
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: GB 0127000.8
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: GB 0202562.5
; PRIOR FILING DATE: 2002-02-04
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Bovine
US-10-494-781-13

Query Match 32.5%; Score 13; DB 6; Length 6;
Best Local Similarity 33.3%; Pred. No. 4.4e+04;
Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 YLW 5
Db 2 FAW 4

RESULT 12
US-10-494-781-15
; Sequence 15, Application US/10494781

; Publication No. US20050244895A1
; GENERAL INFORMATION:
; APPLICANT: King's College London
; TITLE OF INVENTION: Diagnosis of Demyelinating or Spongiform Disease
; FILE REFERENCE: IT/KE/N13246
; CURRENT APPLICATION NUMBER: US/10/494,781
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: GB 0127000.8
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: GB 0202562.5
; PRIOR FILING DATE: 2002-02-04
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Bovine
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (3)..(3)
; OTHER INFORMATION: any amino acid
; NAME/KEY: MISC FEATURE
; LOCATION: (5)..(5)
; OTHER INFORMATION: any amino acid
US-10-494-781-15

Query Match 32.5%; Score 13; DB 6; Length 6;
Best Local Similarity 33.3%; Pred. No. 4.4e+04;
Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 YLW 5
Db 2 FXW 4

RESULT 13
US-10-613-744-15
; Sequence 15, Application US/10613744
; Publication No. US20050272093A1
; GENERAL INFORMATION:
; APPLICANT: Mackinnon, Roderick
; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
; TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
; TITLE OF INVENTION: Channel Proteins, and Uses Thereof
; FILE REFERENCE: 018512-002901US
; CURRENT APPLICATION NUMBER: US/10/613,744
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: US/09/275,252
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: US 09/045,529
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/054,347
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: WO PCT/US99/06307
; PRIOR FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: channel protein
; OTHER INFORMATION: central pore signature sequence
US-10-613-744-15

Query Match 32.5%; Score 13; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GY 3

Db 3 GY 4
||
Query Match 32.5%; Score 13; DB 6; Length 6;
Best Local Similarity 50.0%; Pred. No. 4.4e+04;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 14
US-10-485-788A-138
; Sequence 138, Application US/10485788A
; Publication No. US20050282743A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Rabinowitz, Joshua D.
; APPLICANT: Schweizer, Johannes
; APPLICANT: Carrick, Deanna Marie
; APPLICANT: Arbor Vita Corporation
; TITLE OF INVENTION: Molecular Interactions in Cells
; FILE REFERENCE: 20054-003320US
; CURRENT APPLICATION NUMBER: US/10/485,788A
; CURRENT FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: US 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: WO PCT/US02/24655
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 138
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-485-788A-138

Query Match 32.5%; Score 13; DB 6; Length 6;
Best Local Similarity 50.0%; Pred. No. 4.4e+04;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
:|
DB 2 IW 3

RESULT 15
US-11-079-969-1
; Sequence 1, Application US/11079969
; Publication No. US20050244899A1
; GENERAL INFORMATION:
; APPLICANT: Young, David S.F.
; APPLICANT: Warner, Andrea
; APPLICANT: Kelleher, Michelle
; APPLICANT: McConkey, Fortunata
; APPLICANT: Hahn, Susan E.
; TITLE OF INVENTION: Laminin Receptor 1 Precursor Protein (37LRP) Epitope Delineated B
; TITLE OF INVENTION: Heptocellular Carcinoma Specific Antibody
; FILE REFERENCE: 2056.049
; CURRENT APPLICATION NUMBER: US/11/079,969
; CURRENT FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 10/810,163
; PRIOR FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US 09/415,278
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: US 09/727,361
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 10/713,642
; PRIOR FILING DATE: 2003-11-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: peptide G, a synthetic peptide derived from the sequence of 37LRP
US-11-079-969-1

Search completed: December 30, 2005, 15:48:20
Job time : 12 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:02:01 ; Search time 142.194 Seconds
(without alignments)
49.440 Million cell updates/sec

Title: US-10-735-916A-10

Perfect score: 89

Sequence: 1 YISYDGTNNYKPSLKD 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq_21.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	89	100.0	16	7	ADJ76844 CDR seque
2	89	100.0	16	9	ADZ67014 Murine in
3	89	100.0	117	7	ADJ76903 Anti-IGF-
4	89	100.0	117	7	ADJ76909 Anti-IGF-
5	89	100.0	117	7	ADJ76917 Anti-IGF-
6	89	100.0	117	7	ADJ76913 Anti-IGF-
7	89	100.0	117	9	ADZ67083 Human ant
8	89	100.0	117	9	ADZ67087 Human ant
9	89	100.0	117	9	ADZ67073 Murine im
10	89	100.0	117	9	ADZ67079 Human ant
11	89	100.0	127	7	ADJ76886 Anti-IGF-
12	89	100.0	127	9	ADZ67056 Murine im
13	89	100.0	135	7	ADJ76911 Anti-IGF-
14	89	100.0	135	7	ADJ76915 Anti-IGF-
15	89	100.0	135	9	ADZ67089 Human ant
16	89	100.0	135	9	ADZ67081 Human ant
17	89	100.0	135	9	ADZ67085 Human ant
18	89	100.0	135	9	ADZ67085 Human ant
19	75	84.3	16	9	Aea40141 TNF resis
20	75	84.3	114	9	Aea40137 TNF resis
21	75	84.3	118	2	Aaw00829 Variable
22	75	84.3	118	2	Aaw19015 Anti-huma
23	75	84.3	136	3	Aay94391 Mouse VH
24	73	82.0	16	9	ADZ45407 Murine fa

25	73	82.0	119	9	ADZ45405
26	73	82.0	369	4	AAB73388
27	72	80.9	16	9	ADZ45343
28	72	80.9	16	9	ADZ51256
29	72	80.9	16	9	ADZ42130
30	72	80.9	65	6	ABU56867
31	72	80.9	114	9	AEA40153
32	72	80.9	116	9	ADZ45341
33	72	80.9	116	9	ADZ51254
34	72	80.9	116	9	ADZ42128
35	72	80.9	119	6	ABB98908
36	72	80.9	121	8	ADR38665
37	71	79.8	118	7	ADJ76904
38	71	79.8	118	9	ADZ67074
39	70	78.7	16	9	ADZ45520
40	70	78.7	16	9	ADZ45311
41	70	78.7	16	9	ADZ51224
42	70	78.7	16	9	ADZ42098
43	70	78.7	116	9	ADZ45309
44	70	78.7	116	9	ADZ51222
45	70	78.7	116	9	ADZ42096

ALIGNMENTS

RESULT 1

ADJ76844

ID ADJ76844 standard; peptide; 16 AA.

XX AC ADJ76844;

XX DT 06-MAY-2004 (first entry)

XX DE CDR sequence for anti-IGF-1R antibody.

XX KW cytostatic; antipneumatic; antibody;

XX KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;

XX KW or epidermal growth factor receptor; EGFR; signal transduction pathway;

XX KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;

XX KW CDR.

XX OS Mus musculus.

XX PN WO2003059951-A2.

XX PD 24-JUL-2003.

XX PF 20-JAN-2003; 2003WO-FR000178.

XX PR 18-JAN-2002; 2002FR-00000653.

XX PR 18-JAN-2002; 2002FR-00000654.

XX PR 07-MAY-2002; 2002FR-00005753.

XX PA (FABR) FABRE MEDICAMENT SA PIERRE.

XX PI Goetsch L, Corvaia N, Leger O;

XX DR WPI; 2003-569653/53.

XX DR N-PSDB; ADJ76843.

XX PT New antibodies that bind to human insulin-like growth factor receptor,

XX PT useful for treatment, prevention and diagnosis of cancers.

XX PS Claim 1; SEQ ID NO 10; 164pp; French.

XX CC The invention relates to an isolated antibody (Ab), and its

XX CC fragments, that bind to human insulin-like growth factor-1,

XX CC IR) and optionally: (i) inhibit natural binding of insulin,

XX CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically,

XX CC kinase activity of IGF-1R. Ab and its fragments are used to

XX CC treat diseases associated with overexpression and/or abnorm

XX CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/c

CC hyperactivity of signal transduction pathways mediated by interaction of
 CC these receptors with their ligands. Especially they inhibit
 CC transformation of normal cells to tumor cells, inhibit growth and/or
 CC proliferation of tumor cells, so are useful against cancers of the
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused
 CC by abnormal expression of IGF-IR and/or EGFR. This sequence represents an
 CC CDR sequence used to generate the Ab of the invention.
 XX
 SQ Sequence 16 AA;

Query Match 100.0%; Score 89; DB 7; Length 16;
 Best Local Similarity 100.0%; Pred. No. 6.1e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16
 |||||
 Db 1 YISYDGTNNYKPSLKD 16

RESULT 2
 ADZ67014
 ID ADZ67014 standard; peptide; 16 AA.

XX ADZ67014;

AC ADZ67014;

DT 30-JUN-2005 (first entry)

DE Murine insulin-like growth factor T receptor IGF-IR CDR SEQ ID NO:10.

XX Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
 KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;
 KW musculoskeletal disease; respiratory disease; lung tumor;
 KW endocrine disease; gynecology and obstetrics; breast tumor;
 KW endometrial carcinoma; gastrointestinal disease; colon tumor;
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder.

XX Mus musculus.

OS US2005084906-A1.

PN 21-APR-2005.

PD 16-DEC-2003; 2003US-00735916.

XX 18-JAN-2002; 2002FR-00000653.

PR 07-MAY-2002; 2002FR-00000654.

PR 20-JAN-2003; 2003WO-FR000178.

PR 11-JUL-2003; 2003FR-00008538.

XX (GOET/) GOETSCH L.

PA (CORV/) CORVAIA N.

PA (LEGE/) LEGER O.

PA (DUFL/) DUFLOS A.

PA (HAEU/) HAEUW J.

PA (BECK/) BECK A.

PI Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;

XX WPI; 2005-321968/33.

DR N-PSDB; ADZ67013.

XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)

PT antibody or its functional fragment, being capable of binding human IGF-

PT IR and specifically inhibiting tyrosine kinase activity of receptor,

PT useful for treating cancer.

XX Claim 1; SEQ ID NO 10; 125pp; English.

PS The invention relates to a novel isolated anti-insulin-like growth factor

CC I receptor (IGF-IR) antibody (I) or its functional fragment, being

CC capable of binding to human IGF-IR and, if necessary, capable of

CC specifically inhibiting tyrosine kinase activity of the receptor,
 CC comprising a light or heavy chain having at least one complementary
 CC determining region (CDR) consisting of one of two fully defined 16 amino
 CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in
 CC the preparation of a medicament intended for the prevention or treatment
 CC of an illness connected with an overexpression and/or an abnormal
 CC activation of the IGF-IR and/or EGFR, and/or connected with a
 CC hyperactivation of the transduction pathway of the signal mediated by the
 CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where
 CC the administration of the medicament does not induce or only slightly
 CC induces secondary effects connected with inhibition of the insulin
 CC receptor. The antibody is useful for preparation of a medicament intended
 CC to inhibit the transformation of normal cells into cells with tumoral
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is
 CC useful for preparation of a medicament intended to inhibit the growth
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a
 CC medicament intended for prevention or for the treatment of cancer, where
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the
 CC preparation of a medicament intended for the prevention or for the
 CC treatment of psoriasis. (I) is useful in preparation of a medicament
 CC intended for the specific targeting of a biologically active compound to
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)
 CC is useful for in vitro diagnosis of illnesses induced by an
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor
 CC starting from a biological sample in which the abnormal presence, of IGF-
 CC IR and/or EGFR receptor is suspected, which involves contacting the
 CC biological sample with (I), which is optionally labeled. The present
 CC sequence is used in the exemplification of the invention.
 XX

SQ Sequence 16 AA;

Query Match 100.0%; Score 89; DB 9; Length 16;
 Best Local Similarity 100.0%; Pred. No. 6.1e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16
 |||||
 Db 1 YISYDGTNNYKPSLKD 16

RESULT 3

ADJ76903

ID ADJ76903 standard; protein; 117 AA.

XX ADJ76903;

AC ADJ76903;

DT 06-MAY-2004 (first entry)

XX Anti-IGF-IR related protein #16.

DE Cytostatic; antipsoriatic; antibody;

XX insulin-like growth factor-1 receptor; IGF-IR; tyrosine kinase activity;

KW or epidermal growth factor receptor; EGFR; signal transduction pathway;

KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;

KW CDR.

XX Homo sapiens.

OS WO2003059951-A2.

PN 24-JUL-2003.

PD 20-JAN-2003; 2003WO-FR000178.

PF 18-JAN-2002; 2002FR-00000653.

PR 18-JAN-2002; 2002FR-00000654.

PR 07-MAY-2002; 2002FR-00005753.

XX (FABR) FABRE MEDICAMENT SA PIERRE.


```
XX PI Goetsch L, Corvaia N, Leger O;
XX DR WPI; 2003-569653/53.
XX CC New antibodies that bind to human insulin-like growth factor receptor,
XX PT useful for treatment, prevention and diagnosis of cancers.
XX PT
XX PS Disclosure; SEQ ID NO 69; 164pp; French.
XX CC
XX CC The invention relates to an isolated antibody (Ab), and its functional
XX CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-
XX CC 1R) and optionally: (i) inhibit natural binding of insulin-like growth
XX CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine
XX CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or
XX CC treat diseases associated with overexpression and/or abnormal activity of
XX CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with
XX CC hyperactivity of signal transduction pathways mediated by interaction of
XX CC these receptors with their ligands. Especially they inhibit
XX CC proliferation of normal cells to tumor cells, inhibit growth and/or
XX CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
XX CC also for treating psoriasis. Ab are also used to diagnose diseases caused
XX CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a
XX CC protein sequence used to generate the Ab of the invention.
XX SQ Sequence 117 AA;

Query Match 100.0%; Score 89; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16
DB 51 YISYDGTNNYKPSLKD 66

RESULT 4
ADJ76909
ID ADJ76909 standard; protein; 117 AA.
AC ADJ76909;
DT 06-MAY-2004 (first entry)
DE Anti-IGF-1R related protein #22.
XX cytosolic; antipsoriatic; antibody;
XX insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;
XX or epidermal growth factor receptor; EGFR; signal transduction pathway;
XX ligand; tumor; cancer; osteosarcoma; complementarity determining region;
XX CDR.
XX OS Homo sapiens.
XX WO2003059951-A2.
XX 24-JUL-2003.
XX 20-JAN-2003; 2003WO-FR000178.
XX 18-JAN-2002; 2002FR-00000653.
XX 18-JAN-2002; 2002FR-00000654.
XX 07-MAY-2002; 2002FR-00005753.
XX (FABR ) FABRE MEDICAMENT SA PIERRE.
XX Goetsch L, Corvaia N, Leger O;
XX WPI; 2003-569653/53.
XX New antibodies that bind to human insulin-like growth factor receptor,
XX useful for treatment, prevention and diagnosis of cancers.

Query Match 100.0%; Score 89; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16
DB 51 YISYDGTNNYKPSLKD 66

RESULT 4
ADJ76909
ID ADJ76909 standard; protein; 117 AA.
AC ADJ76909;
DT 06-MAY-2004 (first entry)
DE Anti-IGF-1R related protein #26.
XX cytosolic; antipsoriatic; antibody;
XX insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;
XX or epidermal growth factor receptor; EGFR; signal transduction pathway;
XX ligand; tumor; cancer; osteosarcoma; complementarity determining region;
XX CDR.
XX OS Homo sapiens.
XX WO2003059951-A2.
XX 24-JUL-2003.
XX 20-JAN-2003; 2003WO-FR000178.
XX 18-JAN-2002; 2002FR-00000653.
XX 18-JAN-2002; 2002FR-00000654.
XX 07-MAY-2002; 2002FR-00005753.
XX (FABR ) FABRE MEDICAMENT SA PIERRE.
XX Goetsch L, Corvaia N, Leger O;
XX WPI; 2003-569653/53.
XX New antibodies that bind to human insulin-like growth factor receptor,
XX useful for treatment, prevention and diagnosis of cancers.

Query Match 100.0%; Score 89; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16
DB 51 YISYDGTNNYKPSLKD 66

RESULT 5
ADJ76917
ID ADJ76917 standard; protein; 117 AA.
AC ADJ76917;
DT 06-MAY-2004 (first entry)
DE Anti-IGF-1R related protein #26.
XX cytosolic; antipsoriatic; antibody;
XX insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;
XX or epidermal growth factor receptor; EGFR; signal transduction pathway;
XX ligand; tumor; cancer; osteosarcoma; complementarity determining region;
XX CDR.
XX OS Homo sapiens.
XX WO2003059951-A2.
XX 24-JUL-2003.
XX 20-JAN-2003; 2003WO-FR000178.
XX 18-JAN-2002; 2002FR-00000653.
XX 18-JAN-2002; 2002FR-00000654.
XX 07-MAY-2002; 2002FR-00005753.
XX (FABR ) FABRE MEDICAMENT SA PIERRE.
XX Goetsch L, Corvaia N, Leger O;
XX WPI; 2003-569653/53.
XX New antibodies that bind to human insulin-like growth factor receptor,
XX useful for treatment, prevention and diagnosis of cancers.
XX Disclosure; SEQ ID NO 83; 164pp; French.
XX The invention relates to an isolated antibody (Ab), and its functional
XX CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-
XX CC 1R) and optionally: (i) inhibit natural binding of insulin-like growth
XX CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine
XX CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or
XX CC treat diseases associated with overexpression and/or abnormal activity of
XX CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with
XX CC hyperactivity of signal transduction pathways mediated by interaction of
XX CC these receptors with their ligands. Especially they inhibit
XX CC proliferation of normal cells to tumor cells, inhibit growth and/or
XX CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
XX CC also for treating psoriasis. Ab are also used to diagnose diseases caused
XX CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a
XX CC protein sequence used to generate the Ab of the invention.
XX SQ Sequence 117 AA;
```

CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or
CC treat diseases associated with overexpression and/or abnormal activity of
CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with
CC hyperactivity of signal transduction pathways mediated by interaction of
CC these receptors with their ligands. Especially they inhibit
CC transformation of normal cells to tumor cells, inhibit growth and/or
CC proliferation of tumor cells, so are useful against cancers of the
CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
CC also for treating psoriasis. Ab are also used to diagnose diseases caused
CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a
CC protein sequence used to generate the Ab of the invention.
XX
SQ Sequence 117 AA;

Query Match 100.0%; Score 89; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16
DB 51 YISYDGTNNYKPSLKD 66
|||||

RESULT 6
ADJ76913
ID ADJ76913 standard; protein; 117 AA.

XX AC ADJ76913;
XX DT 06-MAY-2004 (first entry)
XX DE Anti-IGF-1R related protein #24.
XX KW cytotatic; antipsoriatic; antibody;
XX KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;
XX KW or epidermal growth factor receptor; EGFR; signal transduction pathway;
XX KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;
XX KW CDR.
XX OS Homo sapiens.
XX PN WO2003059951-A2.
XX PD 24-JUL-2003.
XX PF 20-JAN-2003; 2003WO-FR000178.
XX PR 18-JAN-2002; 2002FR-0000653.
XX PR 18-JAN-2002; 2002FR-0000654.
XX PR 07-MAY-2002; 2002FR-00005753.
XX PA (FABR) FABRE MEDICAMENT SA PIERRE.
XX PI Goetsch L, Corvaia N, Leger O;
XX DR WPI; 2003-569653/53.

XX New antibodies that bind to human insulin-like growth factor receptor,
XX useful for treatment, prevention and diagnosis of cancers.
XX PS Disclosure; SEQ ID NO 79; 164pp; French.
XX

XX The invention relates to an isolated antibody (Ab), and its functional
XX fragments, that bind to human insulin-like growth factor-1 receptor (IGF-
XX 1R) and optionally; (i) inhibit natural binding of insulin-like growth
XX factors (IGF)-1 and/or -2, and/or (ii) inhibit specifically tyrosine
XX kinase activity of IGF-1R. Ab and its fragments are used to prevent or
XX treat diseases associated with overexpression and/or abnormal activity of
XX IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with
XX hyperactivity of signal transduction pathways mediated by interaction of
XX these receptors with their ligands. Especially they inhibit
XX transformation of normal cells to tumor cells, inhibit growth and/or
XX proliferation of tumor cells, so are useful against cancers of the

CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
CC also for treating psoriasis. Ab are also used to diagnose diseases caused
CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a
CC protein sequence used to generate the Ab of the invention.
XX
SQ Sequence 117 AA;

Query Match 100.0%; Score 89; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16
DB 51 YISYDGTNNYKPSLKD 66
|||||

RESULT 7
ADZ67083
ID ADZ67083 standard; protein; 117 AA.

XX AC ADZ67083;
XX DT 30-JUN-2005 (first entry)
XX DE Human antibody 7C10 2 heavy chain variable region SEQ ID NO:79.
XX KW Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
XX KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;
XX KW musculoskeletal disease; respiratory disease; lung tumor;
XX KW endocrine disease; gynecology and obstetrics; breast tumor;
XX KW endometroid carcinoma; gastrointestinal disease; colon tumor;
XX KW antipsoriatic; psoriasis; dermatological disease; immune disorder;
XX KW heavy chain variable region.

XX OS Homo sapiens.

XX PN US2005084906-A1.

XX PD 21-APR-2005.

XX PF 16-DEC-2003; 2003US-00735916.

XX PR 18-JAN-2002; 2002FR-00000653.

XX PR 18-JAN-2002; 2002FR-0000654.

XX PR 07-MAY-2002; 2002FR-00005753.

XX PR 20-JAN-2003; 2003WO-FR000178.

XX PR 11-JUL-2003; 2003FR-00008538.

XX PA (GOET/) GOETSCH L.

XX PA (CORV/) CORVAIA N.

XX PA (LEGE/) LEGER O.

XX PA (DUFL/) DUFLLOS A.

XX PA (HAEU/) HAEUW J.

XX PA (BECK/) BECK A.

XX PI Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;
XX DR WPI; 2005-321968/33.

XX PT Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)
XX antibody or its functional fragment, being capable of binding human IGF-
XX IR and specifically inhibiting tyrosine kinase activity of receptor,
XX useful for treating cancer.

XX PS Example 13; SEQ ID NO 79; 125pp; English.

XX The invention relates to a novel isolated anti-insulin-like growth factor
XX I receptor (IGF-IR) antibody (I) or its functional fragment, being
XX capable of binding to human IGF-IR and, if necessary, capable of
XX specifically inhibiting tyrosine kinase activity of the receptor,
XX comprising a light or heavy chain having at least one complementary
XX determining region (CDR) consisting of one of two fully defined 16 amino
XX acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in

CC the preparation of a medicament intended for the prevention or treatment
 CC of an illness connected with an overexpression and/or an abnormal
 CC activation of the IGF-IR and/or EGFR, and/or connected with a
 CC hyperactivation of the transduction pathway of the signal mediated by the
 CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGFR with EGFR, where
 CC the administration of the medicament does not induce or only slightly
 CC induces secondary effects connected with inhibition of the insulin
 CC receptor. The antibody is useful for preparation of a medicament intended
 CC to inhibit the transformation of normal cells into cells with tumoral
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is
 CC useful for preparation of a medicament intended to inhibit the growth
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,
 CC especially IGF1- and/or IGF2-dependent and/or EGF-dependent and/or
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a
 CC medicament intended for prevention or for the treatment of cancer, where
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the
 CC preparation of a medicament intended for the prevention or for the
 CC treatment of psoriasis. (I) is useful in preparation of a medicament
 CC intended for the specific targeting of a biologically active compound to
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)
 CC is useful for in vitro diagnosis of illnesses induced by an
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor
 CC starting from a biological sample in which the abnormal presence, of IGF-
 CC IR and/or EGFR receptor is suspected, which involves contacting the
 CC biological sample with (I), which is optionally labeled. The present
 CC sequence is used in the exemplification of the invention.

XX SQ Sequence 117 AA;

Query Match 100.0%; Score 89; DB 9; Length 117;
 Best Local Similarity 100.0%; Pred. No. 5e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16
 |||||
 DB 51 YISYDGTNNYKPSLKD 66

RESULT 8

ID ADZ67087 standard; protein; 117 AA.

XX AC ADZ67087;

XX DT 30-JUN-2005 (first entry)

XX DE Human antibody 7C10 3 heavy chain variable region SEQ ID NO:83.

XX Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
 KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;
 KW musculoskeletal disease; respiratory disease; lung tumor;
 KW endocrine disease; gynecology and obstetrics; breast tumor;
 KW endometrial carcinoma; gastrointestinal disease; colon tumor;
 KW antiproliferative; psoriasis; dermatological disease; immune disorder;
 KW heavy chain variable region.

XX OS Homo sapiens.

XX PN US2005084906-A1.

XX PD 21-APR-2005.

XX PF 16-DEC-2003; 2003US-00735916.

XX PR 18-JAN-2002; 2002FR-00000653.

XX PR 18-JAN-2002; 2002FR-00000654.

XX PR 07-MAY-2002; 2002FR-00005753.

XX PR 20-JAN-2003; 2003WO-FR000178.

XX PR 11-JUL-2003; 2003FR-00008538.

XX FA (GOETSCH L.

PA (CORV/) CORVAIA N.
 PA (LEGE/) LEGER O.
 PA (DUFEL/) DUFLOS A.
 PA (HAEU/) HAEUW J.
 PA (BECK/) BECK A.

XX Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;

XX WPI; 2005-321968/33.

XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)
 PT antibody or its functional fragment, being capable of binding human IGF-
 PT IR and specifically inhibiting tyrosine kinase activity of receptor,
 PT useful for treating cancer.

XX Example 13; SEQ ID NO 83; 125pp; English.

XX The invention relates to a novel isolated anti-insulin-like growth factor
 CC I receptor (IGF-IR) antibody (I) or its functional fragment, being
 CC capable of binding to human IGF-IR and, if necessary, capable of
 CC specifically inhibiting tyrosine kinase activity of the receptor,
 CC comprising a light or heavy chain having at least one complementary
 CC determining region (CDR) consisting of one of two fully defined 16 amino
 CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in
 CC the preparation of a medicament intended for the prevention or treatment
 CC of an illness connected with an overexpression and/or an abnormal
 CC activation of the IGF-IR and/or EGFR, and/or connected with a
 CC hyperactivation of the transduction pathway of the signal mediated by the
 CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGFR with EGFR, where
 CC the administration of the medicament does not induce or only slightly
 CC induces secondary effects connected with inhibition of the insulin
 CC receptor. The antibody is useful for preparation of a medicament intended
 CC to inhibit the transformation of normal cells into cells with tumoral
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is
 CC useful for preparation of a medicament intended to inhibit the growth
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,
 CC especially IGF1- and/or IGF2-dependent and/or EGF-dependent and/or
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a
 CC medicament intended for prevention or for the treatment of cancer, where
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the
 CC preparation of a medicament intended for the prevention or for the
 CC treatment of psoriasis. (I) is useful in preparation of a medicament
 CC intended for the specific targeting of a biologically active compound to
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)
 CC is useful for in vitro diagnosis of illnesses induced by an
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor
 CC starting from a biological sample in which the abnormal presence, of IGF-
 CC IR and/or EGFR receptor is suspected, which involves contacting the
 CC biological sample with (I), which is optionally labeled. The present
 CC sequence is used in the exemplification of the invention.

XX SQ Sequence 117 AA;

Query Match 100.0%; Score 89; DB 9; Length 117;

Best Local Similarity 100.0%; Pred. No. 5e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16
 |||||
 DB 51 YISYDGTNNYKPSLKD 66

RESULT 9

ADZ67073,

ID ADZ67073 standard; protein; 117 AA.

XX AC ADZ67073;

XX DT 30-JUN-2005 (first entry)

XX DE Murine immunoglobulin heavy chain variable region 7C10 VH SEQ ID NO:69.

XX Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
 KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;
 KW musculoskeletal disease; respiratory disease; lung tumor;
 KW endocrine disease; gynecology and obstetrics; breast tumor;
 KW endometroid carcinoma; gastrointestinal disease; colon tumor;
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder;
 KW immunoglobulin; heavy chain variable region.
 XX Mus musculus.
 XX US2005084906-A1.
 XX 21-APR-2005.
 XX 16-DEC-2003; 2003US-00735916.
 XX 18-JAN-2002; 2002FR-00000653.
 XX 18-JAN-2002; 2002FR-00000654.
 XX 07-MAY-2002; 2002FR-00005753.
 XX 20-JAN-2003; 2003WO-FR000178.
 XX 11-JUL-2003; 2003FR-00008538.
 XX (GOET/) GOETSCH L.
 XX (CORV/) CORVAIA N.
 XX (LEGE/) LEGER O.
 XX (DUFL/) DUFLOS A.
 XX (HAEU/) HAEUW J.
 XX (BECK/) BECK A.
 XX Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;
 PI WPI; 2005-321968/33.
 XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)
 PT antibody or its functional fragment, being capable of binding human IGF-
 PT IR and specifically inhibiting tyrosine kinase activity of receptor,
 PT useful for treating cancer.
 XX Example 13; SEQ ID NO 69; 125pp; English.
 XX The invention relates to a novel isolated anti-insulin-like growth factor
 CC I receptor (IGF-IR) antibody (I) or its functional fragment, being
 CC capable of binding to human IGF-IR and, if necessary, capable of
 CC specifically inhibiting tyrosine kinase activity of the receptor,
 CC comprising a light or heavy chain having at least one complementary
 CC determining region (CDR) consisting of one of two fully defined 16 amino
 CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in
 CC the preparation of a medicament intended for the prevention or treatment
 CC of an illness connected with an overexpression and/or an abnormal
 CC activation of the IGF-IR and/or EGFR, and/or connected with a
 CC hyperactivation of the transduction pathway of the signal mediated by the
 CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where
 CC the administration of the medicament does not induce or only slightly
 CC induces secondary effects connected with inhibition of the insulin
 CC receptor. The antibody is useful for preparation of a medicament intended
 CC to inhibit the transformation of normal cells into cells with tumoral
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is
 CC useful for preparation of a medicament intended to inhibit the growth
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a
 CC medicament intended for prevention or for the treatment of cancer, where
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the
 CC preparation of a medicament intended for the prevention or for the
 CC treatment of psoriasis. (I) is useful in preparation of a medicament
 CC intended for the specific targeting of a biologically active compound to
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)
 CC is useful for in vitro diagnosis of illnesses induced by an
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor
 CC starting from a biological sample in which the abnormal presence, of IGF-

CC IR and/or EGFR receptor is suspected, which involves contacting the
 CC biological sample with (I), which is optionally labeled. The present
 CC sequence is used in the exemplification of the invention.
 XX Sequence 117 AA;
 SQ Query Match 100.0%; Score 89; DB 9; Length 117;
 Best Local Similarity 100.0%; Pred. No. 5e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YISYDGTNNYKPSLKD 16
 DB 51 YISYDGTNNYKPSLKD 66
 RESULT 10
 ADZ67079
 ID ADZ67079 standard; protein; 117 AA.
 XX AC ADZ67079;
 XX 30-JUN-2005 (first entry)
 XX Human antibody 7C10 1 heavy chain variable region SEQ ID NO:75.
 XX Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
 KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;
 KW musculoskeletal disease; respiratory disease; lung tumor;
 KW endocrine disease; gynecology and obstetrics; breast tumor;
 KW endometroid carcinoma; gastrointestinal disease; colon tumor;
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder;
 KW heavy chain variable region.
 XX Homo sapiens.
 XX US2005084906-A1.
 XX 21-APR-2005.
 XX 16-DEC-2003; 2003US-00735916.
 XX 18-JAN-2002; 2002FR-00000653.
 XX 18-JAN-2002; 2002FR-00000654.
 XX 07-MAY-2002; 2002FR-00005753.
 XX 20-JAN-2003; 2003WO-FR000178.
 XX 11-JUL-2003; 2003FR-00008538.
 XX (GOET/) GOETSCH L.
 XX (CORV/) CORVAIA N.
 XX (LEGE/) LEGER O.
 XX (DUFL/) DUFLOS A.
 XX (HAEU/) HAEUW J.
 XX (BECK/) BECK A.
 XX Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;
 PI WPI; 2005-321968/33.
 XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)
 PT antibody or its functional fragment, being capable of binding human IGF-
 PT IR and specifically inhibiting tyrosine kinase activity of receptor,
 PT useful for treating cancer.
 XX Example 13; SEQ ID NO 75; 125pp; English.
 XX The invention relates to a novel isolated anti-insulin-like growth factor
 CC I receptor (IGF-IR) antibody (I) or its functional fragment, being
 CC capable of binding to human IGF-IR and, if necessary, capable of
 CC specifically inhibiting tyrosine kinase activity of the receptor,
 CC comprising a light or heavy chain having at least one complementary
 CC determining region (CDR) consisting of one of two fully defined 16 amino
 CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in
 CC the preparation of a medicament intended for the prevention or treatment

CC of an illness connected with an overexpression and/or an abnormal
 CC activation of the IGF-1R and/or EGFR, and/or connected with a
 CC hyperactivation of the transduction pathway of the signal mediated by the
 CC interaction of IGF1 or IGF2 with IGF-1R and/or of EGF with EGFR, where
 CC the administration of the medicament does not induce or only slightly
 CC induces secondary effects connected with inhibition of the insulin
 CC receptor. The antibody is useful for preparation of a medicament intended
 CC to inhibit the transformation of normal cells into cells with tumoral
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is
 CC useful for preparation of a medicament intended to inhibit the growth
 CC and/or the proliferation of tumor cells, preferably IGF-dependent and/or
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a
 CC medicament intended for prevention or for the treatment of cancer, where
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the
 CC preparation of a medicament intended for the prevention or for the
 CC treatment of psoriasis. (I) is useful in preparation of a medicament
 CC intended for the specific targeting of a biologically active compound to
 CC cells expressing or overexpressing the IGF-1R and/or EGFR receptor. (I)
 CC is useful for in vitro diagnosis of illnesses induced by an
 CC overexpression or an underexpression of the IGF-1R and/or EGFR receptor
 CC starting from a biological sample in which the abnormal presence, of IGF-
 CC 1R and/or EGFR receptor is suspected, which involves contacting the
 CC biological sample with (I), which is optionally labeled. The present
 CC sequence is used in the exemplification of the invention.

XX SQ Sequence 117 AA;

Query Match 100.0%; Score 89; DB 9; Length 117;
 Best Local Similarity 100.0%; Pred. No. 5e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLKD 16
 |||||
 Db 51 YISYDGTNNYKPSLKD 66

RESULT 11

ADJ76886
 ID ADJ76886 standard; protein; 127 AA.

XX AC ADJ76886;

XX DT 06-MAY-2004 (first entry)

XX DE Anti-IGF-1R related protein #4.

XX KW cytostatic; antipsoriatic; antibody;
 KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;
 KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;
 KW CDR.

XX OS Mus musculus.

XX FN WO2003059951-A2.

XX PD 24-JUL-2003.

XX PF 20-JAN-2003; 2003WO-FR000178.

XX PR 18-JAN-2002; 2002FR-00000653.

XX PR 18-JAN-2002; 2002FR-00000654.

XX PR 07-MAY-2002; 2002FR-00005753.

XX PA (FABR) FABRE MEDICAMENT SA PIERRE.

XX FI Goetsch L, Corvaia N, Leger O;

XX DR WPI; 2003-569653/53.

PT New antibodies that bind to human insulin-like growth factor receptor,
 PT useful for treatment, prevention and diagnosis of cancers.

XX PS Disclosure; SEQ ID NO 52; 164pp; French.

XX CC The invention relates to an isolated antibody (Ab), and its functional
 CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-
 CC 1R) and optionally: (i) inhibit natural binding of insulin-like growth
 CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine
 CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or
 CC treat diseases associated with overexpression and/or abnormal activity of
 CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with
 CC hyperactivity of signal transduction pathways mediated by interaction of
 CC these receptors with their ligands. Especially they inhibit
 CC transformation of normal cells to tumor cells, inhibit growth and/or
 CC proliferation of tumor cells, so are useful against cancers of the
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a
 CC protein sequence used to generate the Ab of the invention.

XX SQ Sequence 127 AA;

Query Match 100.0%; Score 89; DB 7; Length 127;
 Best Local Similarity 100.0%; Pred. No. 5.5e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLKD 16
 |||||
 Db 61 YISYDGTNNYKPSLKD 76

RESULT 12

ADZ67056
 ID ADZ67056 standard; protein; 127 AA.

XX AC ADZ67056;

XX DT 30-JUN-2005 (first entry)

XX DE Murine immunoglobulin heavy chain variable region 7C10 VH SEQ ID NO:52.

XX KW Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
 KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;
 KW musculoskeletal disease; respiratory disease; lung tumor;
 KW endocrine disease; gynecology and obstetrics; breast tumor;
 KW endometrial carcinoma; gastrointestinal disease; colon tumor;
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder;
 KW immunoglobulin; heavy chain variable region.

XX OS Mus musculus.

XX Key Location/Qualifiers
 FH Peptide 1..10
 FT /note= "leader peptide"

FT Region 41..46
 FT /note= "CDR1"

FT Region 61..76
 FT /note= "CDR2"

FT Region 109..116
 FT /note= "CDR3"

XX US2005084906-A1.

XX PD 21-APR-2005.

XX PF 16-DEC-2003; 2003US-00735916.

XX PR 18-JAN-2002; 2002FR-00000653.

XX PR 18-JAN-2002; 2002FR-00000654.

XX PR 07-MAY-2002; 2002FR-00005753.

XX PR 20-JAN-2003; 2003WO-FR000178.

XX PR 11-JUL-2003; 2003FR-00008538.

XX (GOET/) GOETSCH L.
 PA (CORV/) CORVAIA N.
 PA (LEGE/) LEGER O.
 PA (DUFL/) DUFLOS A.
 PA (HAU/) HAEUW J.
 PA (BECK/) BECK A.
 XX
 XX Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;
 XX WPI; 2005-321968/33.
 XX N-PSDB; ADZ67055.
 XX
 XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)
 PT antibody or its functional fragment, being capable of binding human IGF-
 PT IR and specifically inhibiting tyrosine kinase activity of receptor,
 PT useful for treating cancer.
 XX
 XX Example 8; SEQ ID NO 52; 125pp; English.
 XX
 XX The invention relates to a novel isolated anti-insulin-like growth factor
 CC I receptor (IGF-IR) antibody (I) or its functional fragment, being
 CC capable of binding to human IGF-IR and, if necessary, capable of
 CC specifically inhibiting tyrosine kinase activity of the receptor,
 CC comprising a light or heavy chain having at least one complementary
 CC determining region (CDR) consisting of one of two fully defined 16 amino
 CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in
 CC the preparation of a medicament intended for the prevention or treatment
 CC of an illness connected with an overexpression and/or an abnormal
 CC activation of the IGF-IR and/or EGFR, and/or connected with a
 CC hyperactivation of the transduction pathway of the signal mediated by the
 CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where
 CC the administration of the medicament does not induce or only slightly
 CC induces secondary effects connected with inhibition of the insulin
 CC receptor. The antibody is useful for preparation of a medicament intended
 CC to inhibit the transformation of normal cells into cells with tumoral
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is
 CC useful for preparation of a medicament intended to inhibit the growth
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,
 CC especially IGF1 and/or IGF2-dependent and/or EGF-dependent and/or
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a
 CC medicament intended for prevention or for the treatment of cancer, where
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the
 CC preparation of a medicament intended for the prevention or for the
 CC treatment of psoriasis. (I) is useful in preparation of a medicament
 CC intended for the specific targeting of a biologically active compound to
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)
 CC is useful for in vitro diagnosis of illnesses induced by an
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor
 CC starting from a biological sample in which the abnormal presence, of IGF-
 CC IR and/or EGFR receptor is suspected, which involves contacting the
 CC biological sample with (I), which is optionally labeled. The present
 CC sequence is used in the exemplification of the invention.
 XX
 XX Sequence 127 AA;
 XX
 XX Query Match 100.0%; Score 89; DB 9; Length 127;
 XX Best Local Similarity 100.0%; Pred. No. 5.5e-06;
 XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YISYDGTNNYKPSLKD 16
 Db ||||||||||||||||
 61 YISYDGTNNYKPSLKD 76
 RESULT 13
 ID ADJ76911
 XX ADJ76911 standard; protein; 135 AA.
 XX
 AC ADJ76911;
 XX

DT 06-MAY-2004 (first entry)
 XX
 DE Anti-IGF-IR related protein #23.
 XX
 KW cytotatic; antipsoriatic; antibody;
 KW insulin-like growth factor-1 receptor; IGF-IR; tyrosine kinase activity;
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;
 KW ligand; tumor; cancer; osteosarcoma; complementarily determining region;
 KW CDR.
 XX
 OS Homo sapiens.
 XX
 XX W02003059951-A2.
 PN
 XX 24-JUL-2003.
 PD
 XX
 XX 20-JAN-2003; 2003WO-FR000178.
 PF
 XX 18-JAN-2002; 2002FR-00000653.
 PR
 XX 18-JAN-2002; 2002FR-00000654.
 PR
 XX 07-MAY-2002; 2002FR-00005753.
 XX
 PA (FABR) FABRE MEDICAMENT SA PIERRE.
 XX
 PI Goetsch L, Corvaia N, Leger O;
 XX
 DR WPI; 2003-569653/53.
 XX
 PT New antibodies that bind to human insulin-like growth factor receptor,
 PT useful for treatment, prevention and diagnosis of cancers.
 XX
 XX Disclosure; SEQ ID NO 77; 164pp; French.
 XX
 XX The invention relates to an isolated antibody (Ab), and its functional
 CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-
 CC IR) and optionally: (i) inhibit natural binding of insulin-like growth
 CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine
 CC kinase activity of IGF-IR. Ab and its fragments are used to prevent or
 CC treat diseases associated with overexpression and/or abnormal activity of
 CC IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with
 CC hyperactivity of signal transduction pathways mediated by interaction of
 CC these receptors with their ligands. Especially they inhibit
 CC transformation of normal cells to tumor cells, inhibit growth and/or
 CC proliferation of tumor cells, so are useful against cancers of the
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused
 CC by abnormal expression of IGF-IR and/or EGFR. This sequence represents a
 CC protein sequence used to generate the Ab of the invention.
 XX
 XX Sequence 135 AA;
 XX
 XX Query Match 100.0%; Score 89; DB 7; Length 135;
 XX Best Local Similarity 100.0%; Pred. No. 5.9e-06;
 XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YISYDGTNNYKPSLKD 16
 Db ||||||||||||||||
 69 YISYDGTNNYKPSLKD 84
 RESULT 14
 ADJ76919
 ID ADJ76919 standard; protein; 135 AA.
 XX
 AC ADJ76919;
 XX
 XX 06-MAY-2004 (first entry)
 DT
 XX Anti-IGF-IR related protein #27.
 DE
 XX cytotatic; antipsoriatic; antibody;
 KW insulin-like growth factor-1 receptor; IGF-IR; tyrosine kinase activity;
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;
 KW

KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;
 KW CDR.
 XX
 OS Homo sapiens.
 XX
 PN WO2003059951-A2.
 XX
 XX
 PD 24-JUL-2003.
 XX
 XX 20-JAN-2003; 2003WO-FR000178.
 XX
 XX 18-JAN-2002; 2002FR-0000653.
 PR 18-JAN-2002; 2002FR-0000654.
 PR 07-MAY-2002; 2002FR-00005753.
 XX
 XX (FABR) FABRE MEDICAMENT SA PIERRE.
 XX
 XX Goetsch L, Corvaia N, Leger O;
 PI WPI; 2003-569653/53.
 XX
 DR New antibodies that bind to human insulin-like growth factor receptor,
 XX useful for treatment, prevention and diagnosis of cancers.
 PT
 PS Disclosure; SEQ ID NO 85; 164pp; French.
 XX
 XX The invention relates to an isolated antibody (Ab), and its functional
 CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-
 CC IR) and optionally: (i) inhibit natural binding of insulin-like growth
 CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine
 CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or
 CC treat diseases associated with overexpression and/or abnormal activity of
 CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with
 CC hyperactivity of signal transduction pathways mediated by interaction of
 CC these receptors with their ligands. Especially they inhibit
 CC transformation of normal cells to tumor cells, inhibit growth and/or
 CC proliferation of tumor cells, so are useful against cancers of the
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a
 CC protein sequence used to generate the Ab of the invention.
 XX
 SQ Sequence 135 AA;
 Query Match 100.0%; Score 89; DB 7; Length 135;
 Best Local Similarity 100.0%; Pred. No. 5.9e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YISYDGTNNYKPSLKD 16
 DB 69 YISYDGTNNYKPSLKD 84
 RESULT 15
 ADJ76915
 ID ADJ76915 standard; protein; 135 AA.
 XX
 AC ADJ76915;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Anti-IGF-1R related protein #25.
 XX
 KW cytosolic; antipsoriatic; antibody;
 KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;
 KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;
 KW CDR.
 XX
 XX Homo sapiens.
 OS
 XX WO2003059951-A2.
 PN

PD 24-JUL-2003.
 XX
 PF 20-JAN-2003; 2003WO-FR000178.
 XX
 XX 18-JAN-2002; 2002FR-0000653.
 PR 18-JAN-2002; 2002FR-0000654.
 PR 07-MAY-2002; 2002FR-00005753.
 XX
 XX (FABR) FABRE MEDICAMENT SA PIERRE.
 XX
 XX Goetsch L, Corvaia N, Leger O;
 PI WPI; 2003-569653/53.
 XX
 DR New antibodies that bind to human insulin-like growth factor receptor,
 XX useful for treatment, prevention and diagnosis of cancers.
 PT
 PS Disclosure; SEQ ID NO 81; 164pp; French.
 XX
 XX The invention relates to an isolated antibody (Ab), and its functional
 CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-
 CC IR) and optionally: (i) inhibit natural binding of insulin-like growth
 CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine
 CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or
 CC treat diseases associated with overexpression and/or abnormal activity of
 CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with
 CC hyperactivity of signal transduction pathways mediated by interaction of
 CC these receptors with their ligands. Especially they inhibit
 CC transformation of normal cells to tumor cells, inhibit growth and/or
 CC proliferation of tumor cells, so are useful against cancers of the
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a
 CC protein sequence used to generate the Ab of the invention.
 XX
 SQ Sequence 135 AA;
 Query Match 100.0%; Score 89; DB 7; Length 135;
 Best Local Similarity 100.0%; Pred. No. 5.9e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YISYDGTNNYKPSLKD 16
 DB 69 YISYDGTNNYKPSLKD 84
 Search completed: December 30, 2005, 13:24:01
 Job time : 143.194 secs

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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:11:41 ; Search time 22.7097 Seconds
(without alignments)
67.789 Million cell updates/sec

Title: US-10-735-916A-10
Perfect score: 89
Sequence: 1 YISYDGTNNYKPSLKD 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: Pirl.*
2: Pirl2.*
3: Pirl3.*
4: Pirl4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	75	84.3	104	2 S26467	Ig heavy chain V r
2	75	84.3	116	1 HVMS31	Ig heavy chain pre
3	72	80.9	120	2 A25114	Ig heavy chain v r
4	70	78.7	119	2 B25114	Ig heavy chain v r
5	69	77.5	136	2 S07637	Ig heavy chain v r
6	68	76.4	121	2 S37200	Ig heavy chain v r
7	66	74.2	116	2 S38718	Ig heavy chain v r
8	65	73.0	115	2 F25114	Ig heavy chain v r
9	65	73.0	117	2 C25114	Ig heavy chain v r
10	61	68.5	119	2 D25114	Ig heavy chain v r
11	61	68.5	137	1 AVM335	Ig heavy chain pre
12	61	68.5	106	2 S59639	Ig heavy chain v r
13	58	65.2	106	2 S26464	Ig heavy chain v r
14	57	64.0	134	2 B24672	Ig heavy chain pre
15	57	64.0	97	2 S26906	Ig heavy chain v r
16	56	62.9	97	2 S12416	Ig heavy chain v r
17	56	62.9	99	2 S12412	Ig heavy chain v r
18	56	62.9	105	2 S44125	Ig lambda chain v
19	56	62.9	116	2 B26340	Ig heavy chain pre
20	56	62.9	118	2 A26340	Ig heavy chain pre
21	56	62.9	130	2 S13690	Ig heavy chain v r
22	56	62.9	140	2 I37782	Ig variable region
23	56	62.9	94	2 PH0876	Ig heavy chain v r
24	55	61.8	97	2 S26461	Ig heavy chain v r
25	54	60.7	100	2 S14485	Ig heavy chain v r
26	54	60.7	101	2 S14484	Ig heavy chain v r
27	54	60.7	102	2 S14486	Ig heavy chain v r
28	54	60.7	102	2 S14486	Ig heavy chain v r
29	54	60.7	113	1 G2MS60	Ig heavy chain v r

30	54	60.7	115	2 S57464	Ig heavy chain V-J
31	54	60.7	115	2 D33932	Ig mu chain precu
32	53	59.6	114	2 T01262	Ig heavy chain v r
33	53	59.6	146	2 S09711	Ig heavy chain v r
34	51	57.3	102	2 S14487	Ig heavy chain v r
35	51	57.3	102	2 S14488	Ig heavy chain v r
36	51	57.3	116	1 HVMS1B	Ig heavy chain pre
37	51	57.3	135	2 PL0100	Ig heavy chain pre
38	49	55.1	123	2 S42771	Ig heavy chain - m
39	48	53.9	98	2 S12414	Ig heavy chain v r
40	48	53.9	98	2 S26903	Ig heavy chain v r
41	48	53.9	99	2 S26801	Ig heavy chain v r
42	48	53.9	99	2 S26802	Ig heavy chain v r
43	48	53.9	99	2 S26803	Ig heavy chain v r
44	48	53.9	116	2 S37456	Ig mu chain - huma
45	48	53.9	117	2 E34964	Ig heavy chain pre

ALIGNMENTS

RESULT 1

S26467
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S26467
R;Kavaler, J.
submitted to the EMBL Data Library, April 1991
A;Reference number: S26459
A;Accession: S26467
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-104 <KAV>
A;Cross-references: UNIPARC:UPI0000115F5F; EMBL:X59105; NID:G51939; PIDN:CAA41831.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;6-89/Domain: immunoglobulin homology <IMM>

Query Match 84.3%; Score 75; DB 2; Length 104;
Best Local Similarity 81.2%; Pred. No. 5.2e-05;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16
DB 42 YISYDGTNNYKPSLKN 57
|||||:|||||:
|||||:|||||:

RESULT 2

HVMS31
Ig heavy chain precursor V region (M315) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
C;Accession: J0509
R;Levy, N.S.; Malpietro, U.V.; Lebecque, S.G.; Gearhart, P.J.
J. Exp. Med. 169, 2007-2019, 1989
A;Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary ir
A;Reference number: J0501; MUID:89279149; PMID:2499654
A;Accession: J0509
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-116 <LEV>
A;Cross-references: UNIPROT:P18531; UNIPARC:UPI00000278E0
A;Experimental source: strain BALB/cJ
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-116/Product: Ig heavy chain V region (M315) #status predicted <MAT>
F;33-116/Domain: immunoglobulin homology <IMM>

Query Match 84.3%; Score 75; DB 1; Length 116;
Best Local Similarity 81.2%; Pred. No. 5.8e-05;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16
|||||:|||||:
Db 69 YISYDGSNNYKPSLKN 84

RESULT 3
S07614
Ig heavy chain V region (HP22, HP27) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 21-Jul-2000
C:Accession: A25114
EMBO J. 4, 3681-3688, 1985
R;Ollier, P.; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau, M.
A:Title: The idiotypic network and the internal image: possible regulation of a germ-lin
A:Reference number: A91028; MUID:86136012; PMID:3937730
A:Accession: A25114
A:Molecule type: mRNA
A:Residues: 1-120 <OLL>
A:Cross-references: UNIPARC:UPI0000115D15; GB:X03374; NID:g51983; PIDN:CAA27071.1; PID:g
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 80.9%; Score 72; DB 2; Length 120;
Best Local Similarity 75.0%; Pred. No. 0.00018;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16
|||||:|||||:
Db 51 YINYDGSNNYKPSLKN 66

RESULT 4
E25114
Ig heavy chain V region (HP25) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 20-Jun-2000
C:Accession: E25114
R;Ollier, P.; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau, M.
EMBO J. 4, 3681-3688, 1985
A:Title: The idiotypic network and the internal image: possible regulation of a germ-lin
A:Reference number: A91028; MUID:86136012; PMID:3937730
A:Accession: E25114
A:Molecule type: mRNA
A:Residues: 1-119 <OLL>
A:Cross-references: UNIPARC:UPI0000115D24; GB:X03378; NID:g52007; PIDN:CAA27095.1; PID:g
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 78.7%; Score 70; DB 2; Length 119;
Best Local Similarity 75.0%; Pred. No. 0.00039;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16
|||||:|||||:
Db 51 YISYDGSNNYKPSLKN 66

RESULT 5
S07637
Ig heavy chain V region (PTF.02) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 23-Jul-1999
C:Accession: S07637
R;Urakov, D.N.; Deev, S.M.; Polyanovsky, O.I.
Nucleic Acids Res. 17, 9481, 1989
A:Title: The structure of the expressible VH gene from a hybridoma producing monoclonal
A:Reference number: S07637; MUID:90067954; PMID:2587273
A:Accession: S07637
A:Molecule type: DNA
A:Residues: 1-136 <URA>

A:Cross-references: UNIPARC:UPI0000115E36; EMBL:X16740; NID:g52099; PIDN:CAA34714.1; PID:
A>Note: the authors translated the codon TAT for residue 112 as Ile, TAC for residue 113
C:Genetics:
A:Introns: 15/3
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;33-116/Domain: immunoglobulin homology <IMM>

Query Match 77.5%; Score 69; DB 2; Length 136;
Best Local Similarity 75.0%; Pred. No. 0.00065;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16
|||||:|||||:
Db 69 YISYDGSNNYKPSLKN 84

RESULT 6
S37200
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000
C:Accession: S37200
R;Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Kreuzaler, F.
submitted to the EMBL Data Library, August 1993
A:Description: Production and cloning of TMV-specific monoclonal antibodies.
A:Reference number: S37200
A:Accession: S37200
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-121 <FIS>
A:Cross-references: UNIPARC:UPI00001161AC; EMBL:X74587; NID:g402639; PID:g402640
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 68; DB 2; Length 121;
Best Local Similarity 75.0%; Pred. No. 0.00083;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16
|||||:|||||:
Db 51 YISYDGRNDYKPSLKN 66

RESULT 7
S38718
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C:Accession: S38718
R;Cimani, A.Y.
submitted to the EMBL Data Library, November 1993
A:Reference number: S38713
A:Accession: S38718
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-116 <CIM>
A:Cross-references: UNIPARC:UPI0000117542; EMBL:X76018; NID:g416102; PIDN:CAA53605.1; PI:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.2%; Score 66; DB 2; Length 116;
Best Local Similarity 80.0%; Pred. No. 0.0017;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 15
|||||:|||||:
Db 51 YISYSGTTNNYKPSLKN 65

RESULT 8
F25114

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Ig heavy chain V region (HP12) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 20-Jun-2000
C;Accession: F25114
EMBO J. 4, 3681-3688, 1985
R;Ollier, P.; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau, M.
A;Title: The idiotypic network and the internal image: possible regulation of a germ-line
A;Reference number: A91028; MUID:86136012; PMID:3937730
A;Accession: F25114
A;Molecule type: mRNA
A;Residues: 1-115 <OLL>
A;Cross-references: UNIPARC:UPI0000115D28; GB:X03379; NID:G52013; PIDN:CAA27101.1; PID:G
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 73.0%; Score 65; DB 2; Length 115;
Best Local Similarity 73.3%; Pred. No. 0.0024;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLK 15
: |||||: |||||
Db 51 FIRYDGSNNYPSLK 65

RESULT 9
C25114
Ig heavy chain V region (HP20) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 20-Jun-2000
C;Accession: C25114
EMBO J. 4, 3681-3688, 1985
R;Ollier, P.; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau, M.
A;Title: The idiotypic network and the internal image: possible regulation of a germ-line
A;Reference number: A91028; MUID:86136012; PMID:3937730
A;Accession: C25114
A;Molecule type: mRNA
A;Residues: 1-119 <OLL>
A;Cross-references: UNIPARC:UPI0000115D1A; GB:X03376; NID:G51995; PIDN:CAA27083.1; PID:G
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 73.0%; Score 65; DB 2; Length 119;
Best Local Similarity 68.8%; Pred. No. 0.0025;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLK 16
: |||||: |||||
Db 51 YIKYDGSNNYPSLK 66

RESULT 10
I28195
Ig heavy chain V region (anti-haloperidol antibody D) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 01-Dec-1989 #sequence_revision 30-Sep-1991 #text_change 23-Jul-1999
C;Accession: I28195
R;Sherman, M.A.; Deans, R.J.; Bolger, M.B.
J. Biol. Chem. 263, 4059-4063, 1988
A;Title: Haloperidol binding to monoclonal antibodies. Hypervariable region amino acid s
A;Reference number: A28195; MUID:88153717; PMID:3267217
A;Accession: I28195
A;Molecule type: mRNA
A;Residues: 1-117 <SH>
A;Cross-references: UNIPARC:UPI0000114D72; GB:M19775; NID:g195526; PIDN:AAA38343.1; PID:
A;Note: the authors translated the codon AAC for residue 61 as Thr, and did not translat
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 68.5%; Score 61; DB 2; Length 117;
Best Local Similarity 73.3%; Pred. No. 0.011;

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Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLK 15
: |||||: |||||
Db 51 YISYGTTSYNPSLK 65

RESULT 11
D25114
Ig heavy chain V region (HP21) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 20-Jun-2000
C;Accession: D25114
EMBO J. 4, 3681-3688, 1985
R;Ollier, P.; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau, M.
A;Title: The idiotypic network and the internal image: possible regulation of a germ-line
A;Reference number: A91028; MUID:86136012; PMID:3937730
A;Accession: D25114
A;Molecule type: mRNA
A;Residues: 1-119 <OLL>
A;Cross-references: UNIPARC:UPI0000115D1F; GB:X03377; NID:G52001; PIDN:CAA27089.1; PID:G
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 68.5%; Score 61; DB 2; Length 119;
Best Local Similarity 68.8%; Pred. No. 0.011;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLK 16
: |||||: |||||
Db 51 YISFDGNNYPSLK 66

RESULT 12
AVM535
Ig heavy chain precursor V region (MOPC 315) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 24-Apr-1984 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: FLO102; S03262; A93814; A91462; A93787; S23599
R;Rinfret, A.; Horne, C.; Dorrington, K.J.; Klein, M.
Mol. Immunol. 26, 431-434, 1989
A;Title: Cloning, sequencing and expression of the rearranged MOPC 315 VH gene segment.
A;Reference number: FLO102; MUID:89238351; PMID:2497341
A;Accession: FLO102
A;Molecule type: mRNA
A;Residues: 1-137 <RI>
A;Cross-references: UNIPROT:P01822; UNIPARC:UPI000002727B; GB:M27638; NID:g602706; PIDN:
A;Experimental source: strain MOPC 315
R;Rinfret, A.; Dorrington, K.J.; Klein, M.
submitted to the EMBL Data Library, June 1988
A;Reference number: S03262
A;Accession: S03262
A;Molecule type: DNA
A;Residues: 1-15,'G',16-137 <RI2>
A;Cross-references: UNIPARC:UPI000016CE1C; EMBL:X07880; NID:g51760; PIDN:CAA30727.1; PID
R;Jilka, R.L.; Pectk, S.
Proc. Natl. Acad. Sci. U.S.A. 74, 5692-5696, 1977
A;Title: Amino acid sequence of the precursor region of MOPC-315 mouse immunoglobulin he
A;Reference number: A93814; MUID:78094475; PMID:414225
A;Accession: A93814
A;Molecule type: protein
A;Residues: 1-14,'H',16-31 <JIL>
A;Cross-references: UNIPARC:UPI000017373E
A;Note: the authors translated mRNA in vitro to obtain the precursor protein
R;Schechter, I.; Wolf, O.; Zemall, R.; Burstein, Y.
Fed. Proc. 38, 1839-1845, 1979
A;Title: Structure and function of immunoglobulin genes and precursors.
A;Reference number: A91462; MUID:79148758; PMID:428562
A;Accession: A91462
A;Molecule type: protein
A;Residues: 1,'X',3-11,'X',14-21 <SCH>
A;Cross-references: UNIPARC:UPI000017373F

```

A>Note: the authors translated mRNA in vitro to obtain the precursor protein
R;Francis, S.H.; Leslie, R.G.O.; Hood, L.; Eisen, H.N.
Proc. Natl. Acad. Sci. U.S.A. 71, 1123-1127, 1974
A;Title: Amino-acid sequence of the variable region of the heavy (alpha) chain of a mouse
A;Reference number: A93787; MUID:74170779; PMID:4524622
A;Accession: A93787
A:Molecule type: protein
A:Residues: 19-52, 'K', 53-75, 'BYGB', 80-101, 'D', 103-106, '2B', 109-122, 124-137 <FRA>
A;Cross-references: UNIPARC:UPI0000173740
R;Hood, L.; Margolies, M.; Givol, D.; Zakut, R.
unpublished results, cited by Padlan, E.A., Davies, D.R., Pecht, I., Givol, D., and Wigdalsky, A.
A;Reference number: A94484
A;Contents: annotation; revision to residue 53
R;Chedle, C.; Hook, L.B.; Givol, D.; Ricca, G.A.
Mol. Immunol. 29, 21-30, 1992
A;Title: Cloning and expression of the variable regions of mouse myeloma protein MOPC315
A;Reference number: S23599; MUID:92114886; PMID:1731188
A;Accession: S23599
A:Molecule type: mRNA
A:Residues: 19-137 <CHE>
A;Cross-references: UNIPARC:UPI0000113794; EMBL:X63972; NID:G53532; PIDN:CAA45384.1; PID
C;Comment: This alpha chain was isolated from a myeloma protein that has anti-dinitrophenyl
C;Genetics:
A;Introns: 15/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;1-18/Domain: signal sequence #status experimental <SIG>
F;19-136/Product: Ig heavy chain V region (MOPC 315) #status experimental <MAT>
F;33-116/Domain: immunoglobulin homology <IMM>

Query Match 68.5%; Score 61; DB 1; Length 137;
Best Local Similarity 62.5%; Pred. No. 0.013;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLKD 16
Db 69 FIKYDGSNGYNPSLKN 84

RESULT 13
Ig heavy chain V region N10 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 17-Mar-1999
C;Accession: S59639
R;Bossart-Whitaker, P.; Chang, C.Y.Y.; Novotny, J.; Benjamin, D.C.; Sheriff, S.
J. Mol. Biol. 253, 559-575, 1995
A;Title: The crystal structure of the antibody N10-staphylococcal nuclease complex at 2.
A;Reference number: S59639; MUID:96068846; PMID:7473734
A;Accession: S59639
A;Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-106 <BOS>
A;Cross-references: UNIPARC:UPI0000176905; EMBL:U25121
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;8-91/Domain: immunoglobulin homology <IMM>

Query Match 65.2%; Score 58; DB 2; Length 106;
Best Local Similarity 66.7%; Pred. No. 0.03;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLK 15
Db 44 YITYSGTTSYNPSLK 58

RESULT 14
S26464
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S26464

R;Kavaler, J.
submitted to the EMBL Data Library, April 1991
A;Reference number: S26459
A;Accession: S26464
A;Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-106 <KAV>
A;Cross-references: UNIPARC:UPI0000115P68; EMBL:X59114; NID:G51926; PIDN:CAA41840.1; PID:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;3-86/Domain: immunoglobulin homology <IMM>

Query Match 64.0%; Score 57; DB 2; Length 106;
Best Local Similarity 66.7%; Pred. No. 0.044;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLK 15
Db 39 YIYSYSGSTSYNPSLK 53

RESULT 15
B24672
Ig heavy chain precursor V region (VGAM3-2) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 18-Oct-1996
C;Accession: B24672
R;Winter, E.; Radbruch, A.; Krawinkel, U.
EMBO J. 4, 2861-2867, 1985
A;Reference number: A91022; MUID:86055722; PMID:2998759
A;Accession: B24672
A:Molecule type: DNA
A:Residues: 1-134 <WIN>
A;Cross-references: UNIPARC:UPI00001768F5
A;Note: this sequence was determined from the differentiated gene
C;Genetics:
A;Introns: 15/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-134/Product: Ig heavy chain V region VGAM3-2 #status predicted <MAT>
F;33-116/Domain: immunoglobulin homology <IMM>

Query Match 64.0%; Score 57; DB 2; Length 134;
Best Local Similarity 66.7%; Pred. No. 0.057;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLK 15
Db 69 YIHYSGSTSYNPSLK 83

Search completed: December 30, 2005, 13:34:56
Job time : 23.7097 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:11:26 ; Search time 144 Seconds
(without alignments)
78.392 Million cell updates/sec

Title: US-10-735-916A-10
Perfect score: 89
Sequence: 1 YISYDGTNNYKPSLKD 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75	84.3	116	1 HV60_MOUSE	P18531 mus musculus
2	72	80.9	98	2 Q33VR6_MOUSE	Q33vr6 mus musculus
3	72	80.9	120	2 Q33VR7_MOUSE	Q33vr7 mus musculus
4	72	80.9	479	2 Q99M22_MOUSE	Q99m22 mus musculus
5	70	78.7	98	2 Q53VQ4_MOUSE	Q53vq4 mus musculus
6	70	78.7	119	2 Q53VQ5_MOUSE	Q53vq5 mus musculus
7	69	77.5	136	2 Q53VQ6_MOUSE	Q53vq6 mus musculus
8	68	76.4	483	2 Q50U13_MOUSE	Q50u13 mus musculus
9	65	73.0	98	2 Q53VQ0_MOUSE	Q53vq0 mus musculus
10	65	73.0	98	2 Q53VR2_MOUSE	Q53vr2 mus musculus
11	65	73.0	115	2 Q53VQ1_MOUSE	Q53vq1 mus musculus
12	65	73.0	119	2 Q53VR3_MOUSE	Q53vr3 mus musculus
13	61	68.5	98	2 Q53VQ8_MOUSE	Q53vq8 mus musculus
14	61	68.5	119	2 Q53VQ9_MOUSE	Q53vq9 mus musculus
15	61	68.5	137	1 HV46_MOUSE	P01822 mus musculus
16	56	62.9	139	2 Q86SX2_HUMAN	Q86sx2 homo sapien
17	55	61.8	119	2 Q5UL73_HUMAN	Q5ul73 homo sapien
18	54	60.7	113	1 HV47_MOUSE	P01823 mus musculus
19	52	58.4	615	2 Q569B6_RAT	Q569b6 rattus norv
20	51	57.3	116	1 HV61_MOUSE	P18532 mus musculus
21	51	57.3	477	2 Q6GMX7_HUMAN	Q6gmxi homo sapien
22	50	56.2	358	2 Q4JSK6_CORJK	Q4jsk6 corynebacte
23	49	55.1	262	2 Q65Z11_MOUSE	Q65z11 mus musculus
24	49	55.1	378	2 Q4S891_DICDI	Q4s891 dictyosteli
25	48	53.9	455	2 Q8CXP9_OCEIH	Q8cxp9 oceanobacil
26	48	53.9	476	2 Q6GMX1_HUMAN	Q6gmxi homo sapien
27	47	53.9	590	2 Q569B8_RAT	Q569b8 rattus norv
28	47	52.8	116	2 Q7Z3Y6_HUMAN	Q7z3y6 homo sapien
29	47	52.8	476	2 Q6WZK7_HUMAN	Q6wzk7 homo sapien
30	47	52.8	595	2 Q8WUX4_HUMAN	Q8wux4 homo sapien
31	47	52.8	597	2 Q9BU10_HUMAN	Q9bu10 homo sapien

32	47	52.8	597	2	Q6GMX5_HUMAN	Q6gmxi homo sapien
33	47	52.8	625	2	Q96AA6_HUMAN	Q96aa6 homo sapien
34	47	52.8	1547	2	Q7QV96_GIALA	Q7qv96 giardia lam
35	46	51.7	102	2	Q5A937_CANAL	Q5a937 candida alb
36	46	51.7	119	1	HV40_MOUSE	P01810 mus musculu
37	46	51.7	179	2	Q4T5M8_TETNG	Q4t5m8 tetraodon n
38	46	51.7	321	2	Q8TZN1_PYRFU	Q8tzn1 pyrococcus
39	46	51.7	809	2	Q7SDN1_NEUCR	Q7sdn1 neurospora
40	46	51.7	952	2	Q51W19_MAGGR	Q51w19 magnaporthe
41	46	51.7	1055	2	Q55XG3_CRYNE	Q55xg3 cryptococcu
42	46	51.7	1055	2	Q5KWH0_CRYNE	Q5kwh0 cryptococcu
43	46	51.7	1174	2	Q7QCE8_ANOGA	Q7qce8 anopheles g
44	46	51.7	1533	2	Q54NW5_DICDI	Q54nw5 dictyosteli
45	45	50.6	454	2	Q5WAD9_BACSK	Q5wad9 bacillus cl

ALIGNMENTS

RESULT 1
HV60_MOUSE STANDARD; PRT; 116 AA.
ID HV60_MOUSE
AC P18531;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DB Ig heavy chain V region M315 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALE/CJ;
RX MEDLINE=89279149; PubMed=2499654; DOI=10.1084/jem.169.6.2007;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during the primary immune response".
RL J. Exp. Med. 169:2007-2019(1989).
CC -----
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CC -----
CC PIR; JT0509; HVMS31.
DR PDB; 1EZV; X-ray; X=22-116.
DR SMR; P18531; 19-116.
DR Ensemble; ENSMUSG00000057048; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW 3D-structure; Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 18
FT CHAIN 19 116 Ig heavy chain V region M315.
FT REGION 19 48 Framework-1.
FT REGION 49 53 Complementarity-determining-1.
FT REGION 54 67 Framework-2.
FT REGION 68 84 Complementarity-determining-2.
FT REGION 85 116 Framework-3.
FT DISULFID 40 114 By similarity.
FT NON TER 116
SQ SEQUENCE 116 AA; 4562B03E53DC9E10 CRC64;
Query Match 84.3%; Score 75; DB 1; Length 116;
Best Local Similarity 81.2%; Pred. No. 0.0003;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 YISYDGTNNYKPSLKD 16
|||||:|||||

Db 69 YISYDGSNNYPSLKN 84

RESULT 2

Q53VR6 MOUSE
ID Q53VR6_MOUSE PRELIMINARY; PRT; 98 AA.
AC Q53VR6;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE VH-region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86136012; PubMed=3937730;
RA Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
RT "The idiotypic network and the internal image: possible regulation of
a germ-line network by paucigene encoded Ab2 (anti-idiotypic)
antibodies in the GAT system.";
RL EMBO J. 4:3681-3688(1985).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 28-29.
RA Fougereau M.;
RL Submitted (NOV-1986) to the EMBL/GenBank/DBJ databases.
DR EMBL; X03375; CAA27078.1; -; mRNA.
DR EMBL; X03374; CAA27072.1; -; mRNA.
FT NON_TER 1 1
FT NON_TER 98 98
SQ SEQUENCE 98 AA; 11255 MW; EBC71AA2F8F5FD60 CRC64;

Query Match 80.9%; Score 72; DB 2; Length 98;
Best Local Similarity 75.0%; Pred. No. 0.00077;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16
||:|||||:
Db 51 YINYDGSNNYPSLKN 66

RESULT 3

Q53VR7 MOUSE
ID Q53VR7_MOUSE PRELIMINARY; PRT; 120 AA.
AC Q53VR7;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE VH-D-JH region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86136012; PubMed=3937730;
RA Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
RT "The idiotypic network and the internal image: possible regulation of
a germ-line network by paucigene encoded Ab2 (anti-idiotypic)
antibodies in the GAT system.";
RL EMBO J. 4:3681-3688(1985).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 28-29.
RA Fougereau M.;
RL Submitted (NOV-1986) to the EMBL/GenBank/DBJ databases.
DR EMBL; X03375; CAA27077.1; -; mRNA.
DR EMBL; X03374; CAA27071.1; -; mRNA.
FT NON_TER 1 1
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13892 MW; 013452306EBA33BE CRC64;

Query Match 80.9%; Score 72; DB 2; Length 120;
Best Local Similarity 75.0%; Pred. No. 0.00097;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16
||:|||||:
Db 51 YINYDGSNNYPSLKN 66

RESULT 4

Q99M22 MOUSE
ID Q99M22_MOUSE PRELIMINARY; PRT; 479 AA.
AC Q99M22;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE LOC238447 protein.
GN Name=LOC238447;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Mix FVB/N;
RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.W., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Mix FVB/N;
RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
RG NIH MGC Project;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002091; AA02091.1; -; mRNA.
DR HSSP; P01820; 1G7J.
DR GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Immunoglobulin domain.
SQ SEQUENCE 479 AA; 51992 MW; 768E39A138918892 CRC64;

Query Match 80.9%; Score 72; DB 2; Length 479;
Best Local Similarity 75.0%; Pred. No. 0.0045;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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QY 1 YISYDGTNNYKPSLKD 16
Db 69 YIYDGSNNYNPSLKN 84

RESULT 5
Q53VQ4_MOUSE PRELIMINARY; PRT; 98 AA.
AC Q53VQ4_MOUSE PRELIMINARY; PRT; 98 AA.
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE VH region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86136012; PubMed=3937730;
RA Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
RT "The idiotypic network and the internal image: possible regulation of
a germ-line network by paucigene encoded Ab2 (anti-idiotypic)
antibodies in the CAT system.";
RL EMBO J. 4:3681-3688(1985).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 28-29.
RA Fougereau M.;
RL Submitted (NOV-1986) to the EMBL/GenBank/DBJ databases.
DR EMBL; X03378; CAA27096.1; -; mRNA.
FT NON_TER 1 98
FT NON_TER 1 98
SQ SEQUENCE 98 AA; 11202 MW; 4049CF8C7EB8AAE0 CRC64;

Query Match 78.7%; Score 70; DB 2; Length 98;
Best Local Similarity 75.0%; Pred. No. 0.0016;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16
Db 51 YISYDGSNNYNPSLKN 66

RESULT 6
Q53VQ5_MOUSE PRELIMINARY; PRT; 119 AA.
AC Q53VQ5_MOUSE PRELIMINARY; PRT; 119 AA.
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE VH-D-JH region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86136012; PubMed=3937730;
RA Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
RT "The idiotypic network and the internal image: possible regulation of
a germ-line network by paucigene encoded Ab2 (anti-idiotypic)
antibodies in the CAT system.";
RL EMBO J. 4:3681-3688(1985).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 28-29.
RA Fougereau M.;
RL Submitted (NOV-1986) to the EMBL/GenBank/DBJ databases.
DR EMBL; X03378; CAA27095.1; -; mRNA.
FT NON_TER 1 119
FT NON_TER 1 119
SQ SEQUENCE 119 AA; 13931 MW; 502E51A5213F056E CRC64;

Query Match 78.7%; Score 70; DB 2; Length 119;
Best Local Similarity 75.0%; Pred. No. 0.002;
Matches 12; Conservative 3; Mismatches 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16
Db 51 YISYDGSNNYNPSLKN 66

RESULT 7
Q6LBQ5_MOUSE PRELIMINARY; PRT; 136 AA.
AC Q6LBQ5_MOUSE PRELIMINARY; PRT; 136 AA.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE VH gene product (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=90067954; PubMed=2587273;
RA Urayov D.N., Deev S.M., Polyakov O.L.;
RT "The structure of the expressible VH gene from a hybridoma producing
monoclonal antibodies against porcine transferrin.";
RL Nucleic Acids Res. 17:9481-9481(1989).
DR EMBL; X16740; CAA34714.1; -; Genomic_DNA.
DR HSSP; P18532; IKCV.
DR SMR; Q6LBQ5; 20-136.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1 136
FT NON_TER 1 136
SQ SEQUENCE 136 AA; 15307 MW; 5B0F439CCFB15C3A CRC64;

Query Match 77.5%; Score 69; DB 2; Length 136;
Best Local Similarity 75.0%; Pred. No. 0.0035;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16
Db 69 YISYDGSNNYNPSLKN 84

RESULT 8
Q5U413_MOUSE PRELIMINARY; PRT; 483 AA.
AC Q5U413_MOUSE PRELIMINARY; PRT; 483 AA.
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE LOC544903 protein.
GN Name=LOC544903;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=FVB/N; TISSUE=Colon;
RA MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RG NIH MGC Project;
 RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC085312; AAH85312.1; -; mRNA.
 DR Ensembl; ENSMUSG0000054328; Mus musculus.
 DR GO; GO:0003823; P:antigen binding; IEA.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; C1-set; 2.
 DR SMART; SM00409; IG; 3.
 DR SMART; SM00407; IGC1; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS0835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
 SQ SEQUENCE 483 AA; 52714 MW; 7C272DA501A4A0D1 CRC64;
 Query Match 76.4%; Score 68; DB 2; Length 483;
 Best Local Similarity 80.0%; Pred. No. 0.021;
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 YISYDGTNNYKPSLK 15
 DB 69 YISYSGSNYNPSLK 83
 RESULT 9
 Q53VQ0_MOUSE PRELIMINARY; PRT; 98 AA.
 ID Q53VQ0_MOUSE PRELIMINARY; PRT; 98 AA.
 AC Q53VQ0;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DE VH region (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=86136012; PubMed=3937730;
 RA Ollier P., Rocca-Serra J., Somme G., These J., Fougereau M.;
 RT "The idiotypic network and the internal image; possible regulation of
 RT a germ-line network by paucigene encoded Ab2 (anti-idiotypic)
 RT antibodies in the GAT system.";
 RL EMBO J. 4:3681-3688(1985).
 RN [2]
 RP NUCLEOTIDE SEQUENCE OF 28-29.
 RA Fougereau M.;
 RL Submitted (NOV-1986) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X03379; CAA27102.1; -; mRNA.
 FT NON_TER 1
 SQ SEQUENCE 483 AA; 52714 MW; 7C272DA501A4A0D1 CRC64;
 Query Match 76.4%; Score 68; DB 2; Length 483;
 Best Local Similarity 80.0%; Pred. No. 0.021;
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 YISYDGTNNYKPSLK 15
 DB 69 YISYSGSNYNPSLK 83
 RESULT 9
 Q53VQ0_MOUSE PRELIMINARY; PRT; 98 AA.
 ID Q53VQ0_MOUSE PRELIMINARY; PRT; 98 AA.
 AC Q53VQ0;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DE VH region (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=86136012; PubMed=3937730;
 RA Ollier P., Rocca-Serra J., Somme G., These J., Fougereau M.;
 RT "The idiotypic network and the internal image; possible regulation of
 RT a germ-line network by paucigene encoded Ab2 (anti-idiotypic)
 RT antibodies in the GAT system.";
 RL EMBO J. 4:3681-3688(1985).
 RN [2]
 RP NUCLEOTIDE SEQUENCE OF 28-29.
 RA Fougereau M.;
 RL Submitted (NOV-1986) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X03379; CAA27102.1; -; mRNA.
 FT NON_TER 1

FT NON_TER 98 98
 SQ SEQUENCE 98 AA; 11191 MW; B3585BEB6F080616 CRC64;
 Query Match 73.0%; Score 65; DB 2; Length 98;
 Best Local Similarity 73.3%; Pred. No. 0.011;
 Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 YISYDGTNNYKPSLK 15
 DB 51 FIRYDGSNNYNPSLK 65
 RESULT 10
 Q53VR2_MOUSE PRELIMINARY; PRT; 98 AA.
 ID Q53VR2_MOUSE PRELIMINARY; PRT; 98 AA.
 AC Q53VR2;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE VH region (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=86136012; PubMed=3937730;
 RA Ollier P., Rocca-Serra J., Somme G., These J., Fougereau M.;
 RT "The idiotypic network and the internal image; possible regulation of
 RT a germ-line network by paucigene encoded Ab2 (anti-idiotypic)
 RT antibodies in the GAT system.";
 RL EMBO J. 4:3681-3688(1985).
 RN [2]
 RP NUCLEOTIDE SEQUENCE OF 28-29.
 RA Fougereau M.;
 RL Submitted (NOV-1986) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X03379; CAA27084.1; -; mRNA.
 FT NON_TER 1
 FT NON_TER 98 98
 SQ SEQUENCE 98 AA; 11132 MW; 50878B9A4CF7298B CRC64;
 Query Match 73.0%; Score 65; DB 2; Length 98;
 Best Local Similarity 68.8%; Pred. No. 0.011;
 Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 YISYDGTNNYKPSLK 16
 DB 51 YIKYDGNNSYNPSLKN 66
 RESULT 11
 Q53VQ1_MOUSE PRELIMINARY; PRT; 115 AA.
 ID Q53VQ1_MOUSE PRELIMINARY; PRT; 115 AA.
 AC Q53VQ1;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE VH-D-JH region (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=86136012; PubMed=3937730;
 RA Ollier P., Rocca-Serra J., Somme G., These J., Fougereau M.;
 RT "The idiotypic network and the internal image; possible regulation of
 RT a germ-line network by paucigene encoded Ab2 (anti-idiotypic)
 RT antibodies in the GAT system.";
 RL EMBO J. 4:3681-3688(1985).
 RN [2]

RP NUCLEOTIDE SEQUENCE OF 28-29.
RA Fougereau M.;
RL Submitted (NOV-1986) to the EMBL/GenBank/DBJ databases.
DR EMBL; X03379; CAA27101.1; -; mRNA.
FT NON TER 1 1
FT NON TER 115 115
SQ SEQUENCE 115 AA; 13257 MW; D465A5854DF459A3 CRC64;

Query Match 73.0%; Score 65; DB 2; Length 115;
Best Local Similarity 73.3%; Pred. No. 0.013;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLK 15
Db 51 FIRYDGSNNYNPSLKN 65

RESULT 12
Q53VQ8_MOUSE PRELIMINARY; PRT; 119 AA.
AC Q53VR3;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE VH-D-JH region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86136012; PubMed=3937730;
RA Ollier P., Rocca-Serra J., Somme G., These J., Fougereau M.;
RT "The idiotypic network and the internal image: possible regulation of
a germ-line network by paucigene encoded Ab2 (anti-idiotypic)
antibodies in the GAT system."
RL EMO J. 4:3681-3688(1985).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 28-29.
RA Fougereau M.;
RL Submitted (NOV-1986) to the EMBL/GenBank/DBJ databases.
DR EMBL; X03376; CAA27083.1; -; mRNA.
FT NON TER 1 1
FT NON TER 119 119
SQ SEQUENCE 119 AA; 13799 MW; 36504D1665BFB59 CRC64;

Query Match 73.0%; Score 65; DB 2; Length 119;
Best Local Similarity 68.8%; Pred. No. 0.014;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLK 16
Db 51 YIKYDGSNNYNPSLKN 66

RESULT 13
Q53VQ8_MOUSE PRELIMINARY; PRT; 98 AA.
AC Q53VQ8;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE VH region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86136012; PubMed=3937730;
RA Ollier P., Rocca-Serra J., Somme G., These J., Fougereau M.;

RT "The idiotypic network and the internal image: possible regulation of
a germ-line network by paucigene encoded Ab2 (anti-idiotypic)
antibodies in the GAT system."
RL EMO J. 4:3681-3688(1985).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 28-29.
RA Fougereau M.;
RL Submitted (NOV-1986) to the EMBL/GenBank/DBJ databases.
DR EMBL; X03377; CAA27090.1; -; mRNA.
FT NON TER 1 1
FT NON TER 98 98
SQ SEQUENCE 98 AA; 11191 MW; 5B21146E5DA368C6 CRC64;

Query Match 68.5%; Score 61; DB 2; Length 98;
Best Local Similarity 68.8%; Pred. No. 0.05;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLK 16
Db 51 YISFDGNNYNPSLKN 66

RESULT 14
Q53VQ9_MOUSE PRELIMINARY; PRT; 119 AA.
AC Q53VQ9;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE VH-D-JH region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86136012; PubMed=3937730;
RA Ollier P., Rocca-Serra J., Somme G., These J., Fougereau M.;
RT "The idiotypic network and the internal image: possible regulation of
a germ-line network by paucigene encoded Ab2 (anti-idiotypic)
antibodies in the GAT system."
RL EMO J. 4:3681-3688(1985).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 28-29.
RA Fougereau M.;
RL Submitted (NOV-1986) to the EMBL/GenBank/DBJ databases.
DR EMBL; X03377; CAA27089.1; -; mRNA.
FT NON TER 1 1
FT NON TER 119 119
SQ SEQUENCE 119 AA; 13844 MW; 6B1BC8C7DC77E147 CRC64;

Query Match 68.5%; Score 61; DB 2; Length 119;
Best Local Similarity 68.8%; Pred. No. 0.062;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLK 16
Db 51 YISFDGNNYNPSLKN 66

RESULT 15
HV46_MOUSE STANDARD; PRT; 137 AA.
ID HV46_MOUSE
AC P01822;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE 1g heavy chain V region MOPC 315 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=89238351; PubMed=2497341; DOI=10.1016/0161-5890(89)90133-8;
RA Rinfret A., Horne C., Dorrington K.J., Klein M.;
RT "Cloning, sequencing and expression of the rearranged MOPC 315 VH gene
segment.";
RL Mol. Immunol. 26:431-434 (1989).
RN [2]
RP PROTEIN SEQUENCE OF 1-31.
RX MEDLINE=78094475; PubMed=414225;
RA Jilka R.L., Pestka S.;
RT "Amino acid sequence of the precursor region of MOPC-315 mouse
immunoglobulin heavy chain.";
RL Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696 (1977).
RN [3]
RP PROTEIN SEQUENCE OF 1-21.
RX MEDLINE=79148758; PubMed=428562;
RA Schechter I., Wolf O., Zemell R., Burstein Y.;
RT "Structure and function of immunoglobulin genes and precursors.";
RL Fed. Proc. 38:1839-1845 (1979).
RN [4]
RP PROTEIN SEQUENCE OF 19-136.
RX MEDLINE=74170779; PubMed=4524622;
RA Francis S.H., Leslie R.G.Q., Hood L., Eisen H.N.;
RT "Amino acid sequence of the variable region of the heavy (alpha) chain
of a mouse myeloma protein with anti-hapten activity.";
RL Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127 (1974).
RN [5]
RP SEQUENCE REVISION TO 53.
RX MEDLINE=77244979; PubMed=268248;
RA Hood L., Margolies M.N., Givol D., Zakut R.;
RL Unpublished results, cited by:
RL Padlan E.A., Davies D.R., Pecht I., Givol D., Wright C.;
RL Cold Spring Harb. Symp. Quant. Biol. 41:627-637 (1977).
CC -!- MISCELLANEOUS: This alpha chain was isolated from a myeloma
protein that has anti-dinitrophenyl activity.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC -----
DR EMBL; M27638; AAA61337.1; -; Genomic DNA.
DR EMBL; X07880; CAA30727.1; -; Genomic DNA.
DR PIR; PL0102; AVMS35.
DR HSSP; P01820; 1G7J.
DR SMR; P01822; 20-137.
DR Ensembl; ENSMUSG00000057048; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 18
FT CHAIN 19 137 Ig heavy chain V region MOPC 315.
FT REGION 19 48 Framework-1
FT REGION 49 54 Complementarity-determining-1.
FT REGION 55 68 Framework-2.
FT REGION 69 84 Complementarity-determining-2.
FT REGION 85 116 Framework-3.
FT REGION 117 126 Complementarity-determining-3.
FT REGION 127 137 Framework-4.
FT DISULPID 40 114 By similarity.
FT CONFLICT 15 15 G -> GG (in Ref. 1; CAA30727).
FT CONFLICT 15 15 G -> H (in Ref. 2).
FT CONFLICT 77 78 GY -> YG (in Ref. 4).
FT CONFLICT 102 102 N -> D (in Ref. 4).
FT CONFLICT 123 123 Missing (in Ref. 4).
FT NON_TER 137 137
SQ SEQUENCE 137 AA; 15399 MW; PB3828304C2B81DC CRC64;

Query Match 68.5%; Score 61; DB 1; Length 137;
Best Local Similarity 62.5%; Pred. NO. 0.072;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 VISYDGTNNYKPSLKD 16
Db :||||:||||:
69 FIKYDGSNGYNPSPSLKN 84

Search completed: December 30, 2005, 13:33:30
Job time : 145 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:14:26 ; Search time 35.871 Seconds
(without alignments)
36.877 Million cell updates/sec

Title: US-10-735-916A-10

Perfect score: 89

Sequence: 1 YISYDGTNNYKPSLKD 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75	84.3	118	2	US-09-065-059-11
2	75	84.3	118	2	US-08-913-555-11
3	62	69.7	241	2	US-08-902-486-13
4	62	69.7	496	2	US-08-902-486-15
5	60	67.4	121	1	US-08-887-352B-2
6	60	67.4	121	2	US-08-109-207C-2
7	60	67.4	121	2	US-09-296-005-2
8	60	67.4	121	2	US-09-920-171-2
9	60	67.4	121	2	US-09-716-028-2
10	60	67.4	121	2	US-10-113-996-2
11	60	67.4	134	2	US-08-466-151-3
12	60	67.4	134	2	US-08-466-163B-3
13	60	67.4	134	2	US-09-802-096-3
14	60	67.4	134	2	US-09-802-077-3
15	60	67.4	134	2	US-09-925-179-3
16	58	65.2	451	2	US-09-925-179-66
17	57	64.0	16	2	US-09-170-769A-14
18	57	64.0	119	2	US-08-767-128-18
19	57	64.0	137	2	US-08-466-151-7
20	57	64.0	137	2	US-08-466-163B-7
21	57	64.0	137	2	US-09-802-096-7
22	57	64.0	137	2	US-09-802-077-7
23	57	64.0	137	2	US-09-925-179-7
24	57	64.0	213	2	US-09-170-769A-2
25	56	62.9	16	2	US-09-424-840B-110
26	56	62.9	21	2	US-08-918-148-45
27	56	62.9	21	2	US-09-138-091A-45

Sequence 22, Appl
Sequence 35, Appl
Sequence 101, Appl
Sequence 42, Appl
Sequence 52, Appl
Sequence 53, Appl
Sequence 41, Appl
Sequence 49, Appl
Sequence 69, Appl
Sequence 43, Appl
Sequence 23, Appl
Sequence 23, Appl
Sequence 140, Appl
Sequence 140, Appl
Sequence 13, Appl
Sequence 48, Appl
Sequence 142, Appl

ALIGNMENTS

RESULT 1
US-09-065-059-11
; Sequence 11, Application US/09065059
; Patent No. 6068841
; GENERAL INFORMATION:
; APPLICANT: SEINO, Ken-ichiro
; APPLICANT: KAVAGAKI, No. 6068841uhiko
; APPLICANT: YAGITA, Hideo
; APPLICANT: OKUMURA, Ko
; APPLICANT: NAKATA, Motom1
; TITLE OF INVENTION: THERAPEUTIC AGENT FOR HEPATITIS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDermott, Will & Emery
; STREET: 99 Canal Center Plaza
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/065,059
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Bucca Ph.D., Daniel
; REGISTRATION NUMBER: P-42,368
; REFERENCE/DOCKET NUMBER: 50356-151
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-518-5100
; TELEFAX: 703-684-1124
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-065-059-11

Query Match 84.3%; Score 75; DB 2; Length 118;
Best Local Similarity 81.2%; Pred. No. 9.4e-05;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLKD 16
|||||:|||||

Db 50 YISYDGSNNYPSLKN 65

RESULT 2

US-08-913-555-11

Sequence 11, Application US/08913555

Patent No. 6946255

GENERAL INFORMATION:

APPLICANT: KAYAGAKI, No. 6946255uhiko

APPLICANT: YAGITA, Kideo

APPLICANT: OKUMURA, Ko

APPLICANT: NAKATA, Motomi

TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFICALLY

TITLE OF INVENTION: REACTING WITH Fas LIGAND AND PRODUCTION PROCESS THEREOF

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: McDermott, Will & Emery

STREET: 99 Canal Center Plaza, Suite 300

CITY: Alexandria

STATE: Virginia

COUNTRY: USA

ZIP: 22314

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/913,555

FILING DATE: 19-SEP-1997

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Bucca Ph.D., Daniel

REGISTRATION NUMBER: 42,368

REFERENCE/DOCKET NUMBER: 50356-150

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-756-8690

TELEFAX: 202-756-8699

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 118 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-913-555-11

Query Match 84.3%; Score 75; DB 2; Length 118;

Best Local Similarity 81.2%; Pred. NO. 9.4e-05;

Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16

Db 50 YISYDGSNNYPSLKN 65

RESULT 3

US-08-902-486-13

Sequence 13, Application US/08902486

Patent No. 6140075

GENERAL INFORMATION:

APPLICANT: Russel, David R.

APPLICANT: Fuller, James T.

TITLE OF INVENTION: METHOD FOR PRODUCING ANTIBODIES AND

TITLE OF INVENTION: PROTEIN TOXINS IN PLANT CELLS

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Quarles & Brady

STREET: 1 South Pinckney Street

CITY: Madison

STATE: WI

COUNTRY: US

ZIP: 53701-2113

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/902,486

FILING DATE:

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Seay, Nicholas J.

REGISTRATION NUMBER: 27386

REFERENCE/DOCKET NUMBER: 670513.90261

TELECOMMUNICATION INFORMATION:

TELEPHONE: 608-251-5000

TELEFAX: 608-251-9166

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 496 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-902-486-15

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/902,486

FILING DATE:

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Seay, Nicholas J.

REGISTRATION NUMBER: 27386

REFERENCE/DOCKET NUMBER: 670513.90261

TELECOMMUNICATION INFORMATION:

TELEPHONE: 608-251-5000

TELEFAX: 608-251-9166

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 241 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-902-486-13

Query Match 69.7%; Score 62; DB 2; Length 241;

Best Local Similarity 68.8%; Pred. NO. 0.027;

Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16

Db 180 YIRYDGTSEYTPSLKN 195

RESULT 4

US-08-902-486-15

Sequence 15, Application US/08902486

Patent No. 6140075

GENERAL INFORMATION:

APPLICANT: Russel, David R.

APPLICANT: Fuller, James T.

TITLE OF INVENTION: METHOD FOR PRODUCING ANTIBODIES AND

TITLE OF INVENTION: PROTEIN TOXINS IN PLANT CELLS

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Quarles & Brady

STREET: 1 South Pinckney Street

CITY: Madison

STATE: WI

COUNTRY: US

ZIP: 53701-2113

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/902,486

FILING DATE:

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Seay, Nicholas J.

REGISTRATION NUMBER: 27386

REFERENCE/DOCKET NUMBER: 670513.90261

TELECOMMUNICATION INFORMATION:

TELEPHONE: 608-251-5000

TELEFAX: 608-251-9166

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 496 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-902-486-15

RESULT 9
US-09-716-028-2
; Sequence 2, Application US/09716028
; Patent No. 6723833
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/716,028
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 09/109,207
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 2
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-716-028-2

Query Match 67.4%; Score 60; DB 2; Length 121;
Best Local Similarity 66.7%; Pred. No. 0.027;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ISYDGTNNYKPSLKD 16
|:||||:|||
Db 52 ITYDGSSNYPNSLKN 66

RESULT 10
US-10-113-996-2
; Sequence 2, Application US/10113996
; Patent No. 6761889
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies
; FILE REFERENCE: P1123C3US
; CURRENT APPLICATION NUMBER: US/10/113,996
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: US 09/920,171
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 2
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-113-996-2

Query Match 67.4%; Score 60; DB 2; Length 121;
Best Local Similarity 66.7%; Pred. No. 0.027;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ISYDGTNNYKPSLKD 16
|:||||:|||
Db 52 ITYDGSSNYPNSLKN 66

RESULT 11
US-08-466-151-3
; Sequence 3, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.

; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 3
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-466-163B-3

Query Match 67.4%; Score 60; DB 2; Length 134;
Best Local Similarity 66.7%; Pred. No. 0.03;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
Cy 2 ISYDGTNNYKPSLKD 16
|:||||:|||||
Db 52 ITYDGSNNYPSLKN 66

RESULT 13
US-09-802-096-3
; Sequence 3, Application US/09802096
; Patent No. 6685939
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C3US
; CURRENT APPLICATION NUMBER: US/09/802,096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 3
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-802-096-3

Query Match 67.4%; Score 60; DB 2; Length 134;
Best Local Similarity 66.7%; Pred. No. 0.03;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
Cy 2 ISYDGTNNYKPSLKD 16
|:||||:|||||
Db 52 ITYDGSNNYPSLKN 66

RESULT 14
US-09-802-077-3
; Sequence 3, Application US/09802077
; Patent No. 6699472
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C2US
; CURRENT APPLICATION NUMBER: US/09/802,077
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07

; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 3
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-802-077-3

Query Match 67.4%; Score 60; DB 2; Length 134;
Best Local Similarity 66.7%; Pred. No. 0.03;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
Cy 2 ISYDGTNNYKPSLKD 16
|:||||:|||||
Db 52 ITYDGSNNYPSLKN 66

RESULT 15
US-09-925-179-3
; Sequence 3, Application US/09925179
; Patent No. 6914129
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Anti-IGG Antibodies (as amended)
; FILE REFERENCE: P0718P2C1D1C1US
; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 3
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-925-179-3

Query Match 67.4%; Score 60; DB 2; Length 134;
Best Local Similarity 66.7%; Pred. No. 0.03;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
Cy 2 ISYDGTNNYKPSLKD 16
|:||||:|||||
Db 52 ITYDGSNNYPSLKN 66

Search completed: December 30, 2005, 13:37:19
Job time : 36.871 secs

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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:33:42 ; Search time 118.968 Seconds
(without alignments)
56.194 Million cell updates/sec

Title: US-10-735-916A-10

Perfect score: 89

Sequence: 1 YISYDGTNNYKPSLKD 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main.*

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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	89	100.0	16	5	US-10-735-916A-10
2	89	100.0	117	5	US-10-735-916A-69
3	89	100.0	117	5	US-10-735-916A-75
4	89	100.0	117	5	US-10-735-916A-79
5	89	100.0	117	5	US-10-735-916A-83
6	89	100.0	127	5	US-10-735-916A-52
7	89	100.0	135	5	US-10-735-916A-77
8	89	100.0	135	5	US-10-735-916A-81
9	89	100.0	135	5	US-10-735-916A-85
10	75	84.3	136	3	US-09-858-349-2
11	72	80.9	121	3	US-09-144-886-70
12	72	80.9	121	4	US-10-632-706-67
13	71	79.8	118	5	US-10-735-916A-70
14	70	78.7	118	4	US-10-372-481-17
15	70	78.7	118	4	US-10-371-797-17
16	66	74.2	116	6	US-11-003-819-4
17	65	73.0	120	4	US-10-383-447-2
18	65	73.0	120	4	US-10-383-447-22
19	65	73.0	120	4	US-10-383-447-24
20	65	73.0	120	4	US-10-383-447-26
21	65	73.0	120	4	US-10-383-447-28
22	60	67.4	116	5	US-10-822-306A-26
23	60	67.4	116	5	US-10-822-306A-14
24	60	67.4	121	3	US-09-920-171-2
25	60	67.4	121	4	US-10-113-996-2
26	60	67.4	121	5	US-10-791-619-2
27	60	67.4	134	3	US-09-802-077-3

Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 21, Appli
Sequence 23, Appli
Sequence 9, Appli
Sequence 11, Appli
Sequence 66, Appli
Sequence 66, Appli
Sequence 131, App
Sequence 136, App
Sequence 131, App
Sequence 136, App
Sequence 157, App
Sequence 157, App
Sequence 258, App
Sequence 46, Appli
Sequence 128, App

ALIGNMENTS

RESULT 1

US-10-735-916A-10

; Sequence 10, Application US/10735916A

; Publication No. US20050084906A1

; GENERAL INFORMATION:

; APPLICANT: GOETSCH, Liliane

; APPLICANT: CORVAIA, Nathalie

; APPLICANT: LEGER, Olivier

; APPLICANT: DUFIOS, Alain

; APPLICANT: BECK, Alain

; APPLICANT: HADUM, Jean-Francois

; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF

; FILE REFERENCE: 017753-183

; CURRENT APPLICATION NUMBER: US/10735,916A

; CURRENT FILING DATE: 2003-12-16

; PRIOR APPLICATION NUMBER: FR 03/08 538

; PRIOR FILING DATE: 2003-07-11

; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178

; PRIOR FILING DATE: 2003-01-20

; PRIOR APPLICATION NUMBER: FR 02/00 653

; PRIOR FILING DATE: 2002-01-18

; PRIOR APPLICATION NUMBER: FR 02/00 654

; PRIOR FILING DATE: 2002-01-18

; PRIOR APPLICATION NUMBER: FR 02/05 753

; PRIOR FILING DATE: 2002-05-07

; NUMBER OF SEQ ID NOS: 156

; SOFTWARE: Patentin ver. 2.1

; SEQ ID NO 10

; LENGTH: 16

; TYPE: PRT

; ORGANISM: Mus musculus

US-10-735-916A-10

Query Match 100.0%; Score 89; DB 5; Length 16;

Best Local Similarity 100.0%; Pred. No. 2.7e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLKD 16

Db 1 YISYDGTNNYKPSLKD 16

RESULT 2

US-10-735-916A-69

; Sequence 69, Application US/10735916A

; Publication No. US20050084906A1

; GENERAL INFORMATION:

; APPLICANT: GOETSCH, Liliane

; APPLICANT: CORVAIA, Nathalie

; APPLICANT: LEGER, Olivier

; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10/735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 69
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-735-916A-69

Query Match 100.0%; Score 89; DB 5; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16
|||||

Db 51 YISYDGTNNYKPSLKD 66

RESULT 3
US-10-735-916A-75
; Sequence 75, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10/735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 75
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-735-916A-75

Query Match 100.0%; Score 89; DB 5; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16
|||||

Db 51 YISYDGTNNYKPSLKD 66

RESULT 4
US-10-735-916A-79
; Sequence 79, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10/735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-735-916A-79

Query Match 100.0%; Score 89; DB 5; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16
|||||

Db 51 YISYDGTNNYKPSLKD 66

RESULT 5
US-10-735-916A-83
; Sequence 83, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10/735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 83

Query Match 100.0%; Score 89; DB 5; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-735-916A-83

Query Match      100.0%; Score 89; DB 5; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLKD 16
Db 51 YISYDGTNNYKPSLKD 66

RESULT 6
US-10-735-916A-52
; Sequence 52, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-735-916A-52

Query Match      100.0%; Score 89; DB 5; Length 127;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLKD 16
Db 61 YISYDGTNNYKPSLKD 76

RESULT 7
US-10-735-916A-77
; Sequence 77, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-735-916A-52

Query Match      100.0%; Score 89; DB 5; Length 127;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLKD 16
Db 61 YISYDGTNNYKPSLKD 76

RESULT 8
US-10-735-916A-81
; Sequence 81, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-735-916A-81

Query Match      100.0%; Score 89; DB 5; Length 135;
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLKD 16
Db 69 YISYDGTNNYKPSLKD 84

RESULT 9
US-10-735-916A-85
; Sequence 85, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
```

; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10/735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 85
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-735-916A-85

Query Match 100.0%; Score 89; DB 5; Length 135;
Best Local Similarity 100.0%; Pred. No. 2,7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16
Db 69 YISYDGTNNYKPSLKD 84
|||||

RESULT 10
US-09-858-349-2
; Sequence 2, Application US/09858349
; Patent No. US20020012909A1
; GENERAL INFORMATION:
; APPLICANT: ELAKSIN, Daniel
; TITLE OF INVENTION: SMALL FUNCTIONAL UNITS OF ANTIBODY HEAVY CHAIN VARIABLE REGIONS
; FILE REFERENCE: 87534-2800
; CURRENT APPLICATION NUMBER: US/09/858,349
; CURRENT FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 136
; TYPE: PRT
; ORGANISM: mouse hybridoma specific for H-2D + RGPGRFVTI peptide
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (99)..(107)
; OTHER INFORMATION: variable
US-09-858-349-2

Query Match 84.3%; Score 75; DB 3; Length 136;
Best Local Similarity 81.2%; Pred. No. 0.00047;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16
Db 51 YISYDGSNNYNPSLKN 66
|||||

RESULT 11
US-09-144-886-70
; Sequence 70, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D

; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; TITLE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 70
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BoNT/A clone
; OTHER INFORMATION: 2B6 region VH epitope 3
US-09-144-886-70

Query Match 80.9%; Score 72; DB 3; Length 121;
Best Local Similarity 75.0%; Pred. No. 0.0013;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16
Db 50 YINYDGSNNYNPSLKN 65
|||

RESULT 12
US-10-632-706-67
; Sequence 67, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; APPLICANT: AMERSDORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; TITLE OF INVENTION: NEUROTOXINS
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 67
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody
US-10-632-706-67

Query Match 80.9%; Score 72; DB 4; Length 121;
Best Local Similarity 75.0%; Pred. No. 0.0013;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16
Db 50 YINYDGSNNYNPSLKN 65
|||

RESULT 13
US-10-735-916A-70
; Sequence 70, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF

```
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10/735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-735-916A-70

Query Match      79.8%; Score 71; DB 5; Length 118;
Best Local Similarity 75.0%; Pred. No. 0.0018;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 YISYDGTNNYKPSLKD 16
Db      51 YINYDGNNNYPSLKN 66

RESULT 14
US-10-372-481-17
; Sequence 17, Application US/10372481
; Publication No. US20030202975A1
; GENERAL INFORMATION:
; APPLICANT: Tedder, Thomas F.
; TITLE OF INVENTION: REAGENTS AND TREATMENT METHODS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 5405.306
; CURRENT APPLICATION NUMBER: US/10/372,481
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: PCT/US03/05549
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 60/420,472
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/359,419
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-372-481-17

Query Match      78.7%; Score 70; DB 4; Length 118;
Best Local Similarity 75.0%; Pred. No. 0.0026;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 YISYDGTNNYKPSLKD 16
Db      51 YIRYDGSNNYPSLKN 66

RESULT 15
US-10-371-797-17
; Sequence 17, Application US/10371797
; Publication No. US20040001828A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: TUSCANO, Joseph
; APPLICANT: TEDDER, Thomas
; TITLE OF INVENTION: TREATMENT METHODS USING ANTI-CD22
; TITLE OF INVENTION: ANTIBODIES
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; FILE REFERENCE: 39754-0951
; CURRENT APPLICATION NUMBER: US/10/371,797
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 60/420,472
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/359,419
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 118
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-371-797-17

Query Match      78.7%; Score 70; DB 4; Length 118;
Best Local Similarity 75.0%; Pred. No. 0.0026;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 YISYDGTNNYKPSLKD 16
Db      51 YIRYDGSNNYPSLKN 66

Search completed: December 30, 2005, 14:14:58
Job time : 123.968 secs
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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:35:07 ; Search time 5.93548 Seconds
(without alignments)
20.187 Million cell updates/sec

Title: US-10-735-916a-10

Perfect score: 89

Sequence: 1 YISYDGTNNYKPSLKD 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 57103

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

- 1: /cgn2_6/ptodata/1/pubaa/US08_NEW_PUB pep.*
- 2: /cgn2_6/ptodata/1/pubaa/US06_NEW_PUB pep.*
- 3: /cgn2_6/ptodata/1/pubaa/US07_NEW_PUB pep.*
- 4: /cgn2_6/ptodata/1/pubaa/PCT_NEW_PUB pep.*
- 5: /cgn2_6/ptodata/1/pubaa/US03_NEW_PUB pep.*
- 6: /cgn2_6/ptodata/1/pubaa/US10_NEW_PUB pep.*
- 7: /cgn2_6/ptodata/1/pubaa/US11_NEW_PUB pep.*
- 8: /cgn2_6/ptodata/1/pubaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	89	100.0	16	7 US-11-012-353-10	Sequence 10, Appl
2	89	100.0	117	7 US-11-012-353-69	Sequence 69, Appl
3	89	100.0	117	7 US-11-012-353-75	Sequence 75, Appl
4	89	100.0	117	7 US-11-012-353-79	Sequence 79, Appl
5	89	100.0	117	7 US-11-012-353-83	Sequence 83, Appl
6	89	100.0	127	7 US-11-012-353-52	Sequence 52, Appl
7	89	100.0	135	7 US-11-012-353-77	Sequence 77, Appl
8	89	100.0	135	7 US-11-012-353-81	Sequence 81, Appl
9	89	100.0	135	7 US-11-012-353-85	Sequence 85, Appl
10	71	79.8	118	7 US-11-012-353-70	Sequence 70, Appl
11	70	78.7	259	6 US-10-512-184-34	Sequence 34, Appl
12	70	78.7	371	6 US-10-512-184-71	Sequence 71, Appl
13	70	78.7	626	6 US-10-512-184-49	Sequence 49, Appl
14	56	62.9	97	7 US-11-144-248-36	Sequence 36, Appl
15	56	62.9	97	7 US-11-054-669-42	Sequence 42, Appl
16	56	62.9	97	7 US-11-054-669-52	Sequence 52, Appl
17	56	62.9	97	7 US-11-054-669-53	Sequence 53, Appl
18	56	62.9	97	7 US-11-084-554-54	Sequence 54, Appl
19	56	62.9	97	7 US-11-144-222-36	Sequence 36, Appl
20	56	62.9	99	7 US-11-054-669-43	Sequence 43, Appl
21	56	62.9	99	7 US-11-084-554-55	Sequence 55, Appl
22	56	62.9	113	7 US-11-144-248-20	Sequence 20, Appl
23	56	62.9	113	7 US-11-144-222-20	Sequence 20, Appl
24	55	61.8	98	7 US-11-084-554-10	Sequence 10, Appl
25	55	61.8	114	6 US-10-923-327-5	Sequence 5, Appl

26 55 61.8 229 6 US-10-923-327-13 Sequence 13, Appl
27 55 61.8 233 6 US-10-923-327-18 Sequence 18, Appl
28 55 61.8 248 6 US-10-923-327-15 Sequence 15, Appl
29 55 61.8 451 6 US-10-923-327-7 Sequence 7, Appl
30 55 61.8 451 6 US-10-923-327-9 Sequence 9, Appl
31 54 60.7 118 7 US-11-012-353-71 Sequence 71, Appl
32 53 59.6 249 7 US-11-054-515-2002 Sequence 2002, Ap
33 53 59.6 253 7 US-11-054-515-1339 Sequence 1339, Ap
34 51 57.3 102 7 US-11-185-615-4 Sequence 4, Appl
35 51 57.3 246 7 US-11-054-515-1847 Sequence 1847, Ap
36 51 57.3 247 7 US-11-054-515-1993 Sequence 1993, Ap
37 48 53.9 98 7 US-11-054-669-35 Sequence 35, Appl
38 48 53.9 98 7 US-11-084-554-49 Sequence 49, Appl
39 48 53.9 99 7 US-11-054-669-36 Sequence 36, Appl
40 48 53.9 99 7 US-11-054-669-38 Sequence 38, Appl
41 48 53.9 99 7 US-11-054-669-39 Sequence 39, Appl
42 48 53.9 99 7 US-11-084-554-50 Sequence 50, Appl
43 48 53.9 247 7 US-11-054-515-1981 Sequence 1981, Ap
44 48 53.9 251 7 US-11-054-515-1316 Sequence 1316, Ap
45 48 53.9 253 7 US-11-054-515-1619 Sequence 1619, Ap

ALIGNMENTS

RESULT 1

US-11-012-353-10
; Sequence 10, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GORTSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 01753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 10
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-012-353-10

Query Match 100.0%; Score 89; DB 7; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLKD 16

Db 1 YISYDGTNNYKPSLKD 16

RESULT 2

US-11-012-353-69
; Sequence 69, Application US/11012353

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; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 69
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mus musculus
; US-11-012-353-69

Query Match      100.0%; Score 89; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16
Db 51 YISYDGTNNYKPSLKD 66

RESULT 3
US-11-012-353-75
; Sequence 75, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 75
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-012-353-79

Query Match      100.0%; Score 89; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16
Db 51 YISYDGTNNYKPSLKD 66

RESULT 4
US-11-012-353-79
; Sequence 79, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 79
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-012-353-79

Query Match      100.0%; Score 89; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16
Db 51 YISYDGTNNYKPSLKD 66

RESULT 5
US-11-012-353-83
; Sequence 83, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-198
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; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 83
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-012-353-83

Query Match 100.0%; Score 89; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLKD 16
|||||

Db 51 YISYDGTNNYKPSLKD 66
|||||

RESULT 6

US-11-012-353-52
; Sequence 52, Application US/11/012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 52
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-012-353-52

Query Match 100.0%; Score 89; DB 7; Length 127;
Best Local Similarity 100.0%; Pred. No. 2.2e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLKD 16
|||||

Db 61 YISYDGTNNYKPSLKD 76

RESULT 7

US-11-012-353-77
; Sequence 77, Application US/11/012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 77
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-012-353-77

Query Match 100.0%; Score 89; DB 7; Length 135;
Best Local Similarity 100.0%; Pred. No. 2.4e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLKD 16
|||||

Db 69 YISYDGTNNYKPSLKD 84
|||||

RESULT 8

US-11-012-353-81
; Sequence 81, Application US/11/012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653

; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 81
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-012-353-81

Query Match 100.0%; Score 89; DB 7; Length 135;
Best Local Similarity 100.0%; Pred. No. 2.4e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16
|||||
Db 69 YISYDGTNNYKPSLKD 84

RESULT 9

US-11-012-353-85
; Sequence 85, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN

; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16

; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 85
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-012-353-85

Query Match 100.0%; Score 89; DB 7; Length 135;
Best Local Similarity 100.0%; Pred. No. 2.4e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16
|||||
Db 69 YISYDGTNNYKPSLKD 84

RESULT 10

US-11-012-353-70
; Sequence 70, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN

; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 70
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-012-353-70

Query Match 79.8%; Score 71; DB 7; Length 118;
Best Local Similarity 75.0%; Pred. No. 2.1e-05;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16
|||||
Db 51 YINYDGNNNYPSLKN 66

RESULT 11

US-10-512-184-34
; Sequence 34, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv PL2 with
; OTHER INFORMATION: specificity against Phoma lingam; originates from
; OTHER INFORMATION: Mus musculus.
US-10-512-184-34

Query Match 78.7%; Score 70; DB 6; Length 259;
Best Local Similarity 81.2%; Pred. No. 7.3e-05;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16
|||||
Db 53 YISYDGTNNNPSLKN 68

RESULT 12

US-10-512-184-71
; Sequence 71, Application US/10512184

Publication No. US20050244901A1
GENERAL INFORMATION:
APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
TITLE OF INVENTION: resistance against fungi
FILE REFERENCE: 3581.01US01
CURRENT APPLICATION NUMBER: US/10/512,184
CURRENT FILING DATE: 2004-10-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 71
LENGTH: 371
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: precursor
OTHER INFORMATION: fusion protein comprising ACE - linker -
OTHER INFORMATION: scFv PL2.
US-10-512-184-71
Query Match 78.7%; Score 70; DB 6; Length 371;
Best Local Similarity 81.2%; Pred. No. 0.00011;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 YISYDGTNNYKPSLKD 16
Db 165 YISYDGTNNNNPSLKN 180
RESULT 13
US-10-512-184-49
Sequence 49, Application US/10512184
Publication No. US20050244901A1
GENERAL INFORMATION:
APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
TITLE OF INVENTION: resistance against fungi
FILE REFERENCE: 3581.01US01
CURRENT APPLICATION NUMBER: US/10/512,184
CURRENT FILING DATE: 2004-10-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 49
LENGTH: 626
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: fusion protein
OTHER INFORMATION: comprising the leader peptide - chitinase- linker
OTHER INFORMATION: - scFv PL2 - cmcy/His6.
US-10-512-184-49
Query Match 78.7%; Score 70; DB 6; Length 626;
Best Local Similarity 81.2%; Pred. No. 0.00019;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 YISYDGTNNYKPSLKD 16
Db 394 YISYDGTNNNNPSLKN 409
RESULT 14
US-11-144-248-36
Sequence 36, Application US/11144248
Publication No. US20050244408A1
GENERAL INFORMATION:
APPLICANT: Cohen, Bruce D.
APPLICANT: Beebe, Jean
APPLICANT: Miller, Penelope E.
APPLICANT: Moyer, James D.
APPLICANT: Corvaian, Jose R.

APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
FILE REFERENCE: ABX-PF2
CURRENT APPLICATION NUMBER: US/11/144,248
CURRENT FILING DATE: 2005-06-02
PRIOR APPLICATION NUMBER: US/10/038,591
PRIOR FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 60/259,927
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 36
LENGTH: 97
TYPE: PRT
ORGANISM: Homo sapiens
US-11-144-248-36
Query Match 62.9%; Score 56; DB 7; Length 97;
Best Local Similarity 66.7%; Pred. No. 0.0055;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 YISYDGTNNYKPSLK 15
Db 50 YIYSGSTNNPSLK 64
RESULT 15
US-11-054-669-42
Sequence 42, Application US/11054669
Publication No. US20050261480A1
GENERAL INFORMATION:
APPLICANT: Foote, Jefferson
TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
FILE REFERENCE: 30219/US/3
CURRENT APPLICATION NUMBER: US/11/054,669
CURRENT FILING DATE: 2005-02-08
PRIOR APPLICATION NUMBER: US 10/194,975
PRIOR FILING DATE: 2002-07-12
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 124
SOFTWARE: PatentIn version 3.3
SEQ ID NO 42
LENGTH: 97
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-669-42
Query Match 62.9%; Score 56; DB 7; Length 97;
Best Local Similarity 66.7%; Pred. No. 0.0055;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 YISYDGTNNYKPSLK 15
Db 50 YIYSGSTNNPSLK 64
Search completed: December 30, 2005, 14:15:22
Job time : 6.93548 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:37:27 ; Search time 132.5 seconds

(without alignments)

53.057 Million cell updates/sec

Title: US-10-735-916A-10

Perfect score: 89

Sequence: 1 YISVDTNNYKPSLKD 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 19975

Minimum DB seq length: 16

Maximum DB seq length: 16

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 21.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	89	100.0	16	ADJ76844	ADJ76844 CDR seque
2	89	100.0	16	ADZ67014	Adz67014 Murine in
3	75	84.3	16	AEA40141	Aea40141 TNF resis
4	73	82.0	16	ADZ45407	Adz45407 Murine fa
5	72	80.9	16	ADZ45343	Adz45343 Murine fa
6	72	80.9	16	ADZ51256	Adz51256 Amino aci
7	72	80.9	16	ADZ42130	Adz42130 Mouse ant
8	70	78.7	16	ADZ45520	Adz45520 Murine fa
9	70	78.7	16	ADZ45311	Adz45311 Murine fa
10	70	78.7	16	ADZ51224	Adz51224 Amino aci
11	70	78.7	16	ADZ42098	Adz42098 Mouse ant
12	68	76.4	16	ADZ45479	Adz45479 Murine fa
13	62	69.7	16	ABZ73650	Abz73650 Murine mo
14	58	65.2	16	AAR24718	Aar24718 Sequence
15	57	64.0	16	AEC20782	Aec20782 M-CSF spe
16	56	62.9	16	AAU81236	Aau81236 Human trk
17	56	62.9	16	ADO58086	Ado58086 S9 cell d
18	56	62.9	16	ADZ66143	Adz66143 VH CDR2 f
19	55	61.8	16	AAW90327	Aaw90327 Human ant
20	55	61.8	16	ADX98335	Adx98335 Human ant
21	53	59.6	16	ADL26968	Adl26968 Murine de
22	51	57.3	16	AAW90297	Aaw90297 Human ant
23	51	57.3	16	AAO17789	Aao17789 CDR2 regi
24	50	56.2	16	AUS19315	Aus19315 Heavy cha

25	49	55.1	16	AAW01151	Aaw01151 MAB 1.4 h
26	49	55.1	16	AAW24541	Aaw24541 CDR #2 of
27	49	55.1	16	AAW44174	Aaw44174 Monoclonal
28	49	55.1	16	AEBO0995	Aeb00995 Human IPI
29	48	53.9	16	AAEI0502	Aaei0502 Humanised
30	48	53.9	16	AAEI0499	Aaei0499 Humanised
31	48	53.9	16	AAEI0527	Aaei0527 Humanised
32	48	53.9	16	AAEI0500	Aaei0500 Humanised
33	48	53.9	16	AAU81239	Aau81239 Human trk
34	48	53.9	16	ABP66457	Abp66457 Human RSV
35	48	53.9	16	ABP66395	Abp66395 Human RSV
36	48	53.9	16	ABP66379	Abp66379 Human RSV
37	48	53.9	16	ABP66391	Abp66391 Human RSV
38	48	53.9	16	AAE28034	Aae28034 Human mod
39	48	53.9	16	AAE28046	Aae28046 Human mod
40	48	53.9	16	AAE28050	Aae28050 Human mod
41	48	53.9	16	ABU69320	Abu69320 Respirato
42	48	53.9	16	ABU69242	Abu69242 Respirato
43	48	53.9	16	ABU69254	Abu69254 Respirato
44	48	53.9	16	ABU69258	Abu69258 Respirato
45	48	53.9	16	ADE35749	Ade35749 SYNAGIS a

ALIGNMENTS

RESULT 1

ADJ76844
ID ADJ76844 standard; peptide; 16 AA.

XX AC ADJ76844;

XX AC

DT 06-MAY-2004 (first entry)

XX AC

DE CDR sequence for anti-IGF-1R antibody.

XX AC

KW cytosolic; antipsoriatic; antibody;

KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;

KW or epidermal growth factor receptor; EGFR; signal transduction pathway;

KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;

XX CDR.

XX Mus musculus.

XX WO2003059951-A2.

XX PD

XX 24-JUL-2003.

XX PF

XX 20-JAN-2003; 2003WO-FR000178.

XX PR

XX 18-JAN-2002; 2002FR-00000653.

XX PR

XX 18-JAN-2002; 2002FR-00000654.

XX PR

XX 07-MAY-2002; 2002FR-00005753.

XX PA

XX (FABR) FABRE MEDICAMENT SA PIERRE.

XX FI

XX Goetsch L, Corvaia N, Leger O;

XX DR

XX WPI; 2003-569653/53.

XX DR

XX N-PSDB; ADJ76843.

XX PT

XX New antibodies that bind to human insulin-like growth factor receptor,

XX useful for treatment, prevention and diagnosis of cancers.

XX PS

XX Claim 1; SEQ ID NO 10; 164pp; French.

XX CC

XX The invention relates to an isolated antibody (Ab), and its functional

XX fragments, that bind to human insulin-like growth factor-1 receptor (IGF-

XX IR) and optionally: (i) inhibit natural binding of insulin-like growth

XX factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine

XX kinase activity of IGF-1R. Ab and its fragments are used to prevent or

XX treat diseases associated with overexpression and/or abnormal activity of

XX IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with

CC hyperactivity of signal transduction pathways mediated by interaction of
 CC these receptors with their ligands. Especially they inhibit
 CC transformation of normal cells to tumor cells, inhibit growth and/or
 CC proliferation of tumor cells, so are useful against cancers of the
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused
 CC by abnormal expression of IGF-IR and/or EGFR. This sequence represents an
 CC CDR sequence used to generate the Ab of the invention.
 XX
 SQ Sequence 16 AA;

Query Match 100.0%; Score 89; DB 7; Length 16;
 Best Local Similarity 100.0%; Pred. No. 6.1e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16
 |||||
 Db 1 YISYDGTNNYKPSLKD 16

RESULT 2
 ADZ67014
 ID ADZ67014 standard; peptide; 16 AA.

AC ADZ67014;

XX 30-JUN-2005 (first entry)

DE Murine insulin-like growth factor T receptor IGF-IR CDR SEQ ID NO:10.

XX Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
 KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;
 KW musculoskeletal disease; respiratory disease; lung tumor;
 KW endocrine disease; gynecology and obstetrics; breast tumor;
 KW endometrial carcinoma; gastrointestinal disease; colon tumor;
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder.

XX Mus musculus.

OS US2005084906-A1.

PN 21-APR-2005.

PD 16-DEC-2003; 2003US-00735916.

XX 18-JAN-2002; 2002FR-00000653.

PR 18-JAN-2002; 2002FR-00000654.

PR 07-MAY-2002; 2002FR-00005753.

PR 20-JAN-2003; 2003WO-FR000178.

PR 11-JUL-2003; 2003FR-00008538.

XX (GOET/) GOETSCH L.

PA (CORV/) CORVAIA N.

PA (LEGE/) LEGER O.

PA (DUFL/) DUFLOS A.

PA (HAEU/) HAEUW J.

PA (BECK/) BECK A.

XX Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;

PI WPI; 2005-321968/33.

XX N-PSDB; ADZ67013.

XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)

PT antibody or its functional fragment, being capable of binding human IGF-

PT IR and specifically inhibiting tyrosine kinase activity of receptor,

PT useful for treating cancer.

CC specifically inhibiting tyrosine kinase activity of the receptor,
 CC comprising a light or heavy chain having at least one complementary
 CC determining region (CDR) consisting of one of two fully defined 16 amino
 CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in
 CC the preparation of a medicament intended for the prevention or treatment
 CC of an illness connected with an overexpression and/or an abnormal
 CC activation of the IGF-IR and/or EGFR, and/or connected with a
 CC hyperactivation of the transduction pathway of the signal mediated by the
 CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where
 CC the administration of the medicament does not induce or only slightly
 CC induces secondary effects connected with inhibition of the insulin
 CC receptor. The antibody is useful for preparation of a medicament intended
 CC to inhibit the transformation of normal cells into cells with tumoral
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-
 CC dependent and/or EGF-dependent and/or HSR2/neu-dependent cells. (I) is
 CC useful for preparation of a medicament intended to inhibit the growth
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or
 CC HSR2/neu-dependent cells. (I) is useful in the preparation of a
 CC medicament intended for prevention or for the treatment of cancer, where
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the
 CC preparation of a medicament intended for the prevention or for the
 CC treatment of psoriasis. (I) is useful in preparation of a medicament
 CC intended for the specific targeting of a biologically active compound to
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)
 CC is useful for in vitro diagnosis of illnesses induced by an
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor
 CC starting from a biological sample in which the abnormal presence, of IGF-
 CC IR and/or EGFR receptor is suspected, which involves contacting the
 CC biological sample with (I), which is optionally labeled. The present
 CC sequence is used in the exemplification of the invention.

XX Sequence 16 AA;

Query Match 100.0%; Score 89; DB 9; Length 16;
 Best Local Similarity 100.0%; Pred. No. 6.1e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16
 |||||
 Db 1 YISYDGTNNYKPSLKD 16

RESULT 3

AEA40141

ID AEA40141 standard; peptide; 16 AA.

XX AEA40141;

XX 28-JUL-2005 (first entry)

XX TNF resistant monoclonal antibody VH region, F6VH CDR2.

XX tumor necrosis factor; TNF; monoclonal antibody; F6 mAb;

XX light chain variable region; heavy chain variable region; F6VH.

XX Unidentified.

XX CN1544466-A.

XX 10-NOV-2004.

XX 13-NOV-2003; 2003CN-01105919.

XX 13-NOV-2003; 2003CN-01105919.

XX (UYFO-) UNIV FOURTH MILITARY MEDICAL.

XX Jin B, Liu X, Zhu C;

XX WPI: 2005-153078/17.

XX N-PSDB; AEA40140.

XX Variable region gene of high affinity monoclonal antibody of tumor
 PT necrosis factor and its preparation.
 XX
 XX Claim 1; Page 3; 20pp; Chinese.
 XX
 CC The invention relates to a method for preparing variable region genes of
 CC high affinity tumor necrosis factor (TNF) resistant monoclonal antibody
 CC (F6 mAb). The method comprises using recombinant human TNF immune BALB/c
 CC mouse to prepare mouse anti-TNF monoclonal antibody, screening high
 CC affinity F6 mAb using an indirect enzyme linked immunosorbent assay
 CC (ELISA). By cloning the monoclonal antibody light chain and heavy chain
 CC variable region (VL and VH respectively) genes, the monoclonal antibody
 CC light chain and heavy chain variable region gene sequence and amino acid
 CC sequence can be obtained, and the identity of the gene sequence and
 CC protein sequence can be confirmed. This sequence represents
 CC complementarity determining region, CDR2 of F6VH.
 XX
 XX Sequence 16 AA;
 SQ

Query Match 84.3%; Score 75; DB 9; Length 16;
 Best Local Similarity 81.2%; Pred. No. 0.0001;
 Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLKD 16
 |||||:|||||
 Db 1 YISYDGSNNYNPSLKN 16

RESULT 4
 ADZ45407
 ID ADZ45407 standard; peptide; 16 AA.
 XX
 AC ADZ45407;
 XX
 DT 30-JUN-2005 (first entry)
 XX
 DE Murine factor IX directed antibody CDR2 SEQ ID NO 111.
 XX
 KW bispecific antibody; blood coagulation factor VIII; bleeding;
 KW fibrinolysis; blood coagulation factor X; blood-coagulation factor IX;
 KW factor VIII deficiency; von Willebrand's disease; hemostatic;
 KW immunostimulator; antibody engineering.
 XX
 OS Mus musculus.
 XX
 FN WO2005035756-A1.
 XX
 PD 21-APR-2005.
 XX
 PP 08-OCT-2004; 2004WO-JP014911.
 XX
 PR 10-OCT-2003; 2003WO-JP013062.
 PR 14-OCT-2003; 2003WO-JP013123.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 XX
 PI Hattori K, Kojima T, Miyazaki T, Soeda T;
 XX
 DR WPI; 2005-315563/32.
 XX
 PT Novel bispecific antibody substituting for function of cofactor that
 PT enhances enzyme reaction, and recognizing both enzyme and substrates of
 PT enzyme, useful for treating hemophilia A.
 XX
 PS Disclosure; SEQ ID NO 111; 69pp; Japanese.
 XX

CC This invention describes a novel bispecific antibody which can act as a
 CC cofactor to enhance an enzyme reaction and can recognize the enzyme and
 CC the enzyme substrate. The antibody specifically binds to blood
 CC coagulation factor VIII. The invention also describes a composition
 CC comprising the antibody and a carrier, a kit useful in preventing and/or
 CC treating bleeding associated with a disorder or from a disease caused by

CC bleeding. The composition includes blood coagulation factor VIII. The
 CC antibody of the invention can be a blood-coagulation fibrinolysis related
 CC factor including blood-coagulation factor VIII, blood coagulation factor
 CC X, or blood-coagulation factor IX. The antibody comprises a complementary
 CC determining region (CDR) of anti-blood-coagulation factor IX/IXa factor
 CC antibody. The novel antibody or composition is useful for preventing
 CC and/or treating a disease accompanying bleeding, or the disease resulting
 CC from bleeding, where the disease accompanying bleeding or the disease
 CC resulting from bleeding develops and/or progresses by an active reduction
 CC or deletion of the blood coagulation factor VIII. The disease the
 CC develops and/or progresses by an active reduction or deletion of the
 CC blood coagulation factor VIII and/or activation blood coagulation factor
 CC VIII, is hemophilia A or von Willebrand disease, where the hemophilia is
 CC an acquired hemophilia A. This sequence represents a fragment of the
 CC antibody described in the method of the invention. Note: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 16 AA;
 SQ

Query Match 82.0%; Score 73; DB 9; Length 16;
 Best Local Similarity 81.2%; Pred. No. 0.00021;
 Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLKD 16
 |||||:|||||
 Db 1 YISYDGTNNYNPSLKN 16

RESULT 5
 ADZ45343
 ID ADZ45343 standard; peptide; 16 AA.
 XX
 AC ADZ45343;
 XX
 DT 30-JUN-2005 (first entry)
 XX
 DE Murine factor IX directed antibody CDR2 SEQ ID NO 47.
 XX
 KW bispecific antibody; blood coagulation factor VIII; bleeding;
 KW fibrinolysis; blood coagulation factor X; blood-coagulation factor IX;
 KW factor VIII deficiency; von Willebrand's disease; hemostatic;
 KW immunostimulator; antibody engineering.
 XX
 OS Mus musculus.
 XX
 FN WO2005035756-A1.
 XX
 PD 21-APR-2005.
 XX
 PP 08-OCT-2004; 2004WO-JP014911.
 XX
 PR 10-OCT-2003; 2003WO-JP013062.
 PR 14-OCT-2003; 2003WO-JP013123.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 XX
 PI Hattori K, Kojima T, Miyazaki T, Soeda T;
 XX
 DR WPI; 2005-315563/32.
 XX
 PT Novel bispecific antibody substituting for function of cofactor that
 PT enhances enzyme reaction, and recognizing both enzyme and substrates of
 PT enzyme, useful for treating hemophilia A.
 XX
 PS Claim 5; SEQ ID NO 47; 69pp; Japanese.
 XX

CC This invention describes a novel bispecific antibody which can act as a
 CC cofactor to enhance an enzyme reaction and can recognize the enzyme and
 CC the enzyme substrate. The antibody specifically binds to blood
 CC coagulation factor VIII. The invention also describes a composition
 CC comprising the antibody and a carrier, a kit useful in preventing and/or

CC treating bleeding associated with a disorder or from a disease caused by
 CC bleeding. The composition includes blood coagulation factor VIII. The
 CC antibody of the invention can be a blood-coagulation fibrinolysis related
 CC factor including blood-coagulation factor VIII, blood coagulation factor
 CC X, or blood-coagulation factor IX. The antibody comprises a complementary
 CC determining region (CDR) of anti-blood-coagulation factor IX/IXa factor
 CC antibody. The novel antibody or composition is useful for preventing
 CC and/or treating a disease accompanying bleeding, or the disease resulting
 CC from bleeding, where the disease accompanying bleeding or the disease
 CC resulting from bleeding develops and/or progresses by an active reduction
 CC or deletion of the blood coagulation factor VIII. The disease the
 CC develops and/or progresses by an active reduction or deletion of the
 CC blood coagulation factor VIII and/or activation blood coagulation factor
 CC VIII, is hemophilia A or von Willebrand disease, where the hemophilia is
 CC an acquired hemophilia A. This sequence represents a fragment of the
 CC antibody described in the method of the invention. Note: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX SQ Sequence 16 AA;

Query Match 80.9%; Score 72; DB 9; Length 16;
 Best Local Similarity 75.0%; Pred. No. 0.0003;
 Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16
 ||:|||||
 Db 1 YINYDGSNNYPSLKN 16

RESULT 6
 ADZ51256
 ID ADZ51256 standard; peptide; 16 AA.

AC ADZ51256;
 XX
 XX 30-JUN-2005 (first entry)
 DT
 DE Amino acid sequence of a variable heavy chain region CDR.

XX bispecific antibody; AR1 chain; AR2 chain; hemostatic; bleeding;
 KW antibody therapy; blood coagulation factor VIII; factor VIII deficiency;
 KW von willebrand disease; heavy chain; complementarity determining region;
 KW CDR.

XX Mus musculus.
 XX
 XX WO2005035753-A1.
 PN
 XX 21-APR-2005.

XX 10-OCT-2003; 2003WO-JP013062.

XX 10-OCT-2003; 2003WO-JP013062.

XX (CHUS) CHUGAI SEIYAKU KK.

XX Hattori K, Kojima T, Miyazaki T, Soeda T, Senoo C, Natori O;
 PI Kasutani K, Ishii S;
 XX WPI; 2005-315560/32.

XX Novel bispecific antibody substituting for functional protein or
 PT substituting for ligand for receptor comprising two types of molecules,
 PT useful as pharmaceutical for treating or preventing diseases e.g.
 PT bleeding.

XX Claim 18; SEQ ID NO 73; 143pp; Japanese.

XX The specification describes a bispecific antibody substituting for
 CC functional protein or substituting for a ligand for a receptor comprising
 CC two types of molecules. The antibody comprises AR1 and AR2 chains.

CC Bispecific antibodies of the invention are useful for preventing and
 CC treating bleeding, diseases accompanying bleeding or diseases resulting
 CC from bleeding. These diseases develop or progress by active reduction of
 CC blood coagulation factor VIII/activated blood coagulation factor VIII,
 CC e.g. hemophilia A, acquired hemophilia or von Willebrand disease. The
 CC present sequence represents a complementarity determining region (CDR)
 CC from a variable heavy chain region, which was used to construct
 CC bispecific antibodies of the invention.

XX SQ Sequence 16 AA;

Query Match 80.9%; Score 72; DB 9; Length 16;
 Best Local Similarity 75.0%; Pred. No. 0.0003;
 Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16
 ||:|||||
 Db 1 YINYDGSNNYPSLKN 16

RESULT 7
 ADZ42130
 ID ADZ42130 standard; peptide; 16 AA.

XX AC ADZ42130;

XX 30-JUN-2005 (first entry)

DT Mouse anti-s AR antibody heavy chain CDR 2 SEQ ID NO 73.

DE viral infection; neoplasm; immune disorder; bleeding; infection;
 XX cardiovascular disease; Virucide; Hepatotropic; Antiinflammatory;
 KW Neuroprotective; Hemostatic; Cytostatic; Immunotherapy; antibody.
 XX Mus musculus.

XX WO2005035754-A1.

XX 21-APR-2005.

XX 14-OCT-2003; 2003WO-JP013123.

XX 14-OCT-2003; 2003WO-JP013123.

XX (CHUS) CHUGAI SEIYAKU KK.

XX Hattori K, Kojima T, Miyazaki T, Soeda T, Senoo C, Natori O;
 PI Kasutani K, Ishii S;
 XX WPI; 2005-315561/32.

XX Novel bispecific antibody substituting for functional protein and having
 PT ligand functional alternative activity to receptor containing
 PT heteromolecule, useful for preventing/treating viral disease,
 PT immunological disease or bleeding.

XX Claim 28; SEQ ID NO 73; 151pp; Japanese.

XX The invention relates to a bispecific antibody (I) substituting for: a
 CC functional protein and having ligand functional alternative activity with
 CC respect to receptor containing heteromolecule; or a functional cofactor
 CC which enhances an enzyme reaction and recognizes both substrates of
 CC enzyme. Also claimed are a composition (II) containing (I). (I) and (II)
 CC are useful for preventing and/or treating viral disease, neoplasm, or
 CC immunological disease, or bleeding or disease resulting from bleeding.
 CC The viral disease is a hepatitis C virus or hepatitis B virus infection
 CC such as an acute or chronic liver cirrhosis or hepatic carcinoma. The
 CC neoplasms are chronic myeloid leukemia, malignant melanoma, multiple
 CC myeloma, renal carcinoma, glioblastoma, medulloblastoma, astrocytoma,
 CC hairy cell leukemia, AIDS-related Kaposi's sarcoma, skin T cell lymphoma
 CC or non-Hodgkin's lymphoma. The immunological disease is multiple
 CC sclerosis. The bleeding disease is the disease resulting from the active
 CC reduction or a defect of blood coagulation factor VIII such as hemophilia

CC or von Willebrand disease. (II) is useful for manufacturing (I). (I) has
CC high stability and low antigenicity in blood. The present sequence
CC represents a mouse anti-s AR antibody CDR.
XX
SQ Sequence 16 AA; 80.9%; Score 72; DB 9; Length 16;
Query Match Best Local Similarity 75.0%; Pred. No. 0.0003;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 YISYDGTNNYKPSLKD 16
|:|:|:|:|:|:|:|:|:
DB 1 YINFDGSNNINPSLKN 16
|:|:|:|:|:|:|:|:|:
RESULT 8
ADZ45520
ID ADZ45520 standard; peptide; 16 AA.
XX
XX AC AC
XX ADZ45520;
DT 30-JUN-2005 (first entry)
XX
XX Marine factor IX directed antibody CDR2 SEQ ID NO 224.
DE
XX bispecific antibody; blood coagulation factor VIII; bleeding;
KW fibrinolysis; blood coagulation factor X; blood-coagulation factor IX;
KW factor VIII deficiency; von Willebrand disease; hemostatic;
KW immunostimulator; antibody engineering; ds; gene.
KW
OS Mus musculus.
XX
XX WO2005035756-A1.
XX
XX 21-APR-2005.
XX
XX 08-OCT-2004; 2004WO-JP014911.
XX
XX 10-OCT-2003; 2003WO-JP013062.
PR 14-OCT-2003; 2003WO-JP013123.
XX
XX (CHUS) CHUGAI SEIYAKU KK.
PA
XX
XX Hattori K, Kojima T, Miyazaki T, Soeda T;
XX
XX WPI; 2005-315563/32.
DR N-PSDB; ADZ45519.
XX
XX Novel bispecific antibody substituting for function of cofactor that
PT enhances enzyme reaction, and recognizing both enzyme and substrates of
PT enzyme, useful for treating hemophilia A.
XX
XX Disclosure; SEQ ID NO 224; 69pp; Japanese.
PS
XX
XX This invention describes a novel bispecific antibody which can act as a
CC cofactor to enhance an enzyme reaction and can recognize the enzyme and
CC the enzyme substrate. The antibody specifically binds to blood
CC coagulation factor VIII. The invention also describes a composition
CC comprising the antibody and a carrier, a kit useful in preventing and/or
CC treating bleeding associated with a disorder or from a disease caused by
CC bleeding. The composition includes blood coagulation factor VIII. The
CC antibody of the invention can be a blood-coagulation fibrinolysis related
CC factor including blood-coagulation factor VIII, blood coagulation factor
CC X, or blood-coagulation factor IX. The antibody comprises a complementary
CC determining region (CDR) of anti-blood-coagulation factor IX/IXa factor
CC antibody. The novel antibody or composition is useful for preventing
CC and/or treating a disease accompanying bleeding, or the disease resulting
CC from bleeding, where the disease accompanying bleeding or the disease
CC resulting from bleeding develops and/or progresses by an active reduction
CC or deletion of the blood coagulation factor VIII. The disease the
CC develops and/or progresses by an active reduction or deletion of the
CC blood coagulation factor VIII and/or activation blood coagulation factor
CC VIII, is hemophilia A or von Willebrand disease, where the hemophilia is

CC VIII, is hemophilia A or von Willebrand disease, where the hemophilia is
 CC an acquired hemophilia A. This sequence represents a fragment of the
 CC antibody described in the method of the invention. Note: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 16 AA;

Query Match 78.7%; Score 70; DB 9; Length 16;
 Best Local Similarity 75.0%; Pred. No. 0.00061;
 Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLKD 16
 |||:||||:||||:
 Db 1 YISFDGTNDYNPSLKN 16

RESULT 10

ADZ51224
 ID ADZ51224 standard; peptide; 16 AA.

XX AC ADZ51224;

XX DT 30-JUN-2005 (first entry)

XX DE Amino acid sequence of a variable heavy chain region CDR.

XX KW bispecific antibody; AR1 chain; AR2 chain; hemostatic; bleeding;
 KW antibody therapy; blood coagulation factor VIII; factor VIII deficiency;
 KW von Willebrand disease; heavy chain; complementarity determining region;
 KW CDR.

XX OS Mus musculus.

XX PN WO2005035753-A1.

XX PD 21-APR-2005.

XX PF 10-OCT-2003; 2003WO-JP013062.

XX PR 10-OCT-2003; 2003WO-JP013062.

XX PA (CHUS) CHUGAI SEIYAKU KK.

XX PI Hattori K, Kojima T, Miyazaki T, Soeda T, Senoo C, Natori O;

XX PI Kasutani K, Ishii S;

XX DR WPI; 2005-315560/32.

XX PT Novel bispecific antibody substituting for functional protein or
 PT substituting for ligand for receptor comprising two types of molecules,
 PT useful as pharmaceutical for treating or preventing diseases e.g.
 PT bleeding.

XX PS Claim 18; SEQ ID NO 41; 143pp; Japanese.

XX CC The specification describes a bispecific antibody substituting for
 CC functional protein or substituting for a ligand for a receptor comprising
 CC two types of molecules. The antibody comprises AR1 and AR2 chains.
 CC Bispecific antibodies of the invention are useful for preventing and
 CC treating bleeding, diseases accompanying bleeding or diseases resulting
 CC from bleeding. These diseases develop or progress by active reduction of
 CC blood coagulation factor VIII/activated blood coagulation factor VIII,
 CC e.g. hemophilia A, acquired hemophilia or von Willebrand disease. The
 CC present sequence represents a complementarity determining region (CDR)
 CC from a variable heavy chain region, which was used to construct
 CC bispecific antibodies of the invention.

XX SQ Sequence 16 AA;

Query Match 78.7%; Score 70; DB 9; Length 16;
 Best Local Similarity 75.0%; Pred. No. 0.00061;

Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 YISYDGTNNYKPSLKD 16
 |||:||||:||||:
 Db 1 YISFDGTNDYNPSLKN 16

RESULT 11

ADZ42098
 ID ADZ42098 standard; peptide; 16 AA.

XX AC ADZ42098;

XX DT 30-JUN-2005 (first entry)

XX DE Mouse anti-s AR antibody heavy chain CDR 2 SEQ ID NO 41.

XX KW viral infection; neoplasm; immune disorder; bleeding; infection;
 KW cardiovascular disease; Virucide; Hepatotropic; Antiinflammatory;
 KW Neuroprotective; Hemostatic; Cytostatic; Immunotherapy; antibody.
 XX OS Mus musculus.

XX PN WO2005035754-A1.

XX PD 21-APR-2005.

XX PF 14-OCT-2003; 2003WO-JP013123.

XX PR 14-OCT-2003; 2003WO-JP013123.

XX PA (CHUS) CHUGAI SEIYAKU KK.

XX PI Hattori K, Kojima T, Miyazaki T, Soeda T, Senoo C, Natori O;

XX PI Kasutani K, Ishii S;

XX DR WPI; 2005-315561/32.

XX PT Novel bispecific antibody substituting for functional protein and having
 PT ligand functional alternative activity to receptor containing
 PT heteromolecule, useful for preventing/treating viral disease,
 PT immunological disease or bleeding.

XX PS Claim 28; SEQ ID NO 41; 151pp; Japanese.

XX CC The invention relates to a bispecific antibody (I) substituting for: a
 CC functional protein and having ligand functional alternative activity with
 CC respect to receptor containing heteromolecule; or a functional cofactor
 CC which enhances an enzyme reaction and recognizes both substrates of
 CC enzyme. Also claimed are a composition (II) containing (I). (I) and (II)
 CC are useful for preventing and/or treating viral disease, neoplasm, or
 CC immunological disease, or bleeding or disease resulting from bleeding.
 CC The viral disease is a hepatitis C virus or hepatitis B virus infection
 CC such as an acute or chronic liver cirrhosis or hepatic carcinoma. The
 CC neoplasms are chronic myeloid leukemia, malignant melanoma, multiple
 CC myeloma, renal carcinoma, glioblastoma, medulloblastoma, astrocytoma,
 CC hairy cell leukemia, AIDS-related Kaposi's sarcoma, skin T cell lymphoma
 CC or non-Hodgkin's lymphoma. The immunological disease is multiple
 CC sclerosis. The bleeding disease is the disease resulting from the active
 CC reduction or a defect of blood coagulation factor VIII such as hemophilia
 CC or von Willebrand disease. (II) is useful for manufacturing (I). (I) has
 CC high stability and low antigenicity in blood. The present sequence
 CC represents a mouse anti-s AR antibody CDR.

XX SQ Sequence 16 AA;

Query Match 78.7%; Score 70; DB 9; Length 16;
 Best Local Similarity 75.0%; Pred. No. 0.00061;

Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 YISYDGTNNYKPSLKD 16
 |||:||||:||||:
 Db 1 YISFDGTNDYNPSLKN 16

RESULT 14

AAR24718
ID AAR24718 standard; protein; 16 AA.

AC AAR24718;
XX

DT 25-MAR-2003 (revised)

DT 28-DEC-1992 (first entry)

XX Sequence of an anti-urokinase antibody heavy chain variable region chain designated 'K'.

XX

KW Chimeric monoclonal antibody; anti-urokinase antibody;
KW antithrombotic agent; myocardial infarction therapy.

XX

OS Mus musculus.

XX

PN EP491351-A2.

XX

PD 24-JUN-1992.

XX

PF 17-DEC-1991; 91EP-00121591.

XX

PR 18-DEC-1990; 90JP-00413829.

XX

PR 11-NOV-1991; 91JP-00294464.

XX

PA (TAKE) TAKEDA CHEM IND LTD.

XX

PI Iwasa S, Tada H, Watanabe T;

XX

DR WPI; 1992-209528/26.

XX

XX Chimeric monoclonal antibodies - contain anti-human fibrin antibody light
PT and heavy chain variable and constant for treating thrombotic conditions
PT e.g. myocardial infarction.

XX

PS Claim 21; Page 50; 87pp; English.

XX

CC The inventors claim a chimeric monoclonal antibody which contains a
CC urokinase-recognising antibody heavy chain variable region contg. at least
CC one of the polypeptide chains G, H and I (AAR24717, R24718, AAR24719) and a
CC human antibody heavy chain constant region. The chimeric Abs can be used
CC both in vivo and in vitro and, since they have very low immunogenicity as
CC compared with mouse Abs, they can be administered to humans for
CC diagnostic and therapeutic purposes. They are also more stable and show a
CC longer half-life in the blood as compared with the original mouse Abs.
CC (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 16 AA;

Query Match 65.2%; Score 58; DB 2; Length 16;

Best Local Similarity 66.7%; Pred. No. 0.048; Mismatches 3; Indels 0; Gaps 0;

Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLK 15

||:||||:||||

Db 1 YINYSGTTSYNPSLK 15

RESULT 15

AEC20782
ID AEC20782 standard; peptide; 16 AA.

XX

AC AEC20782;

XX

DT 20-OCT-2005 (first entry)

XX

DE M-CSF specific murine antibody consensus heavy chain CDR2.

XX

DE endocrine-gen.; antiarthritic; antibacterial; antiinflammatory;
KW antirheumatic; antithyroid; bone metastases; calcium antagonist; cancer;

XX

KW cardiovascular-gen.; degeneration; eating-disorders-gen.;
KW endocrine disease; endocrine-gen.; endocrine-gen.;
KW genetic disorder; heavy chain; hepatotropic; hypercalcemia;
KW immune disorder; immunotherapy; inflammation; monoclonal antibody;
KW mouth disease; musculoskeletal disease; neoplasm; nephrotropic;
KW osteopathic; osteopetrosis; osteoporosis; pagets disease;
KW periodontal disease; pharmaceutical; rheumatoid arthritis.

XX Mus musculus.

OS

PN WO2005068503-A2.

XX

PD 28-JUL-2005.

XX

PF 06-JAN-2005; 2005WO-US000546.

XX

PR 07-JAN-2004; 2004US-0535181P.

XX

PR 02-JUN-2004; 2004US-0576417P.

XX

PA (CHIR) CHIRON CORP.

XX

PA (XOMA) XOMA TECHNOLOGY LTD.

XX

PI Liu C, Zimmerman DL, Harrowe GM, Koths K, Kavanaugh WM, Long L;

PI Calderon-Cacia M, Horwitz AH;

XX

DR WPI; 2005-597707/61.

XX

PT Novel non-murine antibody that competes with monoclonal antibody RX1 for
PT binding to macrophage colony stimulating factor, useful for treating
PT hypogonadism, hypercalcemia, rickets, scurvy, homocystinuria, cancer,
PT osteoporosis.

XX

PS Claim 14; SEQ ID NO 21; 269pp; English.

XX

CC The invention describes a non-murine antibody (I) that competes with
CC monoclonal antibody RX1 for binding to macrophage colony stimulating
CC factor (M-CSF) by more than 75%, where the monoclonal antibody RX1 has
CC the heavy chain and light chain amino acid sequences having a fully
CC defined 447 amino acids (SEQ ID NO. 2) and 214 amino acids (SEQ ID NO. 4)
CC sequences given in the specification, respectively. (I) is useful for
CC preventing a subject afflicted with a disease that causes or contributes
CC to osteolysis, where the antibody effectively reduces the severity of
CC bone loss associated with the disease. The disease is chosen from
CC metabolic bone diseases associated with relatively increased osteoclast
CC activity, including endocrinopathies, hypercalcemia, deficiency states,
CC chronic diseases, and hereditary diseases, cancer, osteoporosis,
CC osteopetrosis, inflammation of bone associated with arthritis and
CC rheumatoid arthritis, periodontal disease, fibrous dysplasia, and/or
CC Paget's disease. (I) is useful for preventing or treating metastatic
CC cancer. Antibodies of the invention are useful for preventing or reducing
CC bone loss; osteolysis; metastatic cancer to bone and cancer. (I) is
CC useful for manufacturing a medicament for preventing or reducing bone
CC loss in a patient exhibiting osteolysis, manufacturing a medicament for
CC treating a patient afflicted with a disease that causes or contributes to
CC osteolysis, and metastatic cancer to bone in a patient suffering from
CC metastatic cancer, for manufacturing a medicament for treating a patient
CC having cancer. (I) in synergistic combination, is useful for preparing a
CC medicament for treating a patient exhibiting osteolysis. This is the
CC amino acid sequence of macrophage colony stimulating factor (M-CSF)
CC specific murine antibody consensus heavy chain CDR1.

XX SQ Sequence 16 AA;

Query Match 64.0%; Score 57; DB 9; Length 16;

Best Local Similarity 66.7%; Pred. No. 0.07;

Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLK 15

|||||:||||

Db 1 YISYSGTTSYNPSLK 15

Search completed: December 30, 2005, 14:20:02

Job time : 134.5 secs

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OM protein - protein search, using sw model

Run on: December 30, 2005, 14:07:14 ; Search time 22.5 Seconds
(without alignments)
68.421 Million cell updates/sec

Title: US-10-735-916A-10
Perfect score: 89
Sequence: 1 YISVDGNNYKPSLKD 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 250

Minimum DB seq length: 16
Maximum DB seq length: 16

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: Pirl.*
2: Pirl2.*
3: Pirl3.*
4: Pirl4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	33.7	16	2 PH1589	Ig H chain V-D-J r
2	28	31.5	16	2 PH0749	T-cell receptor be
3	27	30.3	16	2 A49255	T-cell receptor be
4	23	25.8	16	2 A42291	tail fiber protein
5	23	25.8	16	2 A31963	pyruvate dehydroge
6	22	24.7	16	2 PH1351	Ig heavy chain DJ
7	22	24.7	16	2 E28027	protein P8 - curle
8	20	22.5	16	2 C45133	casein kinase II (
9	20	22.5	16	2 S01669	rRNA N-glycosidase
10	20	22.5	16	2 S28213	glutathione transf
11	20	22.5	16	2 PH1778	T cell receptor al
12	20	22.5	16	2 F49039	T-cell receptor be
13	20	22.5	16	2 B60278	24K antigen - Myco
14	19	21.3	16	2 PH0137	redoxendonuclease
15	19	21.3	16	2 S23184	protein kinase, 80
16	19	21.3	16	2 C44896	heat shock protein
17	18	20.2	16	2 S51610	hypothetical prote
18	18	20.2	16	2 B45895	T-cell surface gly
19	18	20.2	16	2 PH1622	Ig H chain V-D-J r
20	17	19.1	16	2 S00123	dihydroliipoamide S
21	17	19.1	16	2 A44101	calmodulin, vasoac
22	17	19.1	16	2 G49039	T-cell receptor be
23	17	19.1	16	2 PH1474	T-cell receptor be
24	17	19.1	16	2 PH1472	T-cell receptor be
25	17	19.1	16	2 PH1477	T-cell receptor be
26	17	19.1	16	2 PH1473	T-cell receptor be
27	17	19.1	16	2 PH1480	T-cell receptor be
28	17	19.1	16	2 A41170	photosystem II 6.1
29	17	19.1	16	2 PA0048	protein QA100047 -

30	17	19.1	16	2 E45066	calcium-dependent
31	16	18.0	16	2 S10807	protein kinase C i
32	16	18.0	16	2 C59045	alpha-conotoxin Au
33	16	18.0	16	2 A59045	alpha-conotoxin Au
34	16	18.0	16	2 A45133	casein kinase II (
35	16	18.0	16	2 PH1346	Ig heavy chain DJ
36	16	18.0	16	2 PH0777	T-cell receptor al
37	16	18.0	16	2 S28433	major outer membra
38	16	18.0	16	2 S22040	cob protein - comm
39	16	18.0	16	2 A11488	taurocyamine kinas
40	16	18.0	16	2 B23692	transcription fact
41	15.5	17.4	16	1 MTDFBS	melanotropin beta
42	15	16.9	16	2 A39109	hypothetical prote
43	15	16.9	16	2 H49039	T-cell receptor be
44	15	16.9	16	2 PH1634	Ig H chain V-D-J r
45	15	16.9	16	2 B36300	T-cell receptor de

ALIGNMENTS

RESULT 1

PH1589
Ig H chain V-D-J region (wild-type clone 140) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1589
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993

A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A;Reference number: PH1580; MUID:93301609; PMID:8315387
A;Accession: PH1589
A;Molecule type: DNA
A;Residues: 1-16 <LEV>
A;Cross-references: UNIPARC:UPI000017C6B0
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin

Query Match 33.7%; Score 30; DB 2; Length 16;
Best Local Similarity 62.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SYDGTNNY 10
|||:|
Db 5 SYDGSFHY 12

RESULT 2

PH0749
T-cell receptor beta chain (B83) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C;Accession: PH0749
R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991

A;Title: T cell receptor genes in a series of class I major histocompatibility complex-
allelic exclusion and antigen-specific repertoire.
A;Reference number: PH0746; MUID:92078846; PMID:1836010
A;Accession: PH0749
A;Molecule type: mRNA
A;Residues: 1-16 <CAS>
A;Cross-references: UNIPARC:UPI0000115FA8; EMBL:X60840; NID:G50116; PIDN:CAA43233.1; PID
A;Experimental source: T lymphocyte
C;Keywords: T-cell receptor

Query Match 31.5%; Score 28; DB 2; Length 16;
Best Local Similarity 71.4%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GTNNYKP 12
|||:|
Db 7 GTNNQAP 13

```
RESULT 3
A49255
T-cell receptor beta chain V-D-J-C region (V beta 7, J beta 1.6) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
C:Accession: A49255
R;Rosenberg, W.M.; Moss, P.A.; Bell, J.I.
Eur. J. Immunol. 22, 541-549, 1992
A;Title: Variation in human T cell receptor V beta and J beta repertoire: analysis using
A;Reference number: A49039; MUID:92164737; PMID:1311263
A;Accession: A49255
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-16 <ROS>
A;Cross-references: UNIPARC:UPI000017C3B9
A;Note: sequence extracted from NCBI backbone (NCBIP:90722)
C;Keywords: T-cell receptor

Query Match 30.3%; Score 27; DB 2; Length 16;
Best Local Similarity 71.4%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 SYDGTNN 9
DB 4 SYPGTQN 10

RESULT 4
A42291
tail fiber protein I - phase P2 (fragment)
C:Species: phage P2
C>Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 09-Jul-2004
C:Accession: A42291
R;Haggard-Ljungquist, E.; Halling, C.; Calendar, R.
J. Bacteriol. 174, 1462-1477, 1992
A;Title: DNA sequences of the tail fiber genes of bacteriophage P2: evidence for horizon
A;Reference number: A42291; MUID:92165720; PMID:1531648
A;Accession: A42291
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-16 <HAG>
A;Cross-references: UNIPROT:P26701; UNIPARC:UPI000017A829; GB:M64677

Query Match 25.8%; Score 23; DB 2; Length 16;
Best Local Similarity 60.0%; Pred. No. 2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISYDG 6
DB 4 VAYDG 8

RESULT 5
A31963
pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) alpha chain type I - pig roundworm (frag
C:Species: Ascaris suum (pig roundworm)
C>Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 09-Jul-2004
C:Accession: A31963
R;Thissen, J.; Komuniecki, R.
J. Biol. Chem. 263, 19092-19097, 1988
A;Title: Phosphorylation and inactivation of the pyruvate dehydrogenase from the anaerob
A;Reference number: A31963; MUID:89066711; PMID:3198613
A;Accession: A31963
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-16 <THI>
A;Cross-references: UNIPROT:P26267; UNIPARC:UPI000017B69C
C;Keywords: mitochondrion; oxidoreductase; phosphoprotein

Query Match 25.8%; Score 23; DB 2; Length 16;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2 ISYDGTNNYK 11
DB 7 MSDPGTSSYR 16

RESULT 6
PH1351
Ig heavy chain DJ region (clone C100-109B) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PH1351
R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A;Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A;Reference number: PH1302; MUID:93094761; PMID:1460419
A;Accession: PH1351
A;Molecule type: DNA
A;Residues: 1-16 <WAS>
A;Cross-references: UNIPARC:UPI000017C21F
C;Keywords: heterotetramer; immunoglobulin

Query Match 24.7%; Score 22; DB 2; Length 16;
Best Local Similarity 30.8%; Pred. No. 2.9e+03;
Matches 4; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 4 YDGTNNYKPSLMD 16
DB 3 YDGPIGSTPGARE 15

RESULT 7
E28027
protein P8 - curled-leaved tobacco (fragment)
C:Species: Nicotiana glauca (curled-leaved tobacco)
C>Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 09-Jul-2004
C:Accession: E28027
R;Bauw, G.; De Loose, M.; Inze, D.; Van Montagu, M.; Vandekerckhove, J.
Proc. Natl. Acad. Sci. U.S.A. 84, 4806-4810, 1987
A;Title: Alterations in the phenotype of plant cells studied by NH2-terminal amino acid-
A;Reference number: A94167
A;Accession: E28027
A;Molecule type: protein
A;Residues: 1-16 <BAU>
A;Cross-references: UNIPROT:Q7M1V7; UNIPARC:UPI000017B09F
A;Note: 10-Lys was also found

Query Match 24.7%; Score 22; DB 2; Length 16;
Best Local Similarity 33.3%; Pred. No. 2.9e+03;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 ISYDGTNNY 10
DB 8 VANDGSKTY 16

RESULT 8
C45133
casein kinase II (EC 2.7.1.-) alpha chain - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C>Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: C45133
R;Ou, W.J.; Thomas, D.Y.; Bell, A.W.; Bergeron, J.J.
J. Biol. Chem. 267, 23789-23796, 1992
A;Title: Casein kinase II phosphorylation of signal sequence receptor alpha and the asso
A;Reference number: A45133; MUID:93054738; PMID:1331100
A;Accession: C45133
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-16 <OUI>
A;Cross-references: UNIPROT:Q9TRK9; UNIPARC:UPI0000088890
A;Experimental source: endoplasmic reticulum, pancreas
A;Note: sequence extracted from NCBI backbone (NCBIP:118799)
```


C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; heterotetramer; phosphotransferase; serine/threonine-specific protein kinase

Query Match 22.5%; Score 20; DB 2; Length 16;
Best Local Similarity 42.9%; Pred. No. 6.1e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 YDGTNNY 10
:|:|:
Db 9 FHGHNDY 15

RESULT 9

S01669
rRNA N-glycosidase (EC 3.2.2.22) trichokirin - Mongolian snake-gourd (fragment)
N;Alternate names: ribosome-inactivating protein trichokirin
C;Species: Trichosanthes kirilowii (Mongolian snake-gourd)
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C;Accession: S01669
R;Casellas, P.; Dussossoy, D.; Falasca, A.I.; Barbieri, L.; Guillemot, J.C.; Ferrara, P.
Eur. J. Biochem. 176, 581-588, 1988
A;Title: Trichokirin, a ribosome-inactivating protein from the seeds of Trichosanthes kirilowii (Mongolian snake-gourd)
A;Reference number: S01669; MUID:89005108; PMID:3262509
A;Accession: S01669
A;Molecule type: protein
A;Residues: 1-16 <CAS>
A;Cross-references: UNIPROT:P16093; UNIPARC:UPI000002BB47
C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
C;Keywords: glycoprotein; glycosidase; hydrolase

Query Match 22.5%; Score 20; DB 2; Length 16;
Best Local Similarity 40.0%; Pred. No. 6.1e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ISYDGTNNYK 11
:|:|:|:
Db 6 LSGGGTASYE 15

RESULT 10

S28213
glutathione transferase (EC 2.5.1.18) - European toad (fragments)
C;Species: Bufo bufo (European toad)
C;Date: 19-Mar-1997 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
C;Accession: S28213
R;Aceto, A.; Dragani, B.; Bucciarrelli, T.; Sacchetta, P.; Martini, F.; Angelucci, S.; Amadio, J. 289, 417-422, 1993
A;Title: Purification and characterization of the major glutathione transferase from adult European toad (Bufo bufo)
A;Reference number: S28213; MUID:93143709; PMID:8424786
A;Accession: S28213
A;Molecule type: protein
A;Residues: 1-16 <ACE>
A;Cross-references: UNIPARC:UPI000017BFA9
A;Experimental source: liver
C;Keywords: transferase

Query Match 22.5%; Score 20; DB 2; Length 16;
Best Local Similarity 28.6%; Pred. No. 6.1e+03;
Matches 4; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSL 14
:|:|:|:
Db 1 FIFWDNEANFLEEL 14

RESULT 11

Phi778
T cell receptor alpha chain V region (clone 1PBL V alpha 24-5) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C;Accession: Phi778
R;Porcellini, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993

A;Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood (PBMC) cells
A;Reference number: PH1754; MUID:93301585; PMID:8391057
A;Accession: PH1778
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-16 <POR>
A;Cross-references: UNIPARC:UPI000017C36C

Query Match 22.5%; Score 20; DB 2; Length 16;
Best Local Similarity 66.7%; Pred. No. 6.1e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 8 NNYKPS 13
:|:|:
Db 10 NDYKLS 15

RESULT 12

F49039
T-cell receptor beta chain V-D-J-C region (V beta 2, J beta 1.5) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
C;Accession: F49039
R;Rosenberg, W.M.; Moss, P.A.; Bell, J.I.
Eur. J. Immunol. 22, 541-549, 1992
A;Title: Variation in human T cell receptor V beta and J beta repertoire: analysis using PCR
A;Reference number: A49039; MUID:92164737; PMID:1311263
A;Accession: F49039
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-16 <ROS>
A;Cross-references: UNIPARC:UPI000017C3B3
A;Note: sequence extracted from NCBI backbone (NCBI:90718)
C;Keywords: T-cell receptor

Query Match 22.5%; Score 20; DB 2; Length 16;
Best Local Similarity 57.1%; Pred. No. 6.1e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 SYDGTNN 9
:|:|:
Db 2 SASGTDN 8

RESULT 13

B60278
24K antigen - Mycobacterium bovis (fragment)
C;Species: Mycobacterium bovis
C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 09-Jul-2004
C;Accession: B60278
R;Fifis, T.; Costopoulos, C.; Radford, A.J.; Basic, A.; Wood, P.R.
Infect. Immun. 59, 800-807, 1991
A;Title: Purification and characterization of major antigens from a Mycobacterium bovis strain
A;Reference number: A60278; MUID:91147217; PMID:1900061
A;Accession: B60278
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-16 <FIF>
A;Cross-references: UNIPROT:Q7M199; UNIPARC:UPI000017AD42

Query Match 22.5%; Score 20; DB 2; Length 16;
Best Local Similarity 66.7%; Pred. No. 6.1e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 10 YKPSLK 15
:|:|:
Db 5 YKPSLK 10

RESULT 14

PL0137
protein kinase, 80K - pig (fragment)

C;Species: Sus scrofa domestica (domestic pig)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 18-Jun-1993
C;Accession: PLO137
R;Dechert, U.; Weber, M.; Weber-Schaeuffelen, M.; Wollny, E.
J. Neurochem. 53, 1268-1275, 1989
A;Title: Isolation and partial characterization of an 80,000-dalton protein kinase from
A;Reference number: PLO137; MUID:89361455; PMID:2769266
A;Accession: PLO137
A;Molecule type: protein
A;Residues: 1-16 <DEC>
A;Cross-references: UNIPARC:UPI0000177D3E
C;Comment: This protein has a novel serine/threonine-specific protein kinase activity.

Query Match 21.3%; Score 19; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 8.8e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISYDGT 7
: |||
Db 4 VDVDGT 9

RESULT 15
S23184
redoxynucleonuclease (EC 4.2.99.-) - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Mar-1997 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
C;Accession: S23184
R;Huq, I.; Haukanes, B.I.; Helland, D.E.
Eur. J. Biochem. 206, 833-839, 1992
A;Title: Purification to homogeneity and characterization of a redoxynucleonuclease from
A;Reference number: S23184; MUID:92299012; PMID:1376689
A;Accession: S23184
A;Molecule type: protein
A;Residues: 1-16 <HUQ>
A;Cross-references: UNIPARC:UPI000017C559
A;Experimental source: thymus
C;Function:
A;Description: recognizes and induces cleavage of DNA damaged by UV
C;Keywords: carbon-oxygen lyase

Query Match 21.3%; Score 19; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 8.8e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 SYDGTN 8
: |||
Db 5 AYTGTD 10

Search completed: December 30, 2005, 14:25:37
Job time : 23.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2005, 14:06:48 ; Search time 141.5 Seconds

(without alignments)
79.777 Million cell updates/sec

Title: US-10-735-916A-10

Perfect score: 89

Sequence: 1 YISYDGTNNYKPSLKD 16

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 1144

Minimum DB seq length: 16

Maximum DB seq length: 16

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	32.6	16	2	Q9UC75_HUMAN
2	26	29.2	16	2	Q50L92_DROBP
3	24	27.0	16	2	Q9KJ10_STAHA
4	23	25.8	16	2	Q7RJE1_PLAYO
5	23	25.8	16	2	Q9F1R9_STRSU
6	23	25.8	16	2	Q9F1S1_STRSU
7	23	25.8	16	2	Q9QVL2_9MURI
8	23	25.8	16	2	Q9YQ11_9CORO
9	22	24.7	16	2	Q7M1V7_NICPL
10	22	24.7	16	2	Q9PRR9_NAVES
11	21	23.6	16	2	Q35214_ONBEB
12	21	23.6	16	2	Q9GIA6_9PHAE
13	20	22.5	16	1	ARCDC_PSEFU
14	20	22.5	16	1	RIPK1_TRIKI
15	20	22.5	16	2	Q9TRK9_CANFA
16	20	22.5	16	2	Q21922_9CAUD
17	20	22.5	16	2	Q7Y0M3_MAIZE
18	20	22.5	16	2	Q79AT0_AGRRH
19	20	22.5	16	2	Q7M1V9_MYCBO
20	20	22.5	16	2	Q9R4J4_PSEPR
21	20	22.5	16	2	Q506K8_9CALI
22	19	21.3	16	2	Q4X7B4_PLACH
23	19	21.3	16	2	Q9PRV4_CHICK
24	18	20.2	16	2	Q96KQ2_HUMAN
25	18	20.2	16	2	Q9T2V8_HUMAN
26	18	20.2	16	2	Q9UCR2_HUMAN
27	18	20.2	16	2	Q50L70_9DIPT
28	18	20.2	16	2	Q50L82_9DIPT
29	18	20.2	16	2	Q6RY72_TRIMO
30	18	20.2	16	2	Q8LLT9_PINRA
31	18	20.2	16	2	Q5YE54_PHOGU

32	17.5	19.7	16	2	Q9F9S4_HELPY	Q9f9s4 helicobacte
33	17	19.1	16	1	FORM1_MYRGU	P81438 myrmecia gu
34	17	19.1	16	1	FORM2_MYRGU	P81437 myrmecia gu
35	17	19.1	16	1	MK2B_FALPR	P80410 palomena pr
36	17	19.1	16	1	MK3_FALPR	P80411 palomena pr
37	17	19.1	16	1	ODO2_BOVIN	P11179 bos taurus
38	17	19.1	16	1	SSIT_STRMB	P83544 streptomyce
39	17	19.1	16	2	Q9TNN9_HUMAN	Q9tnn9 homo sapien
40	17	19.1	16	2	Q9UCG5_HUMAN	Q9ucg5 homo sapien
41	17	19.1	16	2	Q9TRL9_BOVIN	Q9trl9 bos taurus
42	17	19.1	16	2	Q7MIW7_ARATH	Q7miw7 arabidopsis
43	17	19.1	16	2	Q9S8C0_LUPAL	Q9s8c0 lupinus alb
44	17	19.1	16	2	Q9S8G3_ORYSA	Q9s8g3 oryza sativ
45	17	19.1	16	2	Q9S8N2_TOBAC	Q9s8n2 nicotiana t

ALIGNMENTS

RESULT 1

Q9UC75_HUMAN PRELIMINARY; PRT; 16 AA.
AC Q9UC75;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE DIPEPTIDYLPEPTIDASE IV (EC 3.4.14.5) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=95294018; PubMed=7539799; DOI=10.1074/jbc.270.23.14107;
RA Duke-Cohan J.S., Morimoto C., Rocker J.A., Schlossman S.F.;
RT "A novel form of dipeptidylpeptidase IV found in human serum."
RT Isolation, characterization, and comparison with T lymphocyte membrane
RT dipeptidylpeptidase IV (CD26).";
RL J. Biol. Chem. 270:14107-14114(1995).
DR GO; GO:0004274; F:dipeptidyl-peptidase IV activity; IEA.
SQ SEQUENCE 16 AA; 1600 MW; DFB3DD95FEE0A1EB CRC64;

Query Match 32.6%; Score 29; DB 2; Length 16;
Best Local Similarity 71.4%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 DGTNNYK 11
|||
Db 10 DGPNGYK 16

RESULT 2

Q50L92_DROBP PRELIMINARY; PRT; 16 AA.
AC Q50L92;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DR Nos protein (Fragment).
GN Name=nos;
OS Drosophila bipectinata (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=42026;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Nozawa M., Aotsuka T., Tamura K.;
RT "A novel chimeric gene, sirene, found in the Drosophila bipectinata
RT species complex: potential of retroposition with regulatory
RT sequence.";
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AB194429; BAD98205.1; -; Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 16 AA; 1933 MW; BFCABI719C58E7D3 CRC64;

Query Match 29.2%; Score 26; DB 2; Length 16;
Best Local Similarity 66.7%; Pred. No. 3.8e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 YKPSLK 15
   |||
Db 10 YKPMK 15

RESULT 3
Q9KJ10 STAHA PRELIMINARY; PRT; 16 AA.
AC Q9KJ10;
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DE Heparin-binding protein (Fragment).
OS Staphylococcus haemolyticus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1283;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SM131;
RX MEDLINE=21284478; PubMed=11393292;
RA Fallgren C., Utt M., Ljungh A.;
RT Isolation and characterisation of a 17-kDa staphylococcal heparin-
binding protein with broad specificity."
RL J. Med. Microbiol. 50:547-557(2001).
DR EMBL; AF169242; AAF89664.1; -; Genomic_DNA.
FT NON_TER 16
SQ SEQUENCE 16 AA; 1909 MW; 30C19B931B50FF11 CRC64;

Query Match 27.0%; Score 24; DB 2; Length 16;
Best Local Similarity 66.7%; Pred. No. 8e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSYDG 6
   |||
Db 9 YSYSYG 14

RESULT 4
Q7RJEL PLAYO PRELIMINARY; PRT; 16 AA.
AC Q7RJEL;
DT 01-MAR-2004 (TREMELrel. 26, Created)
DT 01-MAR-2004 (TREMELrel. 26, Last sequence update)
DE Hypothetical protein.
GN Name=PY03321;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=17XNL;
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Anguotli S.V., Suh B.B., Kooij T.W., Perteau M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selegut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegan M., Shoaibi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
parasite Plasmodium yoelii yoelii."
```

```
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL01000947; EAA22886.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 16 AA; 1824 MW; AEB5951B681C02A1 CRC64;

Query Match 25.8%; Score 23; DB 2; Length 16;
Best Local Similarity 66.7%; Pred. No. 1.2e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 DGTNNY 10
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Db 9 DDLNNY 14

RESULT 5
Q9FIR9 STRSU PRELIMINARY; PRT; 16 AA.
AC Q9FIR9;
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Phosphoribosyl carboxamide aminoimidazole transformylase (EC 6.3.2.6)
DE (Fragment).
GN Name=purH;
OS Streptococcus suis.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1307;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=212;
RX MEDLINE=20576151; PubMed=11133943; DOI=10.1128/JB.183.2.500-511.2001;
RA Sekizaki T., Otani Y., Osaki M., Takamatsu D., Shimoji Y.;
RT "Evidence for horizontal transfer of the SUDAI1 restriction-
modification genes to the Streptococcus suis genome."
J. Bacteriol. 183:500-511(2001).
DR EMBL; AB045616; BAB20846.1; -; Genomic_DNA.
DR GO; GO:0016874; P:ligase activity; IEA_
DR GO; GO:0004639; P:phosphoribosylaminoimidazolesuccinocarboxam. .; IEA.
KW Ligase.
FT NON_TER 1
SQ SEQUENCE 16 AA; 1980 MW; A73BD79FAE3C0946 CRC64;

Query Match 25.8%; Score 23; DB 2; Length 16;
Best Local Similarity 30.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 ISYDGTNNYK 11
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Db 6 VVYTGVRHYR 15

RESULT 6
Q9FIS1 STRSU PRELIMINARY; PRT; 16 AA.
AC Q9FIS1;
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Phosphoribosyl carboxamide aminoimidazole transformylase (EC 6.3.2.6)
DE (Fragment).
GN Name=purH;
OS Streptococcus suis.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1307;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=211;
RX MEDLINE=20576151; PubMed=11133943; DOI=10.1128/JB.183.2.500-511.2001;
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RX MEDLINE=95159435; PubMed=7856095;
RA Eleuter J., Raeschaert D., Lambert P., Levy L., Vende P., Laude H.;
RT "Complete sequence (20 kilobases) of the polyprotein-encoding gene 1
RL of transmissible gastroenteritis virus.";
RN Virology 206:817-822(1995).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99099045; PubMed=9882359;
RA Izeta A., Smerdou C., Alonso S., Penzes Z., Mendez A., Plana-Duran J.,
RA Enjuanes L.;
RT "Replication and packaging of transmissible gastroenteritis
RT coronavirus-derived synthetic minigenomes.";
RN J. Virol. 73:1535-1545(1999).
DR EMBL; AJ011482; CAA09624.1; -; Genomic_RNA.
RX Hypothetical protein.
SQ SEQUENCE 16 AA; 2015 MW; B37776CE7AP3B62D CRC64;

Query Match 25.8%; Score 23; DB 2; Length 16;
Best Local Similarity 40.0%; Pred. No. 1.2e+04;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISYDGTNNY 10
DB ||::||:
7 YYSFNLTTNW 16

RESULT 9
Q7M1V7 NICPL PRELIMINARY; PRT; 16 AA.
ID 07M1V7;
AC 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Protein P8 (Fragment).
OS Nicotiana plumbaginifolia (Leadwort-leaved tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamnids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4092;
RN [1]
RP PROTEIN SEQUENCE.
RA Bauw G., De Loose M., Inze D., Van Montagu M., Vandekerckhove J.;
RT "Alterations in the phenotype of plant cells studied by NH2-terminal
RT amino acid-sequence analysis of proteins electroblotted from two-
RT dimensional gel-separated total extracts.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:4806-4810(1987).
DR FIR; E28027; E28027.
DR PIR; NON_TER 1
FT NON_TER 16
FT NON_TER 16
SQ SEQUENCE 16 AA; 1637 MW; CB55CCF71E3FFA30 CRC64;

Query Match 24.7%; Score 22; DB 2; Length 16;
Best Local Similarity 33.3%; Pred. No. 1.7e+04;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 ISYDGTNNY 10
DB ::||:|
8 VANDGSKTY 16

RESULT 10
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ID Q9PRR9_9AVES
AC Q9PRR9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE NA/K adenosine triphosphatase alpha subunit (Fragment).
OS Anas (ducks).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archoosauria; Aves; Neognathae; Anseriformes; Anatidae.
OX NCBI_TaxID=8835;
RN [1]

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RP PROTEIN SEQUENCE.
RX MEDLINE=96074598; PubMed=7488178;
RA Boldyrev A.A., Lopina O.D., Kenney M., Johnson P.;
RT "Characterization of the subunit isoforms of duck salt gland Na/K
RL adenosine triphosphatase.";
RL Biochem Biophys Res Commun. 216:1048-1053(1995).
SQ SEQUENCE 16 AA; 1784 MW; 1A3382E2EF6B920 CRC64;

Query Match      24.7%; Score 22; DB 2; Length 16;
Best Local Similarity 37.5%; Pred. No. 1.7e+04;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      6 GTNNYKPS 13
DB      | : | : |
      1 GRDKYEPT 8

RESULT 11
Q35214 OENBE
ID Q35214_OENBE PRELIMINARY; PRT; 16 AA.
AC Q35214;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE ATPase alpha subunit (16 aa) (Fragment).
OS Oenothera lamarckiana (Bertero's evening primrose).
OG Mitochondrion.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Onagraceae; Oenothera.
OX NCBI_TaxID=3950;
[1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86312871; PubMed=2875433;
RA Schuster W., Hiesel R., Isaac P.G., Leaver C.J., Brennicke A.;
RT "Transcript termini of messenger RNAs in higher plant mitochondria.";
RL Nucleic Acids Res. 14:5943-5954(1986).
DR EMBL; X04203; CAA27800.1; -; Genomic DNA.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 1
SQ SEQUENCE 16 AA; 1820 MW; 118AC961C9322C91 CRC64;

Query Match      23.6%; Score 21; DB 2; Length 16;
Best Local Similarity 57.1%; Pred. No. 2.5e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      9 NYKPSLK 15
DB      | | | | |
      9 NAKPYIK 15

RESULT 12
Q9GIA6 9PHAE
ID Q9GIA6_9PHAE PRELIMINARY; PRT; 16 AA.
AC Q9GIA6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit
DE (Fragment).
GN Name=rbcs;
OS Sargassum palmeri.
OG Chloroplast.
OC Eukaryota; stramenopiles; Phaeophyceae; Fucales; Sargassaceae;
OC Sargassum.
OX NCBI_TaxID=129344;
[1]
RP NUCLEOTIDE SEQUENCE.
RA Phillips N.E., Smith C.M., Morden C.W.;
RT "Testing systematic concepts of Sargassum (Fucales, Phaeophyceae)
RT using portions of the rbcLs operon.";
RL Phycol. Res. 53:1-10(2005).
```

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RN NUCLEOTIDE SEQUENCE.
RP Phillips N.E.;
RA "Molecular phylogenetic analysis of the pan-pacific genus Sargassum
RT (Fucales, Phaeophyceae).";
RL Thesis (1998) University of Hawaii.
DR EMBL; AF244335; AAF98104.2; -; Genomic DNA.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0009573; C:ribulose biphosphate carboxylase complex (. . .); IEA.
DR GO; GO:0016984; F:ribulose-bisphosphate carboxylase activity; IEA.
DR GO; GO:0015977; P:carbon utilization by fixation of carbon di. . .; IEA.
DR InterPro; IPR000894; RuBisCO_small.
DR Pfam; PF00101; RuBisCO_small; 1.
DR ProDom; PD000290; RuBisCO_small; 1.
KW Chloroplast.
FT NON TER 16
SQ SEQUENCE 16 AA; 1830 MW; B2096FF5A23D1210 CRC64;

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Best Local Similarity 36.4%; Pred. No. 2.5e+04;
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      6 GCFSFLPDLSD 16

RESULT 13
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AC P41147;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Arginine/ornithine antiporter (Fragment).
GN Name=arcD;
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=303;
[1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 4359;
RA Wilson S.D., Wang M., Filpula D.;
RL Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Catalyzes an electroneutral exchange between arginine
CC and ornithine to allow high-efficiency energy conversion in the
CC arginine deiminase pathway.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (Potential).
CC -!- SIMILARITY: Belongs to the amino acid-polyamine-organocation (APC)
CC superfamily.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
DR EMBL; U07185; AAA16963.1; -; Unassigned DNA.
KW Amino-acid transport; Antiport; Inner membrane; Membrane;
KW Transmembrane; Transport.
FT NON TER 1
SQ SEQUENCE 16 AA; 1644 MW; 90B48A7C8FAA9705 CRC64;

Query Match      22.5%; Score 20; DB 1; Length 16;
Best Local Similarity 66.7%; Pred. No. 3.6e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB      | | | |
      7 YGLYDG 12
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RESULT 14
ID  RIPK_TRIKI  STANDARD;  PRT;  16 AA.
AC  P16093;
DT  01-APR-1990 (Rel. 14, Created)
DT  01-APR-1990 (Rel. 14, Last sequence update)
DT  05-JUL-2004 (Rel. 44, Last annotation update)
DE  Ribosome-inactivating protein trichokirin (EC 3.2.2.22) (rRNA N-
DE  glycosidase) (fragment).
OS  Trichosanthes kirilowii (Mongolian snake-gourd).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC  rosids; eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
OX  NCBI_TaxID=3677;
[1]
RN  PROTEIN SEQUENCE.
RC  TISSUE=Seed;
RX  MEDLINE=89005108; PubMed=3262509;
RA  Casellas P., Dussossy D., Palasca A.I., Barbieri L., Guillemot J.C.,
RA  Ferrara P., Bolognesi A., Ceni P., Stirpe F.;
RT  "Trichokirin, a ribosome-inactivating protein from the seeds of
RT  Trichosanthes kirilowii Maximowicz. Purification, partial
RT  characterization and use for preparation of immunotoxins.";
RL  Eur. J. Biochem. 176:581-588(1988).
CC  -I- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC  specific adenosine on the 28S rRNA.
CC  -I- PTM: Glycosylated.
CC  -I- SIMILARITY: Belongs to the ribosome-inactivating protein family.
CC  Type 1 RIP subfamily.
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CC  This Swiss-Prot entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use as long as its content is in no way modified and this statement is not
CC  removed.
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DR  PIR; S01669; S01669;
DR  InterPro; IPR001574; RIP.
DR  PROSITE; PS00275; SHIGA_RICIN; PARTIAL.
KW  Direct protein sequencing; Glycoprotein; Hydrolase; Plant defense;
KW  Protein synthesis inhibitor; Toxin.
FT  NON TER 16 16
SQ  SEQUENCE 16 AA; 1605 MW; 5E268A7F345935A2 CRC64;

Query Match 22.5%; Score 20; DB 1; Length 16;
Best Local Similarity 40.0%; Pred.No. 3.6e+04;
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: : ||| :|
Db 6 LSGGGTASYE 15

RESULT 15
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ID  Q9TRK9_CANFA PRELIMINARY;  PRT;  16 AA.
AC  Q9TRK9;
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT  01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE  Casein kinase II=24 kDa polypeptide (Fragment).
DE  Canis familiaris (Dog).
OS  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC  Canis.
OX  NCBI_TaxID=9615;
[1]
RN  PROTEIN SEQUENCE.
RC  MEDLINE=93054738; PubMed=1331100;
RA  Ou W.J., Thomas D.Y., Bell A.W., Bergeron J.J.;
RT  "Casein kinase II phosphorylation of signal sequence receptor alpha
RT  and the associated membrane chaperone calnexin.";
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2005, 14:15:20 ; Search time 31.5 Seconds
(without alignments)
41.994 Million cell updates/sec

Title: US-10-735-916A-10
Perfect score: 89
Sequence: 1 YISYDGTNNYKPSLK 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 7712

Minimum DB seq length: 16
Maximum DB seq length: 16

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	64.0	16	2	US-09-170-769A-14
2	56	62.9	16	2	US-09-424-840B-110
3	55	61.8	16	2	US-09-424-840B-112
4	54	60.7	16	1	US-08-137-117D-126
5	54	60.7	16	1	US-08-436-717-126
6	51	57.3	16	2	US-09-424-840B-35
7	49	55.1	16	1	US-08-672-345C-53
8	49	55.1	16	2	US-09-214-095D-53
9	49	55.1	16	2	US-09-940-727B-53
10	48	53.9	16	2	US-09-996-288-25
11	48	53.9	16	2	US-09-996-288-37
12	48	53.9	16	2	US-09-996-288-41
13	48	53.9	16	2	US-09-996-288-103
14	48	53.9	16	2	US-09-996-265-25
15	48	53.9	16	2	US-09-996-265-37
16	48	53.9	16	2	US-09-996-265-41
17	48	53.9	16	2	US-09-996-265-103
18	46	51.7	16	2	US-09-889-480A-2
19	42	47.2	16	2	US-09-996-288-100
20	42	47.2	16	2	US-09-996-288-106
21	42	47.2	16	2	US-09-996-288-114
22	42	47.2	16	2	US-09-996-265-100
23	42	47.2	16	2	US-09-996-265-106
24	42	47.2	16	2	US-09-996-265-114
25	41	46.1	16	2	US-09-996-288-19
26	41	46.1	16	2	US-09-996-288-45
27	41	46.1	16	2	US-09-996-288-86

Sequence 19, Appl
Sequence 45, Appl
Sequence 86, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 15, Appl
Sequence 44, Appl
Sequence 7, Appl
Sequence 2, Appl
Sequence 82, Appl
Sequence 91, Appl
Sequence 93, Appl
Sequence 109, App
Sequence 111, App
Sequence 2, Appl
Sequence 82, Appl
Sequence 91, Appl
Sequence 93, Appl

2 2 US-09-996-265-19
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16 2 US-09-771-415-7
16 2 US-09-996-288-2
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ALIGNMENTS

RESULT 1
US-09-170-769A-14
; Sequence 14, Application US/09170769A
; Patent No. 6444206
; GENERAL INFORMATION:
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
; APPLICANT: LETURCO, Didier
; APPLICANT: MORIATRY, Ann
; APPLICANT: ULEVITCH, Richard
; APPLICANT: TOBIAS, Peter
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING CD14 MEDIATED CELL ACTIVA
; FILE REFERENCE: SCRIP1140-3
; CURRENT APPLICATION NUMBER: US/09/170,769A
; CURRENT FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 08/070,160
; PRIOR FILING DATE: 1993-05-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Murine
US-09-170-769A-14

Query Match 64.0%; Score 57; DB 2; Length 16;
Best Local Similarity 66.7%; Pred. No. 0.0089;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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Db 1 YISYSGTSTYNPSLK 15

RESULT 2
US-09-424-840B-110
; Sequence 110, Application US/09424840B
; Patent No. 6790938
; GENERAL INFORMATION:
; APPLICANT: Berchtold, Peter
; APPLICANT: Escher, Robert F. A.
; TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/09/424,840B
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: DE 19755227.7
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06

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; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 110
; LENGTH: 16
; TYPE: PR
; ORGANISM: Homo sapiens
US-09-424-840B-110

Query Match      62.9%; Score 56; DB 2; Length 16;
Best Local Similarity 66.7%; Pred. No. 0.013;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLK 15
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Db 1 YIYSGSTNNPSLK 15

RESULT 3
US-09-424-840B-112
; Sequence 112, Application US/09424840B
; Patent No. 6790938
; GENERAL INFORMATION:
; APPLICANT: Berchtold, Peter
; APPLICANT: Escher, Robert F. A.
; TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/09/424,840B
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: DE 19755227.7
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 112
; LENGTH: 16
; TYPE: PR
; ORGANISM: Homo sapiens
US-09-424-840B-112

Query Match      61.8%; Score 55; DB 2; Length 16;
Best Local Similarity 66.7%; Pred. No. 0.019;
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLK 15
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Db 1 YIYSGTNNPSLK 15

RESULT 4
US-08-137-117D-126
; Sequence 126, Application US/08137117D
; Patent No. 5795965
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy

Query Match      60.7%; Score 54; DB 1; Length 16;
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Db 1 YIYSGITNNPSLK 15

RESULT 5
US-08-436-717-126
; Sequence 126, Application US/08436717
; Patent No. 5817790
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,717
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117
; FILING DATE: 20-DEC-1993
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APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-436-717-126

Query Match 60.7%; Score 54; DB 1; Length 16;
Best Local Similarity 66.7%; Pred. No. 0.027; 5; Indels
Matches 10; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLK 15
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Db 1 YISYSGITRYNPSLK 15

RESULT 6
US-09-424-840B-35
Sequence 35, Application US/09424840B
Patent No. 6790938
GENERAL INFORMATION:
APPLICANT: Berchtold, Peter
APPLICANT: Escher, Robert F. A.
TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
FILE REFERENCE: 100564-09049
CURRENT APPLICATION NUMBER: US/09/424,840B
CURRENT FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: DE 19820663.1
PRIOR FILING DATE: 1998-05-08
PRIOR APPLICATION NUMBER: DE 19755227.7
PRIOR FILING DATE: 1997-12-12
PRIOR APPLICATION NUMBER: DE 19723904.8
PRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 128
SOFTWARE: PatentIn version 3.1
SEQ ID NO 35
LENGTH: 16
TYPE: PRT
ORGANISM: Homo sapiens
US-09-424-840B-35

Query Match 57.3%; Score 51; DB 2; Length 16;
Best Local Similarity 64.3%; Pred. No. 0.084; 3; Indels
Matches 9; Conservative 2; Mismatches 0; Gaps 0;

Qy 2 ISYDGTNNYKPSLK 15
||| | | | | | | | | | | | | | |
Db 2 ISYSGSTKYKPSLR 15

RESULT 7
US-08-672-345C-53
Sequence 53, Application US/08672345C
Patent No. 5948658
GENERAL INFORMATION:
APPLICANT: Landry Donald, W.

TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-672-345C-53

Query Match 55.1%; Score 49; DB 1; Length 16;
Best Local Similarity 60.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLK 15
||| | | | | | | | | | | | | | |
Db 1 YIRYSGITRYNPSLK 15

RESULT 8
US-09-214-095D-53
Sequence 53, Application US/09214095D
Patent No. 6280987
GENERAL INFORMATION:
APPLICANT: Landry, Donald
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REFERENCE: 51400-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/214,095D
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn version 3.0
SEQ ID NO 53
LENGTH: 16
TYPE: PRT
ORGANISM: Murinae gen. sp.
US-09-214-095D-53

Query Match 55.1%; Score 49; DB 2; Length 16;
Best Local Similarity 60.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLK 15
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Db 1 YIRYSGITRYNPSLK 15

RESULT 9
US-09-940-727B-53
Sequence 53, Application US/09940727B

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; Patent No. 6913917
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIORITY APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIORITY APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIORITY APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53
; LENGTH: 16
; TYPE: PRT
; ORGANISM: mouse
; US-09-940-727B-53

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Query Match 55.1%; Score 49; DB 2; Length 16;
Best Local Similarity 60.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 6; Indels

Qy 1 YISYDGTNNYKPSLK 15
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Db 1 VIRYSGITRYNPSLK 15

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RESULT 10
US-09-996-288-25
; Sequence 25, Application US/09996288
; Patent No. 6818216
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Admini
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/9
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-25

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Query Match 53.9%; Score 48; DB 2; Length 16;
Best Local Similarity 60.0%; Pred. No. 0.26;
Matches 9: Conservative 2; Mismatches 4: Indels

Qy 2 ISYDGTNNYKPSLKD 16
 | : | : | : |
Db**** 2 IWWDGKKHYNP SLKD 16

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RESULT 11
US-09-996-387
; Sequence 37, Application US/09996288
; Patent No. 6818216
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Admini
; TITLE OF INVENTION: and treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/9
; CURRENT FILING DATE: 2001-11-28

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; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-37

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Query Match 53.9%; Score 48; DB 2; Length 16;
Best Local Similarity 60.0%; Pred. No. 0.26;
Matches 9; Conservative 2; Mismatches 4; Indels

```
Qy      2 ISYDGTNNYKPSLKD 16
      | : | | : | | | |
Db      2 IWWDGKKDYNPSLKD 16
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RESULT 12
US-09-936-288-41
; Sequence 41, Application US/09996288
; Patent No. 6818216
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Admini
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10371-047-999
; CURRENT APPLICATION NUMBER: US/09/9
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 41
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-936-288-41

```

Query Match 53.9%; Score 48; DB 2; Length 16;
Best Local Similarity 60.0%; Pred. No. 0.26;
Matches 9; Conservative 2; Mismatches 4; Indels

Qy 2 ISYDGTNNYKPSLKD 16
| : | | : | | | | |
pb 2 IWDGKKSYPNPSLKD 16

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RESULT 13
US-09-996-288-103
; Sequence 103, Application US/09996288
; Patent No. 6818216
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Admin
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/99
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 103
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-103

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Query Match 53.9%; Score 48; DB 2; Length 16;
Best Local Similarity 60.0%; Pred. No. 0.26;
Matches 9; Conservative 2; Mismatches 4; Indels

Qy 2 ISYDGTNNYKPSLKD 16

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Db      |.:||.:| |||||
        2 IWDGKKDYNPSLKD 16

RESULT 14
US-09-996-265-25
; Sequence 25, Application US/09996265
; Patent No. 6855493
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-048-999
; CURRENT APPLICATION NUMBER: US/09/996,265
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-265-25

Query Match      53.9%; Score 48; DB 2; Length 16;
Best Local Similarity 60.0%; Pred. NO. 0.26;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2 ISYDGTNNYKPSLKD 16
        |.:||.:| |||||
Db      2 IWDGKKDYNPSLKD 16

RESULT 15
US-09-996-265-37
; Sequence 37, Application US/09996265
; Patent No. 6855493
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-048-999
; CURRENT APPLICATION NUMBER: US/09/996,265
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-265-37

Query Match      53.9%; Score 48; DB 2; Length 16;
Best Local Similarity 60.0%; Pred. NO. 0.26;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2 ISYDGTNNYKPSLKD 16
        |.:||.:| |||||
Db      2 IWDGKKDYNPSLKD 16
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Job time : 32.5 secs

Page 5 of 5

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2005, 14:25:05 ; Search time 110 Seconds

(without alignments)
60.775 Million cell updates/sec

Title: US-10-735-916A-10

Perfect score: 89

Sequence: 1 YISYDGTNNYKPSLKD 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 11256

Minimum DB seq length: 16

Maximum DB seq length: 16

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:

- 1: /cgm2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgm2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgm2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgm2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 5: /cgm2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 6: /cgm2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	89	100.0	16	5	US-10-735-916A-10
2	60	67.4	16	5	US-10-822-306A-26
3	58	65.2	16	5	US-10-822-306A-21
4	58	65.2	16	5	US-10-822-306A-23
5	56	62.9	16	4	US-10-312-316-8
6	56	62.9	16	4	US-10-844-424-110
7	55	61.8	16	4	US-10-844-424-112
8	55	61.8	16	5	US-10-893-576-107
9	54	60.7	16	3	US-09-791-551-89
10	52	58.4	16	3	US-09-791-551-84
11	51	57.3	16	4	US-10-393-701-5
12	51	57.3	16	4	US-10-844-424-35
13	50	56.2	16	4	US-10-173-551-26
14	50	56.2	16	5	US-10-822-306A-19
15	49	55.1	16	3	US-09-940-727B-53
16	49	55.1	16	5	US-10-822-306A-18
17	49	55.1	16	6	US-11-003-731-23
18	48	53.9	16	3	US-09-796-848A-27
19	48	53.9	16	3	US-09-796-848A-28
20	48	53.9	16	3	US-09-796-848A-30
21	48	53.9	16	3	US-09-796-848A-55
22	48	53.9	16	3	US-09-996-288-25
23	48	53.9	16	3	US-09-996-288-37
24	48	53.9	16	3	US-09-996-288-41
25	48	53.9	16	3	US-09-996-288-103
26	48	53.9	16	3	US-09-996-265-25
27	48	53.9	16	3	US-09-996-265-37

28 48 53.9 16 3 US-09-996-265-41 Sequence 41, Appl
29 48 53.9 16 3 US-09-996-265-103 Sequence 103, App
30 48 53.9 16 4 US-10-020-354-25 Sequence 25, Appl
31 48 53.9 16 4 US-10-020-354-37 Sequence 37, Appl
32 48 53.9 16 4 US-10-020-354-41 Sequence 41, Appl
33 48 53.9 16 4 US-10-461-863-25 Sequence 25, Appl
34 48 53.9 16 4 US-10-461-863-37 Sequence 37, Appl
35 48 53.9 16 4 US-10-461-863-41 Sequence 41, Appl
36 48 53.9 16 4 US-10-461-863-103 Sequence 103, App
37 48 53.9 16 4 US-10-312-316-11 Sequence 11, Appl
38 48 53.9 16 4 US-10-751-744-25 Sequence 25, Appl
39 48 53.9 16 4 US-10-751-744-37 Sequence 37, Appl
40 48 53.9 16 4 US-10-751-744-41 Sequence 41, Appl
41 48 53.9 16 5 US-10-900-230-25 Sequence 25, Appl
42 48 53.9 16 5 US-10-900-230-37 Sequence 37, Appl
43 48 53.9 16 5 US-10-900-230-41 Sequence 41, Appl
44 48 53.9 16 5 US-10-900-230-103 Sequence 103, App
45 48 53.9 16 5 US-10-726-332-67 Sequence 67, Appl

ALIGNMENTS

RESULT 1
US-10-735-916A-10
; Sequence 10, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Lilliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LAGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-735-916A-10

Query Match 100.0%; Score 89; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLKD 16
| | | | | | | | | | | | | | | |
Db 1 YISYDGTNNYKPSLKD 16

RESULT 2
US-10-822-306A-26
; Sequence 26, Application US/10822306A
; Publication No. US20050227289A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Reilly, Edward B.
; APPLICANT: Lacy, Susan E.

```
; APPLICANT: Fung, Emma
; APPLICANT: Belk, Jonathan P.
; APPLICANT: Roguska, Michael
; TITLE OF INVENTION: Antibodies To Erythropoietin Receptor
; FILE REFERENCE: 7349USP1
; CURRENT APPLICATION NUMBER: US/10/822,306A
; PRIOR FILING DATE: 2004-04-12
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-822-306A-26

Query Match      67.4%; Score 60; DB 5; Length 16;
Best Local Similarity 66.7%; Pred. No. 0.012;
Matches 10; Conservative 2; Mismatches 3; Indels 3; Gaps 0;

QY 1 YISYDGTNNYKPSLK 15
   |||:|||||
Db 1 YIGYSGSTNNYPSLK 15

RESULT 3
US-10-822-306A-21
; Sequence 21, Application US/10822306A
; Publication No. US2005027289A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Reilly, Edward B.
; APPLICANT: Lacy, Susan E.
; APPLICANT: Fung, Emma
; APPLICANT: Belk, Jonathan P.
; APPLICANT: Roguska, Michael
; TITLE OF INVENTION: Antibodies To Erythropoietin Receptor
; FILE REFERENCE: 7349USP1
; CURRENT APPLICATION NUMBER: US/10/822,306A
; PRIOR FILING DATE: 2004-04-12
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-822-306A-21

Query Match      65.2%; Score 58; DB 5; Length 16;
Best Local Similarity 66.7%; Pred. No. 0.025;
Matches 10; Conservative 1; Mismatches 4; Indels 4; Gaps 0;

QY 1 YISYDGTNNYKPSLK 15
   |||:|||||
Db 1 YIGYSGSTNNYPSLK 15

RESULT 4
US-10-822-306A-23
; Sequence 23, Application US/10822306A
; Publication No. US2005027289A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Reilly, Edward B.
; APPLICANT: Lacy, Susan E.
; APPLICANT: Fung, Emma
; APPLICANT: Belk, Jonathan P.
; APPLICANT: Roguska, Michael
; TITLE OF INVENTION: Antibodies To Erythropoietin Receptor
; FILE REFERENCE: 7349USP1
; CURRENT APPLICATION NUMBER: US/10/822,306A
; PRIOR FILING DATE: 2004-04-12
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-822-306A-23

Query Match      65.2%; Score 58; DB 5; Length 16;
Best Local Similarity 66.7%; Pred. No. 0.025;
Matches 10; Conservative 2; Mismatches 3; Indels 3; Gaps 0;

QY 1 YISYDGTNNYKPSLK 15
   |||:|||||
Db 1 YIGYSGSTNNYPSLK 15

RESULT 5
US-10-312-316-8
; Sequence 8, Application US/10312316
; Publication No. US20040137513A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Hongo, Jo-Anne S.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shelton, David L.
; TITLE OF INVENTION: AGONIST ANTI-TRK-C MONOCLONAL ANTIBODIES
; FILE REFERENCE: GENENT.04QPC
; CURRENT APPLICATION NUMBER: US/10/312,316
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 60/238,319
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-312-316-8

Query Match      62.9%; Score 56; DB 4; Length 16;
Best Local Similarity 66.7%; Pred. No. 0.053;
Matches 10; Conservative 1; Mismatches 4; Indels 4; Gaps 0;

QY 1 YISYDGTNNYKPSLK 15
   |||:|||||
Db 1 YIYSGSTNNYPSLK 15

RESULT 6
US-10-844-424-110
; Sequence 110, Application US/10844424
; Publication No. US20040202859A1
; GENERAL INFORMATION:
; APPLICANT: Berchtold, Peter
; APPLICANT: Escher, Robert F. A.
; TITLE OF INVENTION: ANTI-GPIIb/IIIa RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/10/844,424
; CURRENT FILING DATE: 2004-05-13
; PRIOR APPLICATION NUMBER: US/09/424,840
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: DE 19755227.7
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; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 110
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-844-424-110

Query Match      62.9%; Score 56; DB 4; Length 16;
Best Local Similarity 66.7%; Pred. No. 0.053;
Matches 10; Conservative 1; Mismatches 4; Indels 4; Gaps 0;

Qy 1 YISYDGTNNYKPSLK 15
   |||:|:|:|:|:|:|
Db 1 YIYSGSTNNYKPSLK 15

RESULT 7
US-10-844-424-112
; Sequence 112, Application US/10844424
; Publication No. US20040202659A1
; GENERAL INFORMATION:
; APPLICANT: BERTHOLD, PETER
; TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/10/844,424
; CURRENT FILING DATE: 2004-05-13
; PRIOR APPLICATION NUMBER: US/09/424,840
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: DE 19755227.7
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 112
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-844-424-112

Query Match      61.8%; Score 55; DB 4; Length 16;
Best Local Similarity 66.7%; Pred. No. 0.076;
Matches 10; Conservative 0; Mismatches 5; Indels 5; Gaps 0;

Qy 1 YISYDGTNNYKPSLK 15
   |||:|:|:|:|:|:|
Db 1 YIYSGSTNNYKPSLK 15

RESULT 8
US-10-893-576-107
; Sequence 107, Application US/10893576
; Publication No. US2005011843A1
; GENERAL INFORMATION:
; APPLICANT: BURGESS, TERESA L.
; APPLICANT: COXON, ANGELA
; APPLICANT: GREEN, LARRY L.
; APPLICANT: ZHANG, KE
; TITLE OF INVENTION: SPECIFIC BINDING AGENTS TO HEPATOCYTE GROWTH FACTOR
; FILE REFERENCE: 06843.0051-00000
; CURRENT APPLICATION NUMBER: US/10/893,576
; CURRENT FILING DATE: 2004-07-16
; PRIOR APPLICATION NUMBER: US 60/488,681
; PRIOR FILING DATE: 2003-07-18
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn Ver. 3.2

; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 110
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic heavy chain
; OTHER INFORMATION: variable region CDR peptide
US-10-893-576-107

Query Match      61.8%; Score 55; DB 5; Length 16;
Best Local Similarity 60.0%; Pred. No. 0.076;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLK 15
   |:|:|:|:|:|:|
Db 1 YIYSGSTNNYKPSLK 15

RESULT 9
US-09-791-551-89
; Sequence 89, Application US/09791551
; Publication No. US20030235584A1
; GENERAL INFORMATION:
; APPLICANT: KLOETZER, WILLIAM S.
; APPLICANT: HANNA, NABIL
; TITLE OF INVENTION: METHOD FOR PREPARING ANTI-MIF ANTIBODIES
; FILE REFERENCE: 037003/0277869
; CURRENT APPLICATION NUMBER: US/09/791,551
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/185,390
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/233,625
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 89
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-791-551-89

Query Match      60.7%; Score 54; DB 3; Length 16;
Best Local Similarity 50.0%; Pred. No. 0.11;
Matches 8; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YISYDGTNNYKPSLK 16
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Db 1 YLSYDGSKSHNPRLN 16

RESULT 10
US-09-791-551-84
; Sequence 84, Application US/09791551
; Publication No. US20030235584A1
; GENERAL INFORMATION:
; APPLICANT: KLOETZER, WILLIAM S.
; APPLICANT: HANNA, NABIL
; TITLE OF INVENTION: METHOD FOR PREPARING ANTI-MIF ANTIBODIES
; FILE REFERENCE: 037003/0277869
; CURRENT APPLICATION NUMBER: US/09/791,551
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/185,390
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/233,625
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-791-551-84
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Query Match      58.4%; Score 52; DB 3; Length 16;
Best Local Similarity 60.0%; Pred. No. 0.23;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLK 15
   |||:|||||
Db 1 YISFGSTGYNPSLK 15

RESULT 11
US-10-399-701-5
; Sequence 5, Application US/10399701
; Publication No. US20040022791A1
; GENERAL INFORMATION:
; APPLICANT: ASAT AG
; TITLE OF INVENTION: Rekombinant anti-GPIIB/IIIA-antibodies as agents for
; FILE OF INVENTION: inhibiting angiogenesis
; FILE REFERENCE: 23600PWO DRAS
; CURRENT APPLICATION NUMBER: US/10/399,701
; CURRENT FILING DATE: 2003-04-21
; PRIOR APPLICATION NUMBER: 100 57 443.2
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDR2-region of
; OTHER INFORMATION: an optimized antibody against GPIIB/IIIA
US-10-399-701-5

Query Match      57.3%; Score 51; DB 4; Length 16;
Best Local Similarity 64.3%; Pred. No. 0.34;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 ISYDGTNNYKPSLK 15
   |||:|||||
Db 2 ISYSGSTKYKPSLR 15

RESULT 12
US-10-844-424-35
; Sequence 35, Application US/10844424
; Publication No. US20040202659A1
; GENERAL INFORMATION:
; APPLICANT: Berchtold, Peter
; APPLICANT: Escher, Robert F. A.
; TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/10/844,424
; CURRENT FILING DATE: 2004-05-13
; PRIOR APPLICATION NUMBER: US/09/424,840
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: DE 19755227.7
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-844-424-35

Query Match      57.3%; Score 51; DB 4; Length 16;
Best Local Similarity 64.3%; Pred. No. 0.34;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLK 15
   |||:|||||
Db 1 YISYDGTNNYKPSLR 15

RESULT 13
US-10-173-551-26
; Sequence 26, Application US/10173551
; Publication No. US20030232387A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Chafen
; TITLE OF INVENTION: Antibodies that bind alphaE Integrin
; FILE REFERENCE: 1855.2025-000
; CURRENT APPLICATION NUMBER: US/10/173,551
; CURRENT FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-173-551-26

Query Match      56.2%; Score 50; DB 4; Length 16;
Best Local Similarity 60.0%; Pred. No. 0.49;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLK 15
   |||:|||||
Db 1 HIYSGNTNYPNPSLK 15

RESULT 14
US-10-822-306A-19
; Sequence 19, Application US/10822306A
; Publication No. US20050227289A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Reilly, Edward B.
; APPLICANT: Lacy, Susan E.
; APPLICANT: Fung, Emma
; APPLICANT: Belk, Jonathan P.
; APPLICANT: Roguska, Michael
; TITLE OF INVENTION: Antibodies To Erythropoietin Receptor
; TITLE OF INVENTION: And Uses Thereof
; FILE REFERENCE: 7349USP1
; CURRENT APPLICATION NUMBER: US/10/822,306A
; CURRENT FILING DATE: 2004-04-12
; PRIOR APPLICATION NUMBER: 10/821,497
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-822-306A-19

Query Match      56.2%; Score 50; DB 5; Length 16;
Best Local Similarity 60.0%; Pred. No. 0.49;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLK 15
   |||:|||||
Db 1 YIGGEGSTNYPNPSLK 15

RESULT 15
US-09-940-727B-53
; Sequence 53, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
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; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53
; LENGTH: 16
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-53

Query Match 55.1%; Score 49; DB 3; Length 16;
Best Local Similarity 60.0%; Pred. No. 0.7;
Matches 9; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 YISYDGTNNYKPSLK 15
Db 1 YIRYSGITRYNPSLK 15

Search completed: December 30, 2005, 14:43:48
Job time : 110 secs

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OM protein - protein search, using sw model

Run on: December 30, 2005, 14:25:45 ; Search time 8 Seconds
(without alignments)
14.978 Million cell updates/sec

Title: US-10-735-916A-10

Perfect score: 89

Sequence: 1 YISVDGNNYKPSLKD 16

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Gapop 10.0 , Gapext 0.5.

Searched: 57103 seqs, 7488799 residues

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Minimum DB seq length: 16

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	89	100.0	16 7	US-11-012-353-10
2	45	50.6	16 7	US-11-009-939-24
3	31	34.8	16 7	US-11-054-515-3140
4	29	32.6	16 6	US-10-502-145-33
5	26	29.2	16 7	US-11-054-515-2799
6	25	28.1	16 6	US-10-507-662-5
7	25	28.1	16 7	US-11-054-515-2263
8	25	28.1	16 7	US-11-128-440-61
9	24	27.0	16 7	US-11-125-837-11
10	24	27.0	16 7	US-11-105-708-15
11	23	25.8	16 7	US-11-054-515-2261
12	23	25.8	16 7	US-11-054-515-2266
13	23	25.8	16 7	US-11-054-515-2223
14	22	24.7	16 7	US-11-055-163-20
15	21	23.6	16 6	US-10-503-575-38
16	21	23.6	16 6	US-10-999-866-59
17	21	23.6	16 7	US-11-054-515-2745
18	21	23.6	16 7	US-11-054-515-2792
19	21	23.6	16 7	US-11-054-515-2891
20	21	23.6	16 7	US-11-093-274-6
21	21	23.6	16 7	US-11-021-305-167
22	20	22.5	16 7	US-11-054-515-2221
23	20	22.5	16 7	US-11-054-515-2274
24	20	22.5	16 7	US-11-054-515-2847
25	20	22.5	16 7	US-11-054-515-3004

ALIGNMENTS

RESULT 1

US-11-012-353-10
; Sequence 10, Application US/11012353
; Publication No. US20050249730A1

GENERAL INFORMATION:

APPLICANT: GOETSCH, LILIANE

APPLICANT: CORVAIA, NATHALIE

APPLICANT: DUFIOS, ALAIN

APPLICANT: HAEUW, JEAN-FRANCOIS

APPLICANT: LEGER, OLIVIER

APPLICANT: BECK, ALAIN

TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF

FILE REFERENCE: 01763-198

CURRENT APPLICATION NUMBER: US/11/012,353

CURRENT FILING DATE: 2004-12-16

PRIOR APPLICATION NUMBER: 10/735,916

PRIOR FILING DATE: 2003-12-16

PRIOR APPLICATION NUMBER: FR 0308538

PRIOR FILING DATE: 2003-07-11

PRIOR APPLICATION NUMBER: PCT/FR03/00178

PRIOR FILING DATE: 2003-01-20

PRIOR APPLICATION NUMBER: FR 0205753

PRIOR FILING DATE: 2002-05-07

PRIOR APPLICATION NUMBER: FR 0200653

PRIOR FILING DATE: 2002-01-18

PRIOR APPLICATION NUMBER: FR 0200654

PRIOR FILING DATE: 2002-01-18

NUMBER OF SEQ ID NOS: 162

SOFTWARE: PatentIn Ver. 3.3

SEQ ID NO 10

LENGTH: 16

TYPE: PRT

ORGANISM: Mus musculus

US-11-012-353-10

Query Match 100.0%; Score 89; DB 7; Length 16;

Best Local Similarity 100.0%; Pred. No. 2.3e-09;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YISVDGNNYKPSLKD 16

Db 1 YISVDGNNYKPSLKD 16

RESULT 2

US-11-009-939-24

; Sequence 24, Application US/11009939

Sequence 2307, Ap
Sequence 2153, Ap
Sequence 2157, Ap
Sequence 2780, Ap
Sequence 2783, Ap
Sequence 3090, Ap
Sequence 183, Appli
Sequence 6, Appli
Sequence 453, Appl
Sequence 33, Appl
Sequence 2137, Ap
Sequence 2143, Ap
Sequence 2145, Ap
Sequence 2214, Ap
Sequence 2215, Ap
Sequence 2216, Ap
Sequence 2217, Ap
Sequence 2218, Ap
Sequence 2219, Ap
Sequence 2220, Ap

16 7 US-11-054-515-2307
16 7 US-11-054-515-2153
16 7 US-11-054-515-2157
16 7 US-11-054-515-2780
16 7 US-11-054-515-2783
16 7 US-11-054-515-3090
16 7 US-11-116-144-183
16 6 US-10-507-662-6
16 6 US-10-623-155-453
16 7 US-11-089-764-33
16 7 US-11-054-515-2137
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16 7 US-11-054-515-2219
16 7 US-11-054-515-2220

26 19.5 21.9
27 19 21.3
28 19 21.3
29 19 21.3
30 19 21.3
31 19 21.3
32 19 21.3
33 18 20.2
34 18 20.2
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; Publication No. US20050265998A1
; GENERAL INFORMATION:
; APPLICANT: Elson, Greg Christopher Andrew
; TITLE OF INVENTION: Neutralizing Antibodies and Methods of Use Thereof
; FILE REFERENCE: 23135-402
; CURRENT APPLICATION NUMBER: US/11/009,939
; CURRENT FILING DATE: 2005-12-10
; PRIOR APPLICATION NUMBER: 60/528,811
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 60/528,812
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 60/528,962
; PRIOR FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-009-939-24

Query Match      50.6%; Score 45; DB 7; Length 16;
Best Local Similarity 53.3%; Pred. No. 0.053;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 YISYDGTNNYKPSLK 15
   |||||:|
Db 1 YIHSGVTDNFPSLK 15

RESULT 3
US-11-054-515-3140
; Sequence 3140, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3140
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-3140

Query Match      34.8%; Score 31; DB 7; Length 16;
Best Local Similarity 44.4%; Pred. No. 12;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 ISYDGTNNY 10
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Db      ::|||:|
      4 LNYDGDY 12

RESULT 4
US-10-502-145-33
; Sequence 33, Application US/10502145
; Publication No. US20050244406A1
; GENERAL INFORMATION:
; APPLICANT: MACKAY, CHARLES REAY
; TITLE OF INVENTION: Anti-C5aR antibodies and uses thereof
; FILE REFERENCE: RICE-032
; CURRENT APPLICATION NUMBER: US/10/502,145
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: USN 60/350,961
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-502-145-33

Query Match      32.6%; Score 29; DB 6; Length 16;
Best Local Similarity 50.0%; Pred. No. 25;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 GTNNYKPSLK 15
   |||||:|
Db 6 GSTNTNSALK 15

RESULT 5
US-11-054-515-2799
; Sequence 2799, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2799
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2799

Query Match      29.2%; Score 26; DB 7; Length 16;
Best Local Similarity 41.7%; Pred. No. 80;
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Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ISYDGTNNYKPS 13
: || ||
Db 1 LDYDILGYTPS 12

RESULT 6

US-10-507-662-5
; Sequence 5, Application US/10507662
; Publication No. US20050255102A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN INC.
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; TITLE OF INVENTION: ANTI-ALPHA-V BETA-6 ANTIBODIES
; FILE REFERENCE: A136PCT
; CURRENT APPLICATION NUMBER: US/10/507,662
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: 60/364,991
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/426,286
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-507-662-5

Query Match 28.1%; Score 25; DB 6; Length 16;
Best Local Similarity 42.9%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ISYDGTNNYKPSLK 15
: || ||:
Db 2 ISSGGSTYYPDSVK 15

RESULT 7

US-11-054-515-2263
; Sequence 2263, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2263
; LENGTH: 16

; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2263

Query Match 28.1%; Score 25; DB 7; Length 16;
Best Local Similarity 45.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 4 YDGTNNYKPSL 14
: || ||:
Db 3 YDTLTSYVPLL 13

RESULT 8

US-11-128-440-61
; Sequence 61, Application US/11128440
; Publication No. US20050261478A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha
; APPLICANT: Brady, William A.
; APPLICANT: Grosmaire, Laura S.
; APPLICANT: Law, Che-Leung
; APPLICANT: Dua, Raj
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATING
; TITLE OF INVENTION: LYMPHOCYTE ACTIVATION
; FILE REFERENCE: 980034.408D1
; CURRENT APPLICATION NUMBER: US/11/128,440
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/646,381
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US 09/252,150
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/108,683
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 60/075,274
; PRIOR FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 61
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-128-440-61

Query Match 28.1%; Score 25; DB 7; Length 16;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YISYDG 6
: || ||
Db 6 YYDYDG 11

RESULT 9

US-11-125-837-11
; Sequence 11, Application US/11125837
; Publication No. US20050266003A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Rong-Hwa
; APPLICANT: Chang, Chung Nan
; APPLICANT: Chen, Pei-Jiun
; APPLICANT: Huang, Chiu-Chen
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 13062-011001
; CURRENT APPLICATION NUMBER: US/11/125,837
; CURRENT FILING DATE: 2005-05-10
; PRIOR APPLICATION NUMBER: US 60/569,892
; PRIOR FILING DATE: 2004-05-10
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 16

```
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-125-837-11

Query Match      27.0%; Score 24; DB 7; Length 16;
Best Local Similarity 40.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 6 GTNNYKPSLK 15
   | : | | |
Db 6 GGTSYNPKFK 15

RESULT 10
US-11-105-708-15
; Sequence 15, Application US/11105708
; Publication No. US20050281821A1
; GENERAL INFORMATION:
; APPLICANT: Pernaesetti, Flavia
; APPLICANT: Freimark, Bruce
; APPLICANT: Van Epps, Dennis
; APPLICANT: Brooks, Peter C
; TITLE OF INVENTION: Method and Composition for Angiogenesis Inhibition
; FILE REFERENCE: 30797-704.501
; CURRENT APPLICATION NUMBER: US/11/105,708
; CURRENT FILING DATE: 2005-04-13
; PRIOR APPLICATION NUMBER: 09/478,977
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: 60/152,496
; PRIOR FILING DATE: 1999-09-02
; PRIOR APPLICATION NUMBER: 60/143,534
; PRIOR FILING DATE: 1999-09-02
; PRIOR APPLICATION NUMBER: 60/114,878
; PRIOR FILING DATE: 1999-01-06
; PRIOR APPLICATION NUMBER: 60/114,877
; PRIOR FILING DATE: 1999-01-06
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-105-708-15

Query Match      27.0%; Score 24; DB 7; Length 16;
Best Local Similarity 42.9%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 2 ISYDGTNNYKPSLK 15
   | : | | |
Db 2 IWDDNKYTNPSLK 15

RESULT 11
US-11-054-515-2261
; Sequence 2261, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16

; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2266

Query Match      25.8%; Score 23; DB 7; Length 16;
Best Local Similarity 44.4%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 YDGTNNYKP 12
   | | | : |
Db 3 YDTLTSYVP 11

RESULT 12
US-11-054-515-2266
; Sequence 2266, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2266
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2266

Query Match      25.8%; Score 23; DB 7; Length 16;
Best Local Similarity 44.4%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 YDGTNNYKP 12
   | | | : |
Db 3 YDTLTSYVP 11
```


Db 3 YDTILTSYVP 11

RESULT 13

US-11-054-515-2323
; Sequence 2323, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 03/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2323
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2323

Query Match 25.8%; Score 23; DB 7; Length 16;
Best Local Similarity 57.1%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 YDGTNNY 10
|||
Db 3 YDTILTY 9

RESULT 14

US-11-055-163-20
; Sequence 20, Application US/11055163
; Publication No. US20050271655A1
; GENERAL INFORMATION:
; APPLICANT: LEE, DANIEL H. S.
; APPLICANT: PEPINSKY, R. BLAKE
; APPLICANT: LI, WEIWEI
; APPLICANT: RABACCHI, SYLVIA A.
; APPLICANT: RELTON, JANE K.
; APPLICANT: WORLEY, DANE S.
; APPLICANT: STRITTMATTER, STEPHEN M.
; APPLICANT: SAH, DINAH Y.W.
; TITLE OF INVENTION: NOGO RECEPTOR ANTAGONISTS
; FILE REFERENCE: A170 CON (00455.271)
; CURRENT APPLICATION NUMBER: US/11/055,163
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: PCT/US03/25004
; PRIOR FILING DATE: 2003-08-07
; PRIOR APPLICATION NUMBER: 60/402,866
; PRIOR FILING DATE: 2002-08-10
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin ver. 2.1

; SEQ ID NO 20
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: heavy chain peptide sequence
US-11-055-163-20

Query Match 24.7%; Score 22; DB 7; Length 16;
Best Local Similarity 55.8%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 7 TNNYKPSLK 15
| | | | |
Db 7 TKYYSLSLK 15

RESULT 15

US-10-503-575-38
; Sequence 38, Application US/10503575
; Publication No. US20050244823A1
; GENERAL INFORMATION:
; APPLICANT: Drijfhout, Jan Wouter
; APPLICANT: van Veelen, Petrus Antonius
; APPLICANT: Koning, Frits
; TITLE OF INVENTION: NOVEL EPITOPES FOR CELIAC DISEASE AND AUTOIMMUNE DISEASES, METHODS
; FILE REFERENCE: 2799/72843-PCT-US
; CURRENT APPLICATION NUMBER: US/10/503,575
; CURRENT FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: PCT/NL03/00077
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: EP 02075456.0
; PRIOR FILING DATE: 2002-02-04
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 38
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-503-575-38

Query Match 23.6%; Score 21; DB 6; Length 16;
Best Local Similarity 37.5%; Pred. No. 5.5e+02;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GTNNYKPS 13
| | | | |
Db 3 GQGSFQPS 10

Search completed: December 30, 2005, 14:44:10
Job time : 8 secs

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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:02:01 ; Search time 71.0968 Seconds
(without alignments)
49.440 Million cell updates/sec

Title: US-10-735-916A-12
Perfect score: 47
Sequence: 1 YGRVFFDY 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 21:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	8	7 ADJ76846	Adj76846 CDR seque
2	47	100.0	8	9 ADZ67016	Adz67016 Murine in
3	47	100.0	117	7 ADJ76903	Adj76903 Anti-IGF-
4	47	100.0	117	7 ADJ76909	Adj76909 Anti-IGF-
5	47	100.0	117	7 ADJ76917	Adj76917 Anti-IGF-
6	47	100.0	117	7 ADJ76913	Adj76913 Anti-IGF-
7	47	100.0	117	9 ADZ67083	Adz67083 Human ant
8	47	100.0	117	9 ADZ67087	Adz67087 Human ant
9	47	100.0	117	9 ADZ67073	Adz67073 Murine im
10	47	100.0	117	9 ADZ67079	Adz67079 Human ant
11	47	100.0	127	7 ADJ76886	Adj76886 Anti-IGF-
12	47	100.0	127	9 ADZ67056	Adz67056 Murine im
13	47	100.0	135	7 ADJ76911	Adj76911 Anti-IGF-
14	47	100.0	135	7 ADJ76919	Adj76919 Anti-IGF-
15	47	100.0	135	7 ADJ76915	Adj76915 Anti-IGF-
16	47	100.0	135	9 ADZ67089	Adz67089 Human ant
17	47	100.0	135	9 ADZ67081	Adz67081 Human ant
18	47	100.0	135	9 ADZ67085	Adz67085 Human ant
19	38	80.9	138	7 AB071408	Ab071408 Pseudomon
20	37	78.7	221	6 ABM70706	Abm70706 Photorhab
21	37	78.7	2920	8 ADG65227	Adg65227 Mcf1 sequ
22	36	76.6	410	3 AAY68969	Aay68969 Cps2T whi
23	35	74.5	233	7 ADH86117	Adh86117 Enterococ
24	35	74.5	390	7 AB084316	Ab084316 Pseudomon

25	35	74.5	395	5	ABB54242	Abb54242 Lactococc
26	35	74.5	1425	4	ABB71908	Abb71908 Drosophil
27	34	72.3	12	2	AAW62012	Aaw62012 Heavy cha
28	34	72.3	12	3	AAW82339	Aay82339 Humanise
29	34	72.3	12	8	ADG39000	Adg39000 Humanise
30	34	72.3	17	2	AAW73928	Aar73928 B.catarrh
31	34	72.3	26	2	AAW73925	Aar73925 B.catarrh
32	34	72.3	71	2	AAW73923	Aar73923 B.catarrh
33	34	72.3	116	2	AAW29452	Aay29452 Human IGG
34	34	72.3	116	3	AAW77755	Aay77755 Human IGG
35	34	72.3	116	3	AAW30312	Ab30312 Human IGG
36	34	72.3	116	6	ABU13789	Abu13789 Human IGG
37	34	72.3	116	6	ABU59502	Abu59502 Human IGG
38	34	72.3	116	7	AAE39085	Aae39085 Human IGG
39	34	72.3	121	2	AAW62013	Aaw62013 Heavy cha
40	34	72.3	121	2	AAW62019	Aaw62019 Rhesusise
41	34	72.3	121	2	AAW63542	Aaw63542 Murine MH
42	34	72.3	121	2	AAW63531	Aaw63531 Murine MH
43	34	72.3	121	2	AAW63532	Aaw63532 Humanise
44	34	72.3	121	3	AAW82348	Aay82348 Rhesusise
45	34	72.3	121	3	AAW82336	Aay82336 Humanise

ALIGNMENTS

RESULT 1
ADJ76846
ID ADJ76846 standard; peptide; 8 AA.
XX
AC ADJ76846;
XX
DT 06-MAY-2004 (first entry)
XX
DE CDR sequence for anti-IGF-1R antibody.
XX
KW cytotstatic; antipsoriatic; antibody;
KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;
KW or epidermal growth factor receptor; EGFR; signal transduction pathway;
KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;
KW CDR.
XX
OS Mus musculus.
XX
EN WO2003059951-A2.
XX
PD 24-JUL-2003.
XX
PF 20-JAN-2003; 2003WO-FR000178.
XX
FR 18-JAN-2002; 2002FR-00000653.
FR 18-JAN-2002; 2002FR-00000854.
FR 07-MAY-2002; 2002FR-00005753.
XX
PA (FABR) FABRE MEDICAMENT SA PIERRE.
XX
FI Goetsch L, Corvaia N, Leger O;
XX WPI; 2003-569653/53.
XX N-PSDB; ADJ76845.
XX
PT New antibodies that bind to human insulin-like growth factor receptor,
XX useful for treatment, prevention and diagnosis of cancers.
XX
PS Claim 1; SEQ ID NO 12; 164pp; French.
XX
CC The invention relates to an isolated antibody (Ab), and its functional
CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-
CC IR) and optionally: (i) inhibit natural binding of insulin-like growth
CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine
CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or
CC treat diseases associated with overexpression and/or abnormal activity of
CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with

CC hyperactivity of signal transduction pathways mediated by interaction of
 CC these receptors with their ligands. Especially they inhibit
 CC transformation of normal cells to tumor cells, inhibit growth and/or
 CC proliferation of tumor cells, so are useful against cancers of the
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused
 CC by abnormal expression of IGF-IR and/or EGFR. This sequence represents an
 CC CDR sequence used to generate the Ab of the invention.
 XX
 SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 7; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2e+06; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0;

QY 1 YGRVFFDY 8
 |||||
 Db 1 YGRVFFDY 8

RESULT 2
 ADZ67016
 ID ADZ67016 standard; peptide; 8 AA.
 XX
 AC ADZ67016;
 XX
 DT 30-JUN-2005 (first entry)
 XX
 DE Murine insulin-like growth factor T receptor IGF-IR CDR SEQ ID NO:12.
 XX
 KW Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
 KW neoplasia; prostate tumor; andrology; genitourinary disease; osteosarcoma;
 KW musculoskeletal disease; respiratory disease; lung tumor;
 KW endocrine disease; gynecology and obstetrics; breast tumor;
 KW endometrial carcinoma; gastrointestinal disease; colon tumor;
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder.
 XX
 OS Mus musculus.
 XX
 PN US2005084906-A1.
 XX
 PD 21-APR-2005.
 XX
 PF 16-DEC-2003; 2003US-00735916.
 XX
 PR 18-JAN-2002; 2002FR-00000653.
 PR 18-JAN-2002; 2002FR-00000654.
 PR 07-MAY-2002; 2002FR-00005753.
 PR 20-JAN-2003; 2003WO-FR000178.
 PR 11-JUL-2003; 2003FR-00008538.
 XX
 PA (GOET/) GOETSCH L.
 PA (CORV/) CORVAIA N.
 PA (LEGE/) LEGER O.
 PA (DUFEL/) DUFLOS A.
 PA (HAEU/) HAEUW J.
 PA (BECK/) BECK A.
 XX
 PI Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;
 XX
 DR WPI; 2005-321968/33.
 DR N-PSDB; ADZ67015.
 XX
 XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)
 PT antibody or its functional fragment, being capable of binding human IGF-
 PT IR and specifically inhibiting tyrosine kinase activity of receptor,
 PT useful for treating cancer.
 XX
 PS Claim 1; SEQ ID NO 12; 125pp; English.
 XX
 PS The invention relates to a novel isolated anti-insulin-like growth factor
 CC I receptor (IGF-IR) antibody (I) or its functional fragment, being
 CC capable of binding to human IGF-IR and, if necessary, capable of

CC specifically inhibiting tyrosine kinase activity of the receptor,
 CC comprising a light or heavy chain having at least one complementary
 CC determining region (CDR) consisting of one of two fully defined 16 amino
 CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in
 CC the preparation of a medicament intended for the prevention or treatment
 CC of an illness connected with an overexpression and/or an abnormal
 CC activation of the IGF-IR and/or EGFR, and/or connected with a
 CC hyperactivation of the transduction pathway of the signal mediated by the
 CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where
 CC the administration of the medicament does not induce or only slightly
 CC induces secondary effects connected with inhibition of the insulin
 CC receptor. The antibody is useful for preparation of a medicament intended
 CC to inhibit the transformation of normal cells into cells with tumoral
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is
 CC useful for preparation of a medicament intended to inhibit the growth
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a
 CC medicament intended for prevention or for the treatment of cancer, where
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the
 CC preparation of a medicament intended for the prevention or for the
 CC treatment of psoriasis. (I) is useful in preparation of a medicament
 CC intended for the specific targeting of a biologically active compound to
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)
 CC is useful for in vitro diagnosis of illnesses induced by an
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor
 CC starting from a biological sample in which the abnormal presence, of IGF-
 CC IR and/or EGFR receptor is suspected, which involves contacting the
 CC biological sample with (I), which is optionally labeled. The present
 CC sequence is used in the exemplification of the invention.
 XX
 SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 9; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2e+06; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0;

QY 1 YGRVFFDY 8
 |||||
 Db 1 YGRVFFDY 8

RESULT 3
 ADJ76903

ID ADJ76903 standard; protein; 117 AA.

XX
 AC ADJ76903;

XX
 DT 06-MAY-2004 (first entry)

XX
 DE Anti-IGF-IR related protein #16.

XX
 KW cytostatic; antipsoriatic; antibody;
 KW insulin-like growth factor-1 receptor; IGF-IR; tyrosine kinase activity;
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;
 KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;
 KW CDR.

XX
 OS Homo sapiens.

XX
 PN WO2003059951-A2.

XX
 PD 24-JUL-2003.

XX
 PF 20-JAN-2003; 2003WO-FR000178.

XX
 PR 18-JAN-2002; 2002FR-00000653.

XX
 PR 18-JAN-2002; 2002FR-00000654.

XX
 PR 07-MAY-2002; 2002FR-00005753.

XX
 PA (FABR) FABRE MEDICAMENT SA PIERRE.

XX PI Goetsch L, Corvaia N, Leger O;
XX DR WPI; 2003-569653/53.
XX PT New antibodies that bind to human insulin-like growth factor receptor,
XX PT useful for treatment, prevention and diagnosis of cancers.
XX PS Disclosure; SEQ ID NO 69; 164pp; French.
XX CC The invention relates to an isolated antibody (Ab), and its functional
XX CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-
XX CC 1R) and optionally: (i) inhibit natural binding of insulin-like growth
XX CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine
XX CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or
XX CC treat diseases associated with overexpression and/or abnormal activity of
XX CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with
XX CC hyperactivity of signal transduction pathways mediated by interaction of
XX CC these receptors with their ligands. Especially they inhibit
XX CC transformation of normal cells to tumor cells, inhibit growth and/or
XX CC proliferation of tumor cells, so are useful against cancers of the
XX CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
XX CC also for treating psoriasis. Ab are also used to diagnose diseases caused
XX CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a
XX CC protein sequence used to generate the Ab of the invention.
XX SQ Sequence 117 AA;
Query Match 100.0%; Score 47; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YGRVFFDY 8
Db 99 YGRVFFDY 106
RESULT 4
ADJ76909
ID ADJ76909 standard; protein; 117 AA.
XX AC ADJ76909;
XX DT 06-MAY-2004 (first entry)
XX DE Anti-IGF-1R related protein #22.
XX KW cytostatic; antipsoriatic; antibody;
XX KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;
XX KW or epidermal growth factor receptor; EGFR; signal transduction pathway;
XX KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;
XX KW CDR.
XX OS Homo sapiens.
XX PN WO2003059951-A2.
XX PD 24-JUL-2003.
XX PF 20-JAN-2003; 2003WO-FR000178.
XX PR 18-JAN-2002; 2002FR-00000653.
XX PR 18-JAN-2002; 2002FR-00000654.
XX PR 07-MAY-2002; 2002FR-00005753.
XX PA (FABR) FABRE MEDICAMENT SA PIERRE.
XX PI Goetsch L, Corvaia N, Leger O;
XX DR WPI; 2003-569653/53.
XX PT New antibodies that bind to human insulin-like growth factor receptor,
XX PT useful for treatment, prevention and diagnosis of cancers.

XX PS Disclosure; SEQ ID NO 75; 164pp; French.
XX CC The invention relates to an isolated antibody (Ab), and its functional
XX CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-
XX CC 1R) and optionally: (i) inhibit natural binding of insulin-like growth
XX CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine
XX CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or
XX CC treat diseases associated with overexpression and/or abnormal activity of
XX CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with
XX CC hyperactivity of signal transduction pathways mediated by interaction of
XX CC these receptors with their ligands. Especially they inhibit
XX CC transformation of normal cells to tumor cells, inhibit growth and/or
XX CC proliferation of tumor cells, so are useful against cancers of the
XX CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
XX CC also for treating psoriasis. Ab are also used to diagnose diseases caused
XX CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a
XX CC protein sequence used to generate the Ab of the invention.
XX SQ Sequence 117 AA;
Query Match 100.0%; Score 47; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YGRVFFDY 8
Db 99 YGRVFFDY 106
RESULT 5
ADJ76917
ID ADJ76917 standard; protein; 117 AA.
XX AC ADJ76917;
XX DT 06-MAY-2004 (first entry)
XX DE Anti-IGF-1R related protein #26.
XX KW cytostatic; antipsoriatic; antibody;
XX KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;
XX KW or epidermal growth factor receptor; EGFR; signal transduction pathway;
XX KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;
XX KW CDR.
XX OS Homo sapiens.
XX PN WO2003059951-A2.
XX PD 24-JUL-2003.
XX PF 20-JAN-2003; 2003WO-FR000178.
XX PR 18-JAN-2002; 2002FR-00000653.
XX PR 18-JAN-2002; 2002FR-00000654.
XX PR 07-MAY-2002; 2002FR-00005753.
XX PA (FABR) FABRE MEDICAMENT SA PIERRE.
XX PI Goetsch L, Corvaia N, Leger O;
XX DR WPI; 2003-569653/53.
XX PT New antibodies that bind to human insulin-like growth factor receptor,
XX PT useful for treatment, prevention and diagnosis of cancers.
XX PS Disclosure; SEQ ID NO 83; 164pp; French.
XX CC The invention relates to an isolated antibody (Ab), and its functional
XX CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-
XX CC 1R) and optionally: (i) inhibit natural binding of insulin-like growth
XX CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine

CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or
 CC treat diseases associated with overexpression and/or abnormal activity of
 CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with
 CC hyperactivity of signal transduction pathways mediated by interaction of
 CC these receptors with their ligands. Especially they inhibit
 CC transformation of normal cells to tumor cells, inhibit growth and/or
 CC proliferation of tumor cells, so are useful against cancers of the
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a
 CC protein sequence used to generate the Ab of the invention.
 XX
 SQ Sequence 117 AA;

Query Match 100.0%; Score 47; DB 7; Length 117;
 Best Local Similarity 100.0%; Pred. No. 0.9;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8
 Db 99 YGRVFFDY 106
 |||||

RESULT 6
 ADJ76913
 ID ADJ76913 standard; protein; 117 AA.

XX AC ADJ76913;
 XX DT 06-MAY-2004 (first entry)
 XX DE Anti-IGF-1R related protein #24.
 XX KW cytostatic; antipsoriatic; antibody;
 KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;
 KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;
 KW CDR.
 XX OS Homo sapiens.

XX PN WO2003059951-A2.
 XX PD 24-JUL-2003.

XX PF 20-JAN-2003; 2003WO-FR000178.

XX PR 18-JAN-2002; 2002FR-0000653.

XX PR 18-JAN-2002; 2002FR-0000654.

XX PR 07-MAY-2002; 2002FR-00005753.

XX PA (FABR) FABRE MEDICAMENT SA PIERRE.

XX PI Goetsch L, Corvaia N, Leger O;

XX DR WPI; 2003-569653/53.

XX PT New antibodies that bind to human insulin-like growth factor receptor,
 XX useful for treatment, prevention and diagnosis of cancers.

XX PS Disclosure; SEQ ID NO 79; 164pp; French.

XX The invention relates to an isolated antibody (Ab), and its functional
 CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-
 CC 1R) and optionally; (i) inhibit natural binding of insulin-like growth
 CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine
 CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or
 CC treat diseases associated with overexpression and/or abnormal activity of
 CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with
 CC hyperactivity of signal transduction pathways mediated by interaction of
 CC these receptors with their ligands. Especially they inhibit
 CC transformation of normal cells to tumor cells, inhibit growth and/or
 CC proliferation of tumor cells, so are useful against cancers of the

CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a
 CC protein sequence used to generate the Ab of the invention.
 XX
 SQ Sequence 117 AA;

Query Match 100.0%; Score 47; DB 7; Length 117;
 Best Local Similarity 100.0%; Pred. No. 0.9;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8
 Db 99 YGRVFFDY 106
 |||||

RESULT 7
 ADZ67083
 ID ADZ67083 standard; protein; 117 AA.

XX AC ADZ67083;
 XX DT 30-JUN-2005 (first entry)

XX DE Human antibody 7C10 2 heavy chain variable region SEQ ID NO:79.
 XX KW Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
 KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;
 KW musculoskeletal disease; respiratory disease; lung tumor;
 KW endocrine disease; gynecology and obstetrics; breast tumor;
 KW endometroid carcinoma; gastrointestinal disease; colon tumor;
 KW antipsoriatic; psoriasis; dermatological disease; immune disorder;
 KW heavy chain variable region.

XX OS Homo sapiens.

XX PN US2005084906-A1.

XX PD 21-APR-2005.

XX PF 16-DEC-2003; 2003US-00735916.

XX PR 18-JAN-2002; 2002FR-0000653.

XX PR 18-JAN-2002; 2002FR-0000654.

XX PR 07-MAY-2002; 2002FR-00005753.

XX PR 20-JAN-2003; 2003WO-FR000178.

XX PR 11-JUL-2003; 2003FR-00008538.

XX PA (GOET/) GOETSCH L.

XX PA (CORV/) CORVAIA N.

XX PA (LEGE/) LEGER O.

XX PA (DUFL/) DUFLOS A.

XX PA (HAEU/) HAEUW J.

XX PA (BECK/) BECK A.

XX PI Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;

XX DR WPI; 2005-321968/33.

XX PT Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)
 XX antibody or its functional fragment, being capable of binding human IGF-
 XX IR and specifically inhibiting tyrosine kinase activity of receptor,
 XX useful for treating cancer.

XX PS Example 13; SEQ ID NO 79; 125pp; English.

XX The invention relates to a novel isolated anti-insulin-like growth factor
 CC I receptor (IGF-IR) antibody (I) or its functional fragment, being
 CC capable of binding to human IGF-IR and, if necessary, capable of
 CC specifically inhibiting tyrosine kinase activity of the receptor,
 CC comprising a light or heavy chain having at least one complementary
 CC determining region (CDR) consisting of one of two fully defined 16 amino
 CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in

CC the preparation of a medicament intended for the prevention or treatment
 CC of an illness connected with an overexpression and/or an abnormal
 CC activation of the IGF-IR and/or EGFR, and/or connected with a
 CC hyperactivation of the transduction pathway of the signal mediated by the
 CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where
 CC the administration of the medicament does not induce or only slightly
 CC induces secondary effects connected with inhibition of the insulin
 CC receptor. The antibody is useful for preparation of a medicament intended
 CC to inhibit the transformation of normal cells into cells with tumoral
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is
 CC useful for preparation of a medicament intended to inhibit the growth
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a
 CC medicament intended for prevention or for the treatment of cancer, where
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the
 CC preparation of a medicament intended for the prevention or for the
 CC treatment of psoriasis. (I) is useful in preparation of a medicament
 CC intended for the specific targeting of a biologically active compound to
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)
 CC is useful for in vitro diagnosis of illnesses induced by an
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor
 CC starting from a biological sample in which the abnormal presence, of IGF-
 CC IR and/or EGFR receptor is suspected, which involves contacting the
 CC biological sample with (I), which is optionally labeled. The present
 CC sequence is used in the exemplification of the invention.

XX SQ Sequence 117 AA;

Query Match 100.0%; Score 47; DB 9; Length 117;
 Best Local Similarity 100.0%; Pred. No. 0.9;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8
 DB 99 YGRVFFDY 106

RESULT 8
 ADZ67087
 ID ADZ67087 standard; protein; 117 AA.

XX AC ADZ67087;

XX DT 30-JUN-2005 (first entry)

XX DE Human antibody 7C10 3 heavy chain variable region SEQ ID NO:83.

XX DE Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
 KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;
 KW musculoskeletal disease; respiratory disease; lung tumor;
 KW endocrine disease; gynecology and obstetrics; breast tumor;
 KW endometrial carcinoma; gastrointestinal disease; colon tumor;
 KW antiproliferative; psoriasis; dermatological disease; immune disorder;
 KW heavy chain variable region.

XX OS Homo sapiens.

XX FN US2005084906-A1.

XX FN 21-APR-2005.

XX PF 16-DEC-2003; 2003US-00735916.

XX PF 18-JAN-2002; 2002FR-00000653.

XX PF 18-JAN-2002; 2002FR-00000654.

XX PF 07-MAY-2002; 2002FR-00005753.

XX PF 20-JAN-2003; 2003WO-FR000178.

XX PF 11-JUL-2003; 2003FR-00008538.

XX PF (GOETSC) GOETSCHE L.

PA (CORV/) CORVAIA N.
 PA (LEGE/) LEGER O.
 PA (DUFIL/) DUFLOS A.
 PA (HAEU/) HAEUW J.
 PA (BECK/) BECK A.

XX PI Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;

XX PI WPI, 2005-321968/33.

XX PT Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)
 PT antibody or its functional fragment, being capable of binding human IGF-
 PT IR and specifically inhibiting tyrosine kinase activity of receptor,
 PT useful for treating cancer.

XX PS Example 13; SEQ ID NO 83; 125pp; English.

XX CC The invention relates to a novel isolated anti-insulin-like growth factor
 CC I receptor (IGF-IR) antibody (I) or its functional fragment, being
 CC capable of binding to human IGF-IR and, if necessary, capable of
 CC specifically inhibiting tyrosine kinase activity of the receptor,
 CC comprising a light or heavy chain having at least one complementary
 CC determining region (CDR) consisting of one of two fully defined 16 amino
 CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in
 CC the preparation of a medicament intended for the prevention or treatment
 CC of an illness connected with an overexpression and/or an abnormal
 CC activation of the IGF-IR and/or EGFR, and/or connected with a
 CC hyperactivation of the transduction pathway of the signal mediated by the
 CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where
 CC the administration of the medicament does not induce or only slightly
 CC induces secondary effects connected with inhibition of the insulin
 CC receptor. The antibody is useful for preparation of a medicament intended
 CC to inhibit the transformation of normal cells into cells with tumoral
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is
 CC useful for preparation of a medicament intended to inhibit the growth
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a
 CC medicament intended for prevention or for the treatment of cancer, where
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the
 CC preparation of a medicament intended for the prevention or for the
 CC treatment of psoriasis. (I) is useful in preparation of a medicament
 CC intended for the specific targeting of a biologically active compound to
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)
 CC is useful for in vitro diagnosis of illnesses induced by an
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor
 CC starting from a biological sample in which the abnormal presence, of IGF-
 CC IR and/or EGFR receptor is suspected, which involves contacting the
 CC biological sample with (I), which is optionally labeled. The present
 CC sequence is used in the exemplification of the invention.

XX SQ Sequence 117 AA;

Query Match 100.0%; Score 47; DB 9; Length 117;
 Best Local Similarity 100.0%; Pred. No. 0.9;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8
 DB 99 YGRVFFDY 106

RESULT 9

ADZ67073

ID ADZ67073 standard; protein; 117 AA.

XX AC ADZ67073;

XX DT 30-JUN-2005 (first entry)

XX DE Murine immunoglobulin heavy chain variable region 7C10 VH SEQ ID NO:69.

XX Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;
KW musculoskeletal disease; respiratory disease; lung tumor;
KW endocrine disease; gynecology and obstetrics; breast tumor;
KW endometrial carcinoma; gastrointestinal disease; colon tumor;
KW antipsoriatic; psoriasis; dermatological disease; immune disorder;
KW immunoglobulin; heavy chain variable region.
XX Mus musculus.
XX US2005084906-A1.
XX 21-APR-2005.
XX 16-DEC-2003; 2003US-00735916.
XX 18-JAN-2002; 2002FR-00000653.
XX 18-JAN-2002; 2002FR-00000654.
XX 07-MAY-2002; 2002FR-00005753.
XX 20-JAN-2003; 2003WO-FR000178.
XX 11-JUL-2003; 2003FR-00008538.
XX (GOET/) GOETSCH L.
XX (CORV/) CORVAIA N.
XX (LEGE/) LEGER O.
XX (DUFU/) DUFLOS A.
XX (HAEU/) HAEUW J.
XX (BECK/) BECK A.
XX Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;
XX WPI; 2005-321968/33.
XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)
XX antibody or its functional fragment, being capable of binding human IGF-
XX IR and specifically inhibiting tyrosine kinase activity of receptor,
XX useful for treating cancer.
XX Example 13; SEQ ID NO 69; 125pp; English.
XX The invention relates to a novel isolated anti-insulin-like growth factor
XX I receptor (IGF-IR) antibody (I) or its functional fragment, being
XX capable of binding to human IGF-IR and, if necessary, capable of
XX specifically inhibiting tyrosine kinase activity of the receptor,
XX comprising a light or heavy chain having at least one complementary
XX determining region (CDR) consisting of one of two fully defined 16 amino
XX acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in
XX the preparation of a medicament intended for the prevention or treatment
XX of an illness connected with an overexpression and/or an abnormal
XX activation of the IGF-IR and/or EGFR, and/or connected with a
XX hyperactivation of the transduction pathway of the signal mediated by the
XX interaction of IGFI or IGf2 with IGF-IR and/or of EGFR with EGFR, where
XX the administration of the medicament does not induce or only slightly
XX induces secondary effects connected with inhibition of the insulin
XX receptor. The antibody is useful for preparation of a medicament intended
XX to inhibit the transformation of normal cells into cells with tumoral
XX character, preferably IGF-dependent, especially IGFI and/or IGf2-
XX dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is
XX useful for preparation of a medicament intended to inhibit the growth
XX and/or the proliferation of tumor cells, preferably IGF-dependent,
XX especially IGFI and/or IGf2-dependent and/or EGF-dependent and/or
XX HER2/neu-dependent cells. (I) is useful in the preparation of a
XX medicament intended for prevention or for the treatment of cancer, where
XX the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,
XX breast cancer, endometrial cancer or colon cancer. (I) is useful in the
XX preparation of a medicament intended for the prevention or for the
XX treatment of psoriasis. (I) is useful in preparation of a medicament
XX intended for the specific targeting of a biologically active compound to
XX cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)
XX is useful for in vitro diagnosis of illnesses induced by an
XX overexpression or an underexpression of the IGF-IR and/or EGFR receptor
XX starting from a biological sample in which the abnormal presence, of IGF-

CC IR and/or EGFR receptor is suspected, which involves contacting the
CC biological sample with (I), which is optionally labeled. The present
CC sequence is used in the exemplification of the invention.
XX Sequence 117 AA;
Query Match 100.0%; Score 47; DB 9; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YGRVFFDY 8
DB 99 YGRVFFDY 106
RESULT 10
ADZ67079
ID ADZ67079 standard; protein; 117 AA.
XX AC ADZ67079;
XX DT 30-JUN-2005 (first entry)
XX DE Human antibody 7C10 1 heavy chain variable region SEQ ID NO:75.
XX KW Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;
KW musculoskeletal disease; respiratory disease; lung tumor;
KW endocrine disease; gynecology and obstetrics; breast tumor;
KW endometrial carcinoma; gastrointestinal disease; colon tumor;
KW antipsoriatic; psoriasis; dermatological disease; immune disorder;
KW heavy chain variable region.
XX OS Homo sapiens.
XX PN US2005084906-A1.
XX PD 21-APR-2005.
XX PF 16-DEC-2003; 2003US-00735916.
XX PR 18-JAN-2002; 2002FR-00000653.
XX PR 18-JAN-2002; 2002FR-00000654.
XX PR 07-MAY-2002; 2002FR-00005753.
XX PR 20-JAN-2003; 2003WO-FR000178.
XX PR 11-JUL-2003; 2003FR-00008538.
XX (GOET/) GOETSCH L.
XX (CORV/) CORVAIA N.
XX (LEGE/) LEGER O.
XX (DUFU/) DUFLOS A.
XX (HAEU/) HAEUW J.
XX (BECK/) BECK A.
XX Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;
XX WPI; 2005-321968/33.
XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)
XX antibody or its functional fragment, being capable of binding human IGF-
XX IR and specifically inhibiting tyrosine kinase activity of receptor,
XX useful for treating cancer.
XX Example 13; SEQ ID NO 75; 125pp; English.
XX The invention relates to a novel isolated anti-insulin-like growth factor
XX I receptor (IGF-IR) antibody (I) or its functional fragment, being
XX capable of binding to human IGF-IR and, if necessary, capable of
XX specifically inhibiting tyrosine kinase activity of the receptor,
XX comprising a light or heavy chain having at least one complementary
XX determining region (CDR) consisting of one of two fully defined 16 amino
XX acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in
XX the preparation of a medicament intended for the prevention or treatment
XX of an illness connected with an overexpression and/or an abnormal
XX activation of the IGF-IR and/or EGFR, and/or connected with a
XX hyperactivation of the transduction pathway of the signal mediated by the
XX interaction of IGFI or IGf2 with IGF-IR and/or of EGFR with EGFR, where
XX the administration of the medicament does not induce or only slightly
XX induces secondary effects connected with inhibition of the insulin
XX receptor. The antibody is useful for preparation of a medicament intended
XX to inhibit the transformation of normal cells into cells with tumoral
XX character, preferably IGF-dependent, especially IGFI and/or IGf2-
XX dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is
XX useful for preparation of a medicament intended to inhibit the growth
XX and/or the proliferation of tumor cells, preferably IGF-dependent,
XX especially IGFI and/or IGf2-dependent and/or EGF-dependent and/or
XX HER2/neu-dependent cells. (I) is useful in the preparation of a
XX medicament intended for prevention or for the treatment of cancer, where
XX the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,
XX breast cancer, endometrial cancer or colon cancer. (I) is useful in the
XX preparation of a medicament intended for the prevention or for the
XX treatment of psoriasis. (I) is useful in preparation of a medicament
XX intended for the specific targeting of a biologically active compound to
XX cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)
XX is useful for in vitro diagnosis of illnesses induced by an
XX overexpression or an underexpression of the IGF-IR and/or EGFR receptor
XX starting from a biological sample in which the abnormal presence, of IGF-

CC of an illness connected with an overexpression and/or an abnormal
CC activation of the IGF-IR and/or EGFR, and/or connected with a
CC hyperactivation of the transduction pathway of the signal mediated by the
CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGFR with EGFR, where
CC the administration of the medicament does not induce or only slightly
CC induces secondary effects connected with inhibition of the insulin
CC receptor. The antibody is useful for preparation of a medicament intended
CC to inhibit the transformation of normal cells into cells with tumoral
CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-
CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is
CC useful for preparation of a medicament intended to inhibit the growth
CC and/or the proliferation of tumor cells, preferably IGF-dependent,
CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or
CC HER2/neu-dependent cells. (I) is useful in the preparation of a
CC medicament intended for prevention or for the treatment of cancer, where
CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,
CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the
CC preparation of a medicament intended for the prevention or for the
CC treatment of psoriasis. (I) is useful in preparation of a medicament
CC intended for the specific targeting of a biologically active compound to
CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)
CC is useful for in vitro diagnosis of illnesses induced by an
CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor
CC starting from a biological sample in which the abnormal presence, of IGF-
CC IR and/or EGFR receptor is suspected, which involves contacting the
CC biological sample with (I), which is optionally labeled. The present
CC sequence is used in the exemplification of the invention.

XX SQ Sequence 117 AA;

Query Match 100.0%; Score 47; DB 9; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRVFFDY 8
| | | | |
Db 99 YGRVFFDY 106

RESULT 11
ADJ76886
ID ADJ76886 standard; protein; 127 AA.

AC ADJ76886;

DT 06-MAY-2004 (first entry)

XX Anti-IGF-IR related protein #4.

XX Cytostatic; antipsoriatic; antibody;
KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;
KW or epidermal growth factor receptor; EGFR; signal transduction pathway;
KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;
KW CDR.

XX Mus musculus.

OS WO2003059951-A2.

XX 24-JUL-2003.

XX 20-JAN-2003; 2003WO-FR000178.

XX 18-JAN-2002; 2002FR-00000653.

XX 18-JAN-2002; 2002FR-00000654.

XX 07-MAY-2002; 2002FR-00005753.

XX (FABR) FABRE MEDICAMENT SA PIERRE.

XX Goetsch L, Corvaia N, Leger O;

XX WPI; 2003-569653/53.

PT New antibodies that bind to human insulin-like growth factor receptor,
PT useful for treatment, prevention and diagnosis of cancers.

XX Disclosure; SEQ ID NO 52; 164pp; French.

XX The invention relates to an isolated antibody (Ab), and its functional
CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-
CC 1R) and optionally; (i) inhibit natural binding of insulin-like growth
CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine
CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or
CC treat diseases associated with overexpression and/or abnormal activity of
CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with
CC hyperactivity of signal transduction pathways mediated by interaction of
CC these receptors with their ligands. Especially they inhibit
CC transformation of normal cells to tumor cells, inhibit growth and/or
CC proliferation of tumor cells, so are useful against cancers of the
CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
CC also for treating psoriasis. Ab are also used to diagnose diseases caused
CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a
CC protein sequence used to generate the Ab of the invention.

XX SQ Sequence 127 AA;

Query Match 100.0%; Score 47; DB 7; Length 127;

Best Local Similarity 100.0%; Pred. No. 0.97;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRVFFDY 8
| | | | |
Db 109 YGRVFFDY 116

RESULT 12

ADZ67056
ID ADZ67056 standard; protein; 127 AA.

AC ADZ67056;

XX 30-JUN-2005 (first entry)

XX Murine immunoglobulin heavy chain variable region 7C10 VH SEQ ID NO:52.

XX Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;
KW musculoskeletal disease; respiratory disease; lung tumor;
KW endocrine disease; gynecology and obstetrics; breast tumor;
KW endometroid carcinoma; gastrointestinal disease; colon tumor;
KW antipsoriatic; psoriasis; dermatological disease; immune disorder;
KW immunoglobulin; heavy chain variable region.

XX Mus musculus.

XX Key Location/Qualifiers
FT Peptide 1..10
/note= "leader peptide"

FT Region 41..46
/note= "CDR1"

FT Region 61..76
/note= "CDR2"

FT Region 109..116
/note= "CDR3"

XX US2005084906-A1.

XX 21-APR-2005.

XX 16-DEC-2003; 2003US-00735916.

XX 18-JAN-2002; 2002FR-00000653.

XX 18-JAN-2002; 2002FR-00000654.

XX 20-JAN-2002; 2002FR-00005753.

XX 11-JUL-2003; 2003FR-00008538.

XX (GOET/) GOETSCH L.
 PA (CORV/) CORVAIA N.
 PA (LEGE/) LEGER O.
 PA (DAFL/) DUFLOS A.
 PA (HAUJ/) HAEUW J.
 PA (BECK/) BECK A.
 XX
 XX Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;
 XX WPI; 2005-321968/33.
 XX N-PSDB; AD267055.
 XX
 XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)
 PT antibody or its functional fragment, being capable of binding human IGF-
 PT IR and specifically inhibiting tyrosine kinase activity of receptor,
 PT useful for treating cancer.
 XX
 XX Example 8; SEQ ID NO 52; 125pp; English.
 XX
 XX The invention relates to a novel isolated anti-insulin-like growth factor
 CC I receptor (IGF-IR) antibody (I) or its functional fragment, being
 CC capable of binding to human IGF-IR and, if necessary, capable of
 CC specifically inhibiting tyrosine kinase activity of the receptor,
 CC comprising a light or heavy chain having at least one complementary
 CC determining region (CDR) consisting of one of two fully defined 16 amino
 CC acids (AD267006 and AD267014). An antibody of the invention is useful in
 CC the preparation of a medicament intended for the prevention or treatment
 CC of an illness connected with an overexpression and/or an abnormal
 CC activation of the IGF-IR and/or EGFR, and/or connected with a
 CC hyperactivation of the transduction pathway of the signal mediated by the
 CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where
 CC the administration of the medicament does not induce or only slightly
 CC induces secondary effects connected with inhibition of the insulin
 CC receptor. The antibody is useful for preparation of a medicament intended
 CC to inhibit the transformation of normal cells into cells with tumoral
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is
 CC useful for preparation of a medicament intended to inhibit the growth
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a
 CC medicament intended for prevention or for the treatment of cancer, where
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the
 CC preparation of a medicament intended for the prevention or for the
 CC treatment of psoriasis. (I) is useful in preparation of a medicament
 CC intended for the specific targeting of a biologically active compound to
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)
 CC is useful for in vitro diagnosis of illnesses induced by an
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor
 CC starting from a biological sample in which the abnormal presence, of IGF-
 CC IR and/or EGFR receptor is suspected, which involves contacting the
 CC biological sample with (I), which is optionally labeled. The present
 CC sequence is used in the exemplification of the invention.
 XX
 XX Sequence 127 AA;
 XX
 XX Query Match 100.0%; Score 47; DB 9; Length 127;
 XX Best Local Similarity 100.0%; Pred. No. 0.97; Mismatches 0; Gaps 0;
 XX Matches 8; Conservative 0; Indels 0; Indels 0; Gaps 0;
 QY 1 YGRVFFDY 8
 Db 109 YGRVFFDY 116
 |||||
 RESULT 13
 ID ADJ76911
 XX ADJ76911 standard; protein; 135 AA.
 XX
 AC ADJ76911,
 XX

DT 06-MAY-2004 (first entry)
 XX
 DE Anti-IGF-IR related protein #23.
 XX
 KW cytotatic; antipsoriatic; antibody;
 KW insulin-like growth factor-1 receptor; IGF-IR; tyrosine kinase activity;
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;
 KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;
 KW CDR.
 XX
 OS Homo sapiens.
 XX
 PN WO2003059951-A2.
 XX
 PD 24-JUL-2003.
 XX
 PF 20-JAN-2003; 2003WO-FR000178.
 XX
 PR 18-JAN-2002; 2002FR-00000653.
 PR 18-JAN-2002; 2002FR-00000654.
 PR 07-MAY-2002; 2002FR-00005753.
 XX
 PA (FABR) FABRE MEDICAMENT SA PIERRE.
 XX
 PI Goetsch L, Corvaia N, Leger O;
 XX WPI; 2003-569653/53.
 XX
 XX New antibodies that bind to human insulin-like growth factor receptor,
 PT useful for treatment, prevention and diagnosis of cancers.
 XX
 XX Disclosure; SEQ ID NO 77; 164pp; French.
 XX
 XX The invention relates to an isolated antibody (Ab), and its functional
 CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-
 CC IR) and optionally: (i) inhibit natural binding of insulin-like growth
 CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine
 CC kinase activity of IGF-IR. Ab and its fragments are used to prevent or
 CC treat diseases associated with overexpression and/or abnormal activity of
 CC IGF-IR and/or epidermal growth factor receptor (EGFR) and/or with
 CC hyperactivity of signal transduction pathways mediated by interaction of
 CC these receptors with their ligands. Especially they inhibit
 CC transformation of normal cells to tumor cells, inhibit growth and/or
 CC proliferation of tumor cells, so are useful against cancers of the
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused
 CC by abnormal expression of IGF-IR and/or EGFR. This sequence represents a
 CC protein sequence used to generate the Ab of the invention.
 XX
 XX Sequence 135 AA;
 XX
 XX Query Match 100.0%; Score 47; DB 7; Length 135;
 XX Best Local Similarity 100.0%; Pred. No. 1;
 XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YGRVFFDY 8
 Db 117 YGRVFFDY 124
 |||||
 RESULT 14
 ID ADJ76919
 XX ADJ76919 standard; protein; 135 AA.
 XX
 AC ADJ76919;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Anti-IGF-IR related protein #27.
 XX
 KW cytotatic; antipsoriatic; antibody;
 KW insulin-like growth factor-1 receptor; IGF-IR; tyrosine kinase activity;
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;
 KW

KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;
 KW CDR.
 XX
 OS Homo sapiens.
 XX
 PN WO2003059951-A2.
 XX
 XX
 PD 24-JUL-2003.
 XX
 XX 20-JAN-2003; 2003WO-FR000178.
 XX
 XX 18-JAN-2002; 2002FR-00000653.
 PR 18-JAN-2002; 2002FR-00000654.
 PR 07-MAY-2002; 2002FR-00005753.
 XX
 XX (FABR) FABRE MEDICAMENT SA PIERRE.
 PA
 XX Goetsch L, Corvaia N, Leger O;
 PI WPI; 2003-569653/53.
 XX
 XX New antibodies that bind to human insulin-like growth factor receptor,
 PR useful for treatment, prevention and diagnosis of cancers.
 PT
 XX Disclosure; SEQ ID NO 85; 164pp; French.
 PS
 XX The invention relates to an isolated antibody (Ab), and its functional
 CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-
 CC 1R) and optionally: (i) inhibit natural binding of insulin-like growth
 CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine
 CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or
 CC treat diseases associated with overexpression and/or abnormal activity of
 CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with
 CC hyperactivity of signal transduction pathways mediated by interaction of
 CC these receptors with their ligands. Especially they inhibit
 CC transformation of normal cells to tumor cells, inhibit growth and/or
 CC proliferation of tumor cells, so are useful against cancers of the
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a
 CC protein sequence used to generate the Ab of the invention.
 XX
 SQ Sequence 135 AA;
 Query Match 100.0%; Score 47; DB 7; Length 135;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 YGRVFFDY 8
 Db 117 YGRVFFDY 124
 RESULT 15
 ADJ76915
 ID ADJ76915 standard; protein; 135 AA.
 XX
 XX AC ADJ76915;
 DT 06-MAY-2004 (first entry)
 XX
 XX DE Anti-IGF-1R related protein #25.
 XX
 KW cytosolic; antipsoriatic; antibody;
 KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;
 KW or epidermal growth factor receptor; EGFR; signal transduction pathway;
 KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;
 KW CDR.
 XX
 XX Homo sapiens.
 OS
 XX WO2003059951-A2.
 PN

PD 24-JUL-2003.
 XX
 XX 20-JAN-2003; 2003WO-FR000178.
 XX
 XX 18-JAN-2002; 2002FR-00000653.
 PR 18-JAN-2002; 2002FR-00000654.
 PR 07-MAY-2002; 2002FR-00005753.
 XX
 XX (FABR) FABRE MEDICAMENT SA PIERRE.
 PA
 XX Goetsch L, Corvaia N, Leger O;
 PI WPI; 2003-569653/53.
 XX
 XX New antibodies that bind to human insulin-like growth factor receptor,
 PR useful for treatment, prevention and diagnosis of cancers.
 PT
 XX Disclosure; SEQ ID NO 81; 164pp; French.
 PS
 XX The invention relates to an isolated antibody (Ab), and its functional
 CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-
 CC 1R) and optionally: (i) inhibit natural binding of insulin-like growth
 CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine
 CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or
 CC treat diseases associated with overexpression and/or abnormal activity of
 CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with
 CC hyperactivity of signal transduction pathways mediated by interaction of
 CC these receptors with their ligands. Especially they inhibit
 CC transformation of normal cells to tumor cells, inhibit growth and/or
 CC proliferation of tumor cells, so are useful against cancers of the
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused
 CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a
 CC protein sequence used to generate the Ab of the invention.
 XX
 SQ Sequence 135 AA;
 Query Match 100.0%; Score 47; DB 7; Length 135;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 YGRVFFDY 8
 Db 117 YGRVFFDY 124
 Search completed: December 30, 2005, 13:24:02
 Job time : 72.0968 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2005, 13:11:41 ; Search time 11.3548 Seconds
(without alignments)
67.789 Million cell updates/sec

Title: US-10-735-916A-12
Perfect score: 47
Sequence: 1 YGRVFFDY 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
PIR_80:*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	74.5	90	AC1030	hypothetical prote
2	35	74.5	293	D90456	oxydoreductase, pr
3	35	74.5	384	A11566	B. subtilis TagF p
4	35	74.5	395	F86740	teichoic acid bios
5	35	74.5	682	C84295	UDP-sugar hydrolas
6	34	72.3	87	E81191	hypothetical prote
7	34	72.3	117	S01822	Ig heavy chain V-D
8	34	72.3	125	D69523	hypothetical prote
9	34	72.3	142	D69515	hypothetical prote
10	34	72.3	297	C84509	hypothetical prote
11	34	72.3	453	S39866	outer membrane pro
12	34	72.3	477	T33531	hypothetical prote
13	34	72.3	483	A38560	nitrate transport
14	34	72.3	731	S16595	gene CARSR12 prote
15	34	72.3	739	A81430	outer membrane pr
16	33	70.2	119	S03077	Ig heavy chain V r
17	33	70.2	174	C69037	hypothetical prote
18	33	70.2	220	D71946	hypothetical prote
19	33	70.2	222	F64563	hypothetical prote
20	33	70.2	255	AB2109	hypothetical prote
21	33	70.2	285	F95289	conserved hypothet
22	33	70.2	317	T20302	hypothetical prote
23	33	70.2	341	CTNH22	site-specific DNA-
24	33	70.2	363	S42379	hypothetical prote
25	33	70.2	363	JC6053	glycerol-3-phospha
26	33	70.2	427	AB3025	methionine gamma-1
27	33	70.2	427	G98259	methionine gamma-1
28	33	70.2	450	D97885	conserved hypothet
29	33	70.2	603	T28278	ORF MSV117 probabl

ALIGNMENTS

RESULT 1

AC1030

hypothetical protein STY4564 [imported] - Salmonella enterica subsp. enterica serovar Typhimurium
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AC1030
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhimurium
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AC1030
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-90 <PAR>
A;Cross-references: UNIPARC:UPI000005A8A2; GB:AL513382; PIDN:CAD09340.1; PID:g16505340; C;Genetics;
A;Gene: STY4564

Query Match 74.5%; Score 35; DB 2; Length 90;

Best Local Similarity 85.7%; Pred. No. 6.3;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GRVFFDY 8

Db |||||

44 GRVFFDY 50

RESULT 2

D90456

oxydoreductase, probable [imported] - Sulfolobus solfataricus

C;Species: Sulfolobus solfataricus

C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004

C;Accession: D90456

R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan, J.; Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.; arrett, R.A.; Ragan, M.A.; Sengen, C.W.; Van der Oost, J.

submitted to GenBank, April 2001

A;Description: Sulfolobus solfataricus complete genome.

A;Reference number: A99139

A;Accession: D90456

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-293 <KUR>

A;Cross-references: UNIPROT:Q97V38; UNIPARC:UPI0000064866; GB:AE006641; NID:g13816140; P

C;Genetics:

A;Gene: SS02794

Query Match 74.5%; Score 35; DB 2; Length 293;

```

Best Local Similarity 75.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8
Db 159 YGNRFFDY 166

RESULT 3
B. subtilis TagF protein (probable CDPglycerol glycerophosphotransferase) homolog lin107
A:Accession: A11566
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: A11566
R.; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunat, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlant,
A.; Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: A11566
A:Status: preliminary
A:Gene: lin1074
A:Molecule type: DNA
A:Residues: 1-384 <GLA>
A:Cross-references: UNIPROT:Q92CU7; UNIPARC:UPI000000CC457; GB:AL592022; PIDN:CAC96305.1;
A:Experimental source: strain Clp11262
C:Genetics:
A:Gene: lin1074

Query Match 74.5%; Score 35; DB 2; Length 384;
Best Local Similarity 75.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8
Db 292 YSSVFFDY 299

RESULT 4
F86740
telchoic acid biosynthesis protein F [imported] - Lactococcus lactis subsp. lactis (stra
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C:Accession: F86740
R.; Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: F86740
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-395 <STO>
A:Cross-references: UNIPROT:Q9CH15; UNIPARC:UPI000000C6947; GB:AE005176; PID:g12723861; F
A:Experimental source: strain ILI403
C:Genetics:
A:Gene: tagF

Query Match 74.5%; Score 35; DB 2; Length 395;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8
Db 304 YSSVFFDY 311

RESULT 5
C84295
UDP-sugar hydrolase [imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

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C:Accession: C84295
R.; Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.
.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablor
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: A84160; MUID:20504483; PMID:11016950
A:Accession: C84295
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-682 <STO>
A:Cross-references: UNIPROT:Q9HPZ0; UNIPARC:UPI00000638A1; GB:AE004437; NID:g10580911; P
C:Genetics:
A:Gene: ush

Query Match 74.5%; Score 35; DB 2; Length 682;
Best Local Similarity 75.0%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8
Db 494 YGTVLFDY 501

RESULT 6
E81191
hypothetical protein NMB0510 [imported] - Neisseria meningitidis (strain MCS8 serogroup I
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: E81191
R.; Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.;
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
xi, H.; Qin, H.; Vamathavan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8.
A:Reference number: A81000; MUID:20175755; PMID:10710307
A:Accession: E81191
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-87 <TET>
A:Cross-references: UNIPROT:Q9JR23; UNIPARC:UPI000000C4E2B; GB:AE002407; GB:AE002098; NID:
A:Experimental source: serogroup B, strain MCS8
C:Genetics:
A:Gene: NMB0510

Query Match 72.3%; Score 34; DB 2; Length 87;
Best Local Similarity 62.5%; Pred. No. 9.6;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8
Db 49 YGKDFDY 56

RESULT 7
S01822
Ig heavy chain V-D-J region (hybridoma 10B10S) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
C:Accession: S01822
R.; Foerster, I.; Gu, H.; Rajewsky, K.
EMBO J. 7, 3693-3703, 1988
A:Title: Germ-line antibody V regions as determinants of clonal persistence and malignant
A:Reference number: S01822; MUID:89091115; PMID:3264787
A:Accession: S01822
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-117 <FOE>
A:Cross-references: UNIPARC:UPI0000176B35; EMBL:X12388; NID:g51924; PIDN:CAA30945.1; PID:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

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F;11-94/Domain: immunoglobulin homology <IMM>

Query Match 72.3%; Score 34; DB 2; Length 117;
Best Local Similarity 62.5%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 YGRVFFDY 8
| | | | |
Db 99 YGNYYFDY 106
| | | | |
RESULT 8
G69523
hypothetical protein AF2191 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: G69523
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: G69523
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-125 <KLE>
A;Cross-references: UNIPROT:O28092; UNIPARC:UPI0000056A38; GB:AE000954; GB:AE000782; NID

Query Match 72.3%; Score 34; DB 2; Length 125;
Best Local Similarity 71.4%; Pred. No. 14;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 YGRVFFD 7
| | | | |
Db 3 YGRIFFN 9
| | | | |

RESULT 9
D69515
hypothetical protein AF2124 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: D69515
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: D69515
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-142 <KLE>
A;Cross-references: UNIPROT:O28156; UNIPARC:UPI0000056A66; GB:AE000957; GB:AE000782; NID

Query Match 72.3%; Score 34; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YGRVFF 6
| | | | |
Db 72 YGRVFF 77
| | | | |

RESULT 10
C84509
hypothetical protein At2g13630 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 31-Dec-2004
C;Accession: C84509
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; P
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
eues, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: C84509
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-297 <STO>
A;Cross-references: UNIPROT:Q9S1T4; UNIPARC:UPI000000248E; GB:AE002093; NID:94558667; PI

C;Genetics:
A;Gene: At2g13630
A;Map position: 2
C;Superfamily: hypothetical protein containing F-box domain

Query Match 72.3%; Score 34; DB 2; Length 297;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RVFFDY 8
| | | | |
Db 281 RVFFDY 286
| | | | |

RESULT 11

S39866
outer membrane protein CD precursor - Moraxella catarrhalis
C;Species: Moraxella catarrhalis
C;Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C;Accession: S39866
R;Murphy, T.F.; Kirkham, C.; Lesse, A.J.
Mol. Microbiol. 10, 87-97, 1993
A;Title: The major heat-modifiable outer membrane protein CD is highly conserved among s
A;Reference number: S39866; MUID:95058186; PMID:7968522
A;Accession: S39866
A;Molecule type: DNA
A;Residues: 1-453 <MUR>
A;Cross-references: UNIPROT:Q08657; UNIPARC:UPI000000B8DE; EMBL:L10755; NID:G149756; PID

C;Keywords: membrane protein
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-453/Product: outer membrane protein CD #status predicted <MAT>

Query Match 72.3%; Score 34; DB 2; Length 453;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RVFFDY 8
| | | | |
Db 329 RVFFDY 334
| | | | |

RESULT 12

T33531
hypothetical protein F58E1.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T33531
R;Wamsley, P.; Twyman, B.
submitted to the EMBL Data Library, October 1998
A;Description: The sequence of C. elegans cosmid F58E1.
A;Reference number: Z21365
A;Accession: T33531
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-477 <WAM>
A;Cross-references: UNIPROT:Q9TZG7; UNIPARC:UPI0000007C654; EMBL:AF098995; PIDN:AAC67482.

A;Experimental source: strain Bristol N2; clone F58E1
C;Genetics:
A;Gene: CESP:F58E1.4
A;Map position: 2

A;Introns: 32/1; 104/1; 269/3; 424/3

C;Superfamily: Caenorhabditis elegans hypothetical protein T05A6.4

Query Match 72.3%; Score 34; DB 2; Length 477;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRVFF 6
Db 472 YGRVFF 477

RESULT 13

A38560

nitrate transport protein crnA - Emericella nidulans

C;Species: Emericella nidulans, Aspergillus nidulans

C;Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 09-Jul-2004

C;Accession: A38560

R;Unkies, S.B.; Hawker, K.L.; Grieve, C.; Campbell, E.I.; Montague, P.; Kinghorn, J.R.

Proc. Natl. Acad. Sci. U.S.A. 88, 204-208, 1991

A;Title: crnA encodes a nitrate transporter in Aspergillus nidulans.

A;Reference number: A38560; MUID:91095428; PMID:1986367

A;Accession: A38560

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-483 <UNK>

A;Cross-references: UNIPROT:P22152; UNIPARC:UPI0000178CA8; GB:M57647

C;Superfamily: nitrate transporter component

C;Keywords: transmembrane protein

Query Match 72.3%; Score 34; DB 2; Length 483;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRVFF 6
Db 32 YGRVFF 37

RESULT 14

S16595

gene CARSR12 protein - clove pink

C;Species: Dianthus caryophyllus (clove pink)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C;Accession: S16595

R;Raghothama, K.G.; Lawton, K.A.; Goldsbrough, P.B.; Woodson, W.R.

Plant Mol. Biol. 17, 61-71, 1991

A;Title: Characterization of an ethylene-regulated flower senescence-related gene from clove pink

A;Reference number: S16595; MUID:91329738; PMID:1868223

A;Accession: S16595

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-731 <RAG>

A;Cross-references: UNIPROT:Q00662; UNIPARC:UPI00001268DC; EMBL:X57171; NID:g18327; PIDN

C;Genetics:

A;Introns: 60/3; 92/3; 130/2; 152/3; 183/3; 232/3; 262/2; 297/3; 326/1; 365/3; 423/3; 48

C;Superfamily: beta-galactosidase bga

Query Match 72.3%; Score 34; DB 2; Length 731;
Best Local Similarity 62.5%; Pred. No. 82;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8
Db 28 YGNVWIDY 35

RESULT 15

A81430

outer membrane protein Cj0129c [imported] - Campylobacter jejuni (strain NCTC 11168)

C;Species: Campylobacter jejuni

C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C;Accession: A81430

R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrall
Nature 403, 665-668, 2000

A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp

A;Reference number: A81250; MUID:20150912; PMID:10688204

A;Accession: A81430

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-739 <PAR>

A;Cross-references: UNIPROT:O9PIZ8; UNIPARC:UPI00000C2051; GB:AL139074; GB:AL1111168; NID:

A;Experimental source: serotype O2, strain NCTC 11168

C;Genetics:

A;Gene: Cj0129c

Query Match 72.3%; Score 34; DB 2; Length 739;
Best Local Similarity 85.7%; Pred. No. 82;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GRVFFDY 8
Db 677 GSVFFDY 683

Search completed: December 30, 2005, 13:34:58
Job time : 13.3548 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:11:26 ; Search time 72 Seconds
(without alignments)

78.392 Million cell updates/sec

Title: US-10-735-916A-12

Perfect score: 47

Sequence: 1 YGRVFFDY 8

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	85.1	345	2	Q7M880 WOLSU
2	39	83.0	149	2	Q4IUN5 AZOVI
3	37	78.7	213	2	Q7N273 FHOHL
4	37	78.7	331	2	Q93HL7 STRAW
5	37	78.7	366	2	Q5VLJ6 HEVER
6	37	78.7	366	2	Q6T4P0 HEVER
7	37	78.7	552	2	Q8LJB0 ARATH
8	37	78.7	1838	2	Q8IDZ6 PLAF7
9	36	76.6	298	2	Q8RAL0 THETN
10	35	74.5	90	2	Q821K0 SALT1
11	35	74.5	113	2	Q6GUD4 EDWIC
12	35	74.5	270	2	Q96ZJ6 SULFO
13	35	74.5	289	1	END4 MYCPE
14	35	74.5	293	2	Q97V38 SULSO
15	35	74.5	298	2	Q5L810 BACFN
16	35	74.5	298	2	Q64N90 BACFR
17	35	74.5	300	2	Q8A9T6 BACTN
18	35	74.5	305	2	Q8A7X8 BACTN
19	35	74.5	382	2	Q6LNN6 PHOPR
20	35	74.5	384	2	Q720Y4 LISMP
21	35	74.5	384	2	Q92CU7 LISIN
22	35	74.5	395	2	Q9CH15 LACLA
23	35	74.5	398	2	Q4MJH6 BACCE
24	35	74.5	401	2	Q5WDC3 BACSK
25	35	74.5	443	2	Q5TVP9 ANOGA
26	35	74.5	455	2	Q9HJZ7 THEAC
27	35	74.5	493	2	Q7QGY9 ANOGA
28	35	74.5	514	2	Q5TVQ3 ANOGA
29	35	74.5	560	2	Q82YV7 ENTFA
30	35	74.5	568	2	Q7PSH8 ANOGA
31	35	74.5	682	2	Q9HPZ0 HALSA

32	35	74.5	710	2	Q4MJH5 BACCE	Q4mjh5 bacillus ce
33	35	74.5	722	2	Q5WDC6 BACSK	Q5wdc6 bacillus cl
34	35	74.5	775	2	Q8CQJ9 STAP	Q8cqj9 staphylococ
35	35	74.5	839	2	Q8DS18 VIRVU	Q8ds18 vibrio vuln
36	35	74.5	858	2	Q7MBV1 VIRVY	Q7mbv1 vibrio vuln
37	35	74.5	1496	2	Q9VIT9 DROME	Q9vit9 drosophila
38	35	74.5	1496	2	Q9NFV5 DROME	Q9nfvs drosophila
39	34	72.3	77	2	Q4ZS80 PLABE	Q4z580 plasmodium
40	34	72.3	87	2	Q9JR23 NEIME	Q9jrd3 neisseria m
41	34	72.3	87	2	Q7DDN6 NEIMB	Q7ddn6 neisseria m
42	34	72.3	125	1	Y2191_ARCFU	Q28092 archaeoglob
43	34	72.3	142	1	Y2124_ARCFU	Q28156 archaeoglob
44	34	72.3	159	2	Q5GTD1 WOLTR	Q5gttd1 wolbachia s
45	34	72.3	199	2	Q856Z7_9CAUD	Q856z7 mycobacteri

ALIGNMENTS

RESULT 1

Q7M880 WOLSU
ID Q7M880_WOLSU PRELIMINARY; PRT; 345 AA.

AC Q7M880;

DT 01-MAR-2004 (Tremblrel. 26, Created)

DT 01-MAR-2004 (Tremblrel. 26, Last sequence update)

DE MEMBRANE PROTEIN-Predicted permease.

GN Name=AMAA; OrderedLocusNames=WS1824;

OS Wolinella succinogenes.

OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;

OC Helicobacteraceae; Wolinella.

OX NCBI_TaxID=844;

RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=DSMZ 1740;

RX MEDLINE=22882897; PubMed=14500908; DOI=10.1073/pnas.1932838100;

RA Baar C., Eppinger M., Radatz G., Simon J., Lanz C., Klimmek O.,

RA Nandakumar R., Gross R., Rosinus A., Keller H., Jagtap P., Linke B.,

RA Meyer P., Lederer H., Schuster S.C.;

RT "Complete genome sequence and analysis of Wolinella succinogenes.";

RL Proc. Natl. Acad. Sci. U.S.A. 100:11690-11695(2003).

DR EMBL; BX571661; CAS10839.1; -; Genomic_DNA.

DR InterPro; IPR002549; UPF0118.

DR Pfam; PF01594; UPF0118; 1.

KW Complete proteome.

SQ SEQUENCE 345 AA; 38928 MW; 595AF3430F1C444E CRC64;

Query Match 85.1%; Score 40; DB 2; Length 345;

Best Local Similarity 75.0%; Pred. No. 16;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YGRVFFDY 8

||| |||

Db 163 YGRAFYDY 170

RESULT 2

Q4IUN5 AZOVI

ID Q4IUN5_AZOVI PRELIMINARY; PRT; 149 AA.

AC Q4IUN5;

DT 13-SEP-2005 (Tremblrel. 31, Created)

DT 13-SEP-2005 (Tremblrel. 31, Last sequence update)

DE 13-SEP-2005 (Tremblrel. 31, Last annotation update)

DE Hypothetical protein.

GN ORFNames=AvindRAFT 1630;

OS Azotobacter vinelandii AvOP.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

OC Pseudomonadaceae; Azotobacter.

OX NCBI_TaxID=322710;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=AvOP;

RG US DOE Joint Genome Institute (JGI-PGF);

RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
 RA Hammon N., Israni S., Pitluck S., Richardson P.,
 RT "Sequencing of the draft genome assembly of *Azotobacter vinelandii*
 AVOP";
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=AVOP;
 RG US DOE Joint Genome Institute (JGI-ORNL);
 RA Larimer F., Land M.,
 RT "Annotation of the draft genome assembly of *Azotobacter vinelandii*
 AVOP";
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 [3]
 RN NUCLEOTIDE SEQUENCE.
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=AVOP;
 RG US DOE Joint Genome Institute;
 RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
 RA Hammon N., Israni S., Pitluck S., Richardson P.,
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAU03000012; EAM04553.1; -; Genomic_DNA.
 KW Hypochemical protein.
 SQ SEQUENCE 149 AA; 16436 MW; B03FD0348C8ACFDE CRC64;

Query Match 83.0%; Score 39; DB 2; Length 149;
 Best Local Similarity 87.5%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8
 |||
 DB 119 YGVFFDY 126

RESULT 3
 Q7NZ73_PHOLL PRELIMINARY; PRT; 213 AA.
 AC Q7NZ73;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Complete genome; segment 11/17.
 GN OrderedLocusNames=plu3218;
 OS *Photobacterium luminescens* (subsp. *laumondii*).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Photobacterium.
 OX NCBI_TaxID=141679;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=TT01;
 RX MEDLINE=22957627; PubMed=14528314; DOI=10.1038/nbt886;
 RA Duchaud E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A.,
 RA Taourit S., Bocs S., Boursaux-Eude C., Chandler M., Charles J.-F.,
 RA Dassa E., Berose R., Derzelle S., Freysinet G., Gaudriault S.,
 RA Medigue C., Lanois A., Powell K., Sigulier P., Vincent R., Wingate V.,
 RA Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.,
 RT "The genome sequence of the entomopathogenic bacterium *Photobacterium*
 RT *luminescens*."
 RL Nat. Biotechnol. 21:1307-1313 (2003).
 DR EMBL; BX571869; CAF15592.1; -; Genomic_DNA.
 DR PhotoList; plu3218; -;
 KW Complete proteome.
 SQ SEQUENCE 213 AA; 24684 MW; FB69E290F8C4116C CRC64;

Query Match 78.7%; Score 37; DB 2; Length 213;
 Best Local Similarity 85.7%; Pred. No. 40;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GRVFFDY 8
 |||
 DB 121 GKVFFDY 127

RESULT 4
 Q93HL7_STRAW PRELIMINARY; PRT; 331 AA.
 ID Q93HL7;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE O-methyltransferase.
 GN OrderedLocusNames=SAV2843;
 OS Streptomyces avermitilis.
 OC Bacteria; Actinobacteria; Actinomycetales; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=33903;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
 RX MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
 RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
 RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
 RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.,
 RT "Genome sequence of an industrial microorganism *Streptomyces*
 RT *avermitilis*: deducing the ability of producing secondary
 RT metabolites.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220 (2001).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
 RX MEDLINE=22608306; PubMed=12692562; DOI=10.1038/nbt820;
 RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
 RA Sakaki Y., Hattori M., Omura S.,
 RT "Complete genome sequence and comparative analysis of the industrial
 RT microorganism *Streptomyces avermitilis*.";
 RL Nat. Biotechnol. 21:526-531 (2003).
 DR EMBL; AB070937; BAB69170.1; -; Genomic_DNA.
 DR EMBL; BA000030; BAC70554.1; -; Genomic_DNA.
 DR GO; GO:0008171; F:O-methyltransferase activity; IEA.
 DR GO; GO:0008757; F:S-adenosylmethionine-dependent methyltransf. .; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR InterPro; IPR001601; Methyltransf.
 DR InterPro; IPR001077; O-Met transf.
 DR InterPro; IPR000051; SAM_bind.
 DR InterPro; IPR011951; Wing_hlx_DNA_bd.
 DR Pfam; PF00891; Methyltransf_2; 1.
 KW Complete proteome; Methyltransferase; Transferase.
 SQ SEQUENCE 331 AA; 36302 MW; A13E700B/F81AB5B CRC64;

Query Match 78.7%; Score 37; DB 2; Length 331;
 Best Local Similarity 75.0%; Pred. No. 63;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8
 |||
 DB 121 YGVFFDY 128

RESULT 5
 Q5VLJ6_HEVBR PRELIMINARY; PRT; 366 AA.
 ID Q5VLJ6;
 AC Q5VLJ6;
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE 50 kDa protein.
 OS *Hevea brasiliensis* (Para rubber tree).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

```

RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20363099; PubMed=10907853;
RA kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RT "structural analysis of Arabidopsis thaliana chromosome 3.II.
RT sequence features of the 4,251,695 bp regions covered by 90 Fl, TAC
RT and BAC clones.";
RL DNA Res. 7:217-221(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RA Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP006506; BAB01195.1; -; Genomic DNA.
SQ SEQUENCE 552 AA; 63036 MW; 740EA16CDEBB2447 CRC64;

Query Match 78.7%; Score 37; DB 2; Length 552;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8
DB 283 WGRVFFDY 290
:|||||

RESULT 8
Q8IDZ6_PLAF7
ID Q8IDZ6_PLAF7 PRELIMINARY; PRT; 1838 AA.
AC Q8IDZ6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein PF13_0182.
GN Name=PF13_0182;
OS Plasmodium falciparum (isolate 3D7)
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
CX NCBI_TaxID=36329;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=3D7;
RA Harris B., Lennard N., Clark L., Line A., Barron A., Corton C.,
RA Brannan M., Pain A., Hall N., Atkin R., Chillingworth C., Doggett J.,
RA Ormond D., Sanders M., Hayes R., Hall S., Quail M., Barrell B.;
RA Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL844509; CA52471.1; -; Genomic DNA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0004839; F:ubiquitin activating enzyme activity; IEA.
DR GO; GO:0006512; P:ubiquitin cycle; IEA.
DR InterPro; IPR000594; Thif domain.
DR InterPro; IPR000127; UBact repeat.
DR InterPro; IPR000011; UBQ-activ_enz_E1.
DR Pfam; PF00899; Thif; 2.
DR Pfam; PF02134; UBACT; 1.
DR PRINTS; PR01849; UBIQUITINACT.
DR Hypothetical protein.
SQ SEQUENCE 1838 AA; 218523 MW; 460029B7943F3143 CRC64;

Query Match 78.7%; Score 37; DB 2; Length 1838;
Best Local Similarity 75.0%; Pred. No. 3.8e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8
DB 309 FGRVFFDY 316
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RESULT 9
Q8RAL0_THETN
ID Q8RAL0_THETN PRELIMINARY; PRT; 298 AA.
AC Q8RAL0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CheY-like receiver domains.

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GN Name=ChetY6; OrderedLocusNames=TTE1203;
OS Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
OC Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=119072;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MB4 / JCM 11007;
RX MEDLINE=2192816; PubMed=11997336; DOI=10.1101/gr.219302;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of the T. tengcongensis genome.";
RL Genome Res. 12:689-700 (2002).
CC -|- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
DR EMBL; AE013083; AA024433.1; -; Genomic_DNA.
DR HSSP; Q56312; 1TWY.
DR GO; GO:0003577; P:DNA binding; IEA.
DR GO; GO:0001567; P:two-component response regulator activity; IEA.
DR GO; GO:0000156; P:two-component response regulator activity; IEA.
DR GO; GO:0007600; P:sensory perception; IEA.
DR GO; GO:0000160; P:two-component signal transduction system (p. . .; IEA.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF00072; Response_reg.1.
DR ProDom; PD000039; Response_reg; 1.
DR SMART; SM00448; REC; 1.
DR PROSITE; PS01110; RESPONSE REGULATORY; 1.
DR Complete proteome; DNA-binding; Sensory transduction; Transcription;
KW Transcription regulation; Two-component regulatory system.
SQ SEQUENCE 298 AA; 34210 MW; ABB5DE49DDC3C539 CRC64;

Query Match 76.6%; Score 36; DB 2; Length 298;
Best Local Similarity 75.0%; Pred. No. 90;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8
DB 253 YGHVLFY 260

RESULT 10
Q821K0_SALTI PRELIMINARY; PRT; 90 AA.
ID Q821K0_SALTI PRELIMINARY; PRT; 90 AA.
AC Q821K0; Q7C5G8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein STY4564
GN OrderedLocusNames=STY4564, t4262;
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feitwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
enterica serovar Typhi CT18.";
RL Nature 413:848-852 (2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RX DOI=10.1128/JB.185.7.2330-2337.2003;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,

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RA Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT and CT18.";
RL J. Bacteriol. 185:2330-2337 (2003).
DR EMBL; AL627282; CAD09340.1; -; Genomic_DNA.
DR EMBL; AE016848; AAO71720.1; -; Genomic_DNA.
DR InterPro; IPR010040; Plasmid_RAQPRD.
DR TIGRFAMs; TIGR01690; plasmid_RAQPRD; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 90 AA; 10309 MW; 133893BEF86FEDF0 CRC64;

Query Match 74.5%; Score 35; DB 2; Length 90;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GRVFFDY 8
DB 44 GRVFFDY 50

RESULT 11
Q6GUD4_EDWIC PRELIMINARY; PRT; 113 AA.
ID Q6GUD4_EDWIC PRELIMINARY; PRT; 113 AA.
AC Q6GUD4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Edwardsiella ictaluri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Edwardsiella.
OX NCBI_TaxID=67780;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Thune R.L., Fernandez D.H., Benoit J.L., Kelly-Smith M., Rogge M.L.,
RA Booth N.J., Bologna R.A.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY641981; AAT47192.1; -; Genomic_DNA.
DR InterPro; IPR010040; Plasmid_RAQPRD.
DR TIGRFAMs; TIGR01690; plasmid_RAQPRD; 1.
KW Hypothetical protein.
SQ SEQUENCE 113 AA; 12533 MW; 4F556CE8590CC469 CRC64;

Query Match 74.5%; Score 35; DB 2; Length 113;
Best Local Similarity 85.7%; Pred. No. 52;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GRVFFDY 8
DB 68 GRVFFDY 74

RESULT 12
Q96ZJ6_SULTO PRELIMINARY; PRT; 270 AA.
ID Q96ZJ6_SULTO PRELIMINARY; PRT; 270 AA.
AC Q96ZJ6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE 270aa long hypothetical thiosulfate reductase electron transport
protein phsB.
GN OrderedLocusNames=ST1839;
OS Sulfolobus tokodaii.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=111955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JCM 10545 / 7;
RX MEDLINE=21456156; PubMed=11572479;
RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA Sekine M., Baba S.-I., Anka A., Kosugi H., Hosoyama A., Fukui S.,
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,

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RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
 RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
 RA Ohshima T., Kikuchi H.;
 RT "Complete genome sequence of an aerobic thermoacidophilic
 RT Crenarchaeon, Sulfolobus tokodaii strain7.";
 RL DNA Res. 8:123-140(2001).
 DR ENBL; BA000023; BAB66929.1; -; Genomic_DNA.
 DR HSP; P11349; 1R27.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0005506; F:iron ion binding; IEA.
 DR GO; GO:0046872; F:metal ion binding; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR001450; 4Fe4S_Fe_S_bd.
 DR Pfam; PF00037; Fer4; 1.
 DR PRINTS; PR00353; 4FE4SPRDOXIN.
 DR 4Fe-4S; Complete proteome; Electron transport; Hypothetical protein;
 KW Iron; Iron-sulfur; Metal-binding; Transprot.
 KW Iron; Iron-sulfur; Metal-binding; Transprot.
 SQ SEQUENCE 270 AA; 30000 MW; 4600F746DBF1685 CRC64;
 Query Match 74.5%; Score 35; DB 2; Length 270;
 Best Local Similarity 75.0%; Pred. No. 1.3e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 YGRVFFDY 8
 DB 138 YGNRFFDY 145
 RESULT 13
 ENDA MYCPE
 ID _END4_MYCPE STANDARD; PRT; 289 AA.
 AC QSEW72; 2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Probable endonuclease IV (EC 3.1.21.2) (Endodeoxyribonuclease IV).
 GN Name=info; OrderedLocusNames=MYPE1190;
 OS Mycoplasma penetrans.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OC NCBI_TaxID=28227;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=HF-2;
 RX MEDLINE=22354719; PubMed=12466555; DOI=10.1093/nar/gkf667;
 RA Sasaki Y., Ishikawa J., Yamashita A., Ohshima K., Kenri T., Furuya K.,
 RA Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;
 RT "The complete genomic sequence of Mycoplasma penetrans, an
 RT intracellular bacterial pathogen in humans.";
 RL Nucleic Acids Res. 30:5293-5300(2002).
 CC -1- FUNCTION: Endonuclease IV plays a role in DNA repair. It cleaves
 CC phosphodiester bonds at apurinic or apyrimidinic sites (AP sites)
 CC to produce new 5' ends that are base-free deoxyribose 5-phosphate
 CC residues. It preferentially attacks modified AP sites created by
 CC bleomycin and neocarzinostatin (By similarity).
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
 CC phosphooligonucleotide end-products.
 CC -1- COFACTOR: Binds 3 zinc ions (By similarity).
 CC -1- SIMILARITY: Belongs to the AP endonuclease 2 family.
 CC
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 CC EMBL; BA000026; BAC43911.1; ALT_INIT; Genomic_DNA.
 DR HSP; P12638; 1QTW.
 DR HAWAP; MF_00152; -; 1.
 DR InterPro; IPR001719; AP endonuclease2.
 DR InterPro; IPR012307; Xylisom TIMbar1.
 DR Pfam; PF01261; AP endonuc 2; 1.
 DR TIGRFAMs; TIGR00587; nfo; 1.
 DR PROSITE; PS00729; AP_NUCLEASE_F2_1; 1.

DR PROSITE; PS00730; AP_NUCLEASE_F2_2; 1.
 DR PROSITE; PS00731; AP_NUCLEASE_F2_3; 1.
 KW Complete proteome; DNA damage; DNA repair; Endonuclease; Hydrolase;
 KW Metal-binding; Nuclease; Zinc
 FT METAL 76 Zinc 1 (By similarity).
 FT METAL 116 Zinc 1 (By similarity).
 FT METAL 152 Zinc 1 and 2 (By similarity).
 FT METAL 186 Zinc 2 (By similarity).
 FT METAL 189 Zinc 3 (By similarity).
 FT METAL 220 Zinc 2 (By similarity).
 FT METAL 220 Zinc 3 (By similarity).
 FT METAL 233 Zinc 3 (By similarity).
 FT METAL 235 Zinc 3 (By similarity).
 FT METAL 265 Zinc 2 (By similarity).
 SQ SEQUENCE 289 AA; 32583 MW; 985835176E016EB9 CRC64;
 Query Match 74.5%; Score 35; DB 1; Length 289;
 Best Local Similarity 75.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 YGRVFFDY 8
 DB 240 YGKVGFDY 247

RESULT 14
 Q97V38 SULSO
 ID Q57V38 SULSO PRELIMINARY; PRT; 293 AA.
 AC Q97V38; 2001 (TREMBlrel. 18, Created)
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Oxydoreductase, putative.
 GN OrderedLocusNames=SSO2794;
 OS Sulfolobus solfataricus.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 OC NCBI_TaxID=2287;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ATCC 35092 / DSM 1617 / P2;
 RX MEDLINE=21332296; PubMed=11427726; DOI=10.1073/pnas.141222098;
 RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
 RA Wayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
 RA De Moors A., Etrauso G., Fletcher C., Gordon P.M.K.,
 RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
 RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
 RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland I.,
 RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
 RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
 DR EMBL; AE006873; AAK42907.1; -; Genomic_DNA.
 DR PIR; D90456; D90456.
 DR HSP; P00214; 2PD2.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0005506; F:iron ion binding; IEA.
 DR GO; GO:0046872; F:metal ion binding; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR001450; 4Fe4S_Fe_S_bd.
 DR Pfam; PF00037; Fer4; 1.
 DR PRINTS; PR00353; 4FE4SPRDOXIN.
 KW 4Fe-4S; Complete proteome; Electron transport; Iron; Iron-sulfur;
 KW Metal-binding; Transport.
 KW Metal-binding; Transport.
 SQ SEQUENCE - 293 AA; 32382 MW; C13A04963619EDAD CRC64;
 Query Match 74.5%; Score 35; DB 2; Length 293;
 Best Local Similarity 75.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 YGRVFFDY 8
 DB 159 YGNRFFDY 166

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RESULT 15
Q5L810_BACFN
ID Q5L810_BACFN PRELIMINARY; PRT; 298 AA.
AC Q5L810;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Putative AraC-family transcriptional regulator.
GN OrderedLocusNames=BF4113;
OS Bacteroides fragilis (strain ATCC 25285 / NCTC 9343).
OC Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=272559;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15746427; DOI=10.1126/science.1107008;
RA Cerdeno-Tarraga A.-M., Patrick S., Crossman L.C., Blakely G.,
RA Abratt V., Lennard N., Poxton I., Duerden B., Harris B., Quail M.A.,
RA Barron A., Clark L., Corton C., Doggett J., Holden M.T.G., Larke N.,
RA Line A., Lord A., Norbertczak H., Ormond D., Price C.,
RA Rabinowitsch E., Woodward J., Barrell B.G., Parkhill J.;
RT "Extensive DNA inversions in the B. fragilis genome control variable
RT gene expression.";
RL Science 307:1463-1465(2005).
DR EMBL; CR626927; CAH09787.1; -; Genomic_DNA.
DR InterPro; IPR012287; Homeodomain-rel.
DR InterPro; IPR000005; HTHARAC.
DR Pfam; PF00165; HTH_AraC; 1.
DR PRINTS; PR00032; HTHARAC.
DR SMART; SM00342; HTH_ARAC; 1.
DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; 1.
DR PROSITE; PS01124; HTH_ARAC_FAMILY_2; 1.
KW Activator; Complete proteome; DNA-binding; Transcription;
KW Transcription regulation.
SQ SEQUENCE 298 AA; 34641 MW; A08394D705F34AD1 CRC64;

Query Match 74.5%; Score 35; DB 2; Length 298;
Best Local Similarity 62.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8
Db ||| :||
61 YGRKYDY 68

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Search completed: December 30, 2005, 13:33:33
Job time : 75 secs

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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:14:26 ; Search time 17.9355 Seconds
(without alignments)
36.877 Million cell updates/sec

Title: US-10-735-916A-12

Perfect score: 47

Sequence: 1 YGRVFFDY 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*

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2: /cgm2_6/ptodata/1/iaa/6_COMB.pep.*

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5: /cgm2_6/ptodata/1/iaa/RE_COMB.pep.*

6: /cgm2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	80.9	138	2	US-09-252-991A-20154
2	35	74.5	72	2	US-09-248-796A-21727
3	35	74.5	233	2	US-09-134-000C-4002
4	35	74.5	390	2	US-09-252-991A-33062
5	34	72.3	12	2	US-08-974-899-12
6	34	72.3	12	2	US-09-795-798-12
7	34	72.3	17	1	US-08-306-871-41
8	34	72.3	17	1	US-08-569-959-41
9	34	72.3	26	1	US-08-306-871-33
10	34	72.3	26	1	US-08-569-959-33
11	34	72.3	71	1	US-08-306-871-28
12	34	72.3	71	1	US-08-569-959-28
13	34	72.3	92	2	US-09-270-767-61481
14	34	72.3	116	2	US-09-027-449-50
15	34	72.3	116	2	US-08-804-444A-50
16	34	72.3	116	2	US-09-026-985-50
17	34	72.3	116	2	US-09-121-952A-50
18	34	72.3	116	2	US-09-234-340A-50
19	34	72.3	116	2	US-09-355-014-50
20	34	72.3	121	2	US-08-974-899-4
21	34	72.3	121	2	US-08-974-899-5
22	34	72.3	121	2	US-08-974-899-24
23	34	72.3	121	2	US-09-795-798-4
24	34	72.3	121	2	US-09-795-798-5
25	34	72.3	121	2	US-09-795-798-24
26	34	72.3	133	2	US-09-540-236-3221
27	34	72.3	142	1	US-08-860-174A-7

28 34 72.3 274 1 US-08-860-174A-12 Sequence 12, Appl

29 34 72.3 282 1 US-08-860-174A-10 Sequence 10, Appl

30 34 72.3 306 2 US-09-270-767-45943 Sequence 45943, A

31 34 72.3 514 2 US-09-902-540-12330 Sequence 12330, A

32 34 72.3 731 1 US-08-696-944-20 Sequence 20, Appl

33 33 70.2 375 2 US-09-248-796A-15005 Sequence 15005, A

34 33 70.2 878 2 US-09-937-908-1 Sequence 1, Appl

35 32 68.1 10 2 US-09-406-535-7 Sequence 7, Appl

36 32 68.1 119 2 US-09-406-535-2 Sequence 2, Appl

37 32 68.1 120 1 US-08-497-312-26 Sequence 26, Appl

38 32 68.1 120 1 US-08-497-312-28 Sequence 28, Appl

39 32 68.1 122 2 US-10-092-246-10 Sequence 10, Appl

40 32 68.1 122 2 US-10-092-246-11 Sequence 11, Appl

41 32 68.1 122 2 US-10-096-246A-10 Sequence 10, Appl

42 32 68.1 122 2 US-10-096-246A-11 Sequence 11, Appl

43 32 68.1 123 2 US-09-840-459-91 Sequence 91, Appl

44 32 68.1 123 2 US-09-497-625A-91 Sequence 91, Appl

45 32 68.1 139 2 US-08-454-899G-15 Sequence 15, Appl

ALIGNMENTS

RESULT 1

US-09-252-991A-20154
; Sequence 20154, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; PRIOR FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 20154

; LENGTH: 138

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-20154

Query Match 80.9%; Score 38; DB 2; Length 138;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YGRVFFDY 8

Db 98 YGRIFRY 105

RESULT 2

US-09-248-796A-21727
; Sequence 21727, Application US/09248796A

; Patent No. 6747137

; GENERAL INFORMATION:

; APPLICANT: Keith Weinstock et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.132

; CURRENT APPLICATION NUMBER: US/09/248,796A

; CURRENT FILING DATE: 1999-02-12

; PRIOR APPLICATION NUMBER: US 60/074,725

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: US 60/096,409

; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 28208

; SEQ ID NO 21727

; LENGTH: 72

; TYPE: PRT

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; ORGANISM: Candida albicans
US-09-248-796A-21727

Query Match      74.5%; Score 35; DB 2; Length 72;
Best Local Similarity 71.4%; Pred. No. 20;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRVFFD 7
Db 11 YGRIFFE 17

RESULT 3
US-09-134-000C-4002
; Sequence 4002, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US/09/134,000C
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4002
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-4002

Query Match      74.5%; Score 35; DB 2; Length 233;
Best Local Similarity 62.5%; Pred. No. 64;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8
Db 131 YGKISFDY 138

RESULT 4
US-09-252-991A-33062
; Sequence 33062, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 33062
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-33062

Query Match      74.5%; Score 35; DB 2; Length 390;
Best Local Similarity 62.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8
Db 350 YGRIYFRY 357

; ORGANISM: Candida albicans
US-08-974-899-12
; Sequence 12, Application US/08974899
; Patent No. 6037454
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,899
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 11/27/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1014R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-974-899-12

Query Match      72.3%; Score 34; DB 2; Length 12;
Best Local Similarity 62.5%; Pred. No. 5.1;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8
Db 5 YGTYTFDY 12

RESULT 6
US-09-795-798-12
; Sequence 12, Application US/09795798
; Patent No. 6703018
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/09/795,798
FILING DATE: 28-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,899
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-795-798-12

Query Match 72.3%; Score 34; DB 2; Length 12;
Best Local Similarity 62.5%; Pred. No. 5.1;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8
DB 5 YGTTTFDY 12

RESULT 7
US-08-306-871-41
Sequence 41, Application US/08306871
Patent No. 5712118
GENERAL INFORMATION:
APPLICANT: Timothy F. Murphy
TITLE OF INVENTION: Vaccine For Branhamella catarrhalis
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
STREET: 1800 One M&T Plaza
CITY: Buffalo
STATE: New York
COUNTRY: United States
ZIP: 14203-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS/ Microsoft Windows 3.1
SOFTWARE: Wordperfect for Windows 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,871
FILING DATE: 20-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/129,719
FILING DATE: September 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Nelson, M. Bud
REGISTRATION NUMBER: 35,300
REFERENCE/DOCKET NUMBER: 11520.0053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 856-4000
TELEFAX: (716) 849-0349
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 residues
TYPE: amino acid
TOPOLOGY: linear
ORIGINAL SOURCE:
ORGANISM: Branhamella catarrhalis
STRAIN: 25240
FEATURE:
LOCATION: CD amino acid positions 295-311

US-08-306-871-41

Query Match 72.3%; Score 34; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RVFFDY 8
DB 9 RVFFDY 14

RESULT 8
US-08-569-959-41
Sequence 41, Application US/08569959
Patent No. 5725862
GENERAL INFORMATION:
APPLICANT: Timothy F. Murphy
TITLE OF INVENTION: Vaccine For Branhamella catarrhalis
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
STREET: 1800 One M&T Plaza
CITY: Buffalo
STATE: New York
COUNTRY: United States
ZIP: 14203-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS/ Microsoft Windows 3.1
SOFTWARE: Wordperfect for Windows 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,959
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/129,719
FILING DATE: September 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Nelson, M. Bud
REGISTRATION NUMBER: 35,300
REFERENCE/DOCKET NUMBER: 11520.0053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 856-4000
TELEFAX: (716) 849-0349
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 residues
TYPE: amino acid
TOPOLOGY: linear
ORIGINAL SOURCE:
ORGANISM: Branhamella catarrhalis
STRAIN: 25240
FEATURE:
LOCATION: CD amino acid positions 295-311

US-08-569-959-41

Query Match 72.3%; Score 34; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RVFFDY 8
DB 9 RVFFDY 14

RESULT 9
US-08-306-871-33
Sequence 33, Application US/08306871
Patent No. 5712118
GENERAL INFORMATION:
APPLICANT: Timothy F. Murphy
TITLE OF INVENTION: Vaccine For Branhamella catarrhalis

```
/
/
/ NUMBER OF SEQUENCES: 52
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
/ STREET: 1800 One M&T Plaza
/ CITY: Buffalo
/ STATE: New York
/ COUNTRY: United States
/ ZIP: 14203-2391
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: MS-DOS/ Microsoft Windows 3.1
/ SOFTWARE: Wordperfect for Windows 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/306,871
/ FILING DATE: 20-SEP-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/129,719
/ FILING DATE: September 29, 1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Nelson, M. Bud
/ REGISTRATION NUMBER: 35,300
/ REFERENCE/DOCKET NUMBER: 11520.0053
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (716) 856-4000
/ TELEFAX: (716) 849-0349
/ INFORMATION FOR SEQ ID NO: 33:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 26 residues
/ TYPE: amino acid
/ TOPOLOGY: linear
/ ORGANISM: Branhamella catarrhalis
/ STRAIN: 25240
/ FEATURE:
/ LOCATION: CD amino acid positions 286-311
/ US-08-306-871-33

Query Match 72.3%; Score 34; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RVFFDY 8
Db 18 RVFFDY 23

RESULT 10
US-08-569-959-33
/ Sequence 33, Application US/08569959
/ Patent No. 5725862
/ GENERAL INFORMATION:
/ APPLICANT: Timothy F. Murphy
/ TITLE OF INVENTION: Vaccine For Branhamella catarrhalis
/ NUMBER OF SEQUENCES: 52
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
/ STREET: 1800 One M&T Plaza
/ CITY: Buffalo
/ STATE: New York
/ COUNTRY: United States
/ ZIP: 14203-2391
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: MS-DOS/ Microsoft Windows 3.1
/ SOFTWARE: Wordperfect for Windows 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/569,959
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: U.S. 08/129,719
```

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/
/
/ FILING DATE: September 29, 1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Nelson, M. Bud
/ REGISTRATION NUMBER: 35,300
/ REFERENCE/DOCKET NUMBER: 11520.0053
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (716) 856-4000
/ TELEFAX: (716) 849-0349
/ INFORMATION FOR SEQ ID NO: 33:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 26 residues
/ TYPE: amino acid
/ TOPOLOGY: linear
/ ORGANISM: Branhamella catarrhalis
/ STRAIN: 25240
/ FEATURE:
/ LOCATION: CD amino acid positions 286-311
/ US-08-569-959-33

Query Match 72.3%; Score 34; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RVFFDY 8
Db 18 RVFFDY 23

RESULT 11
US-08-306-871-28
/ Sequence 28, Application US/08306871
/ Patent No. 5712118
/ GENERAL INFORMATION:
/ APPLICANT: Timothy F. Murphy
/ TITLE OF INVENTION: Vaccine For Branhamella catarrhalis
/ NUMBER OF SEQUENCES: 52
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
/ STREET: 1800 One M&T Plaza
/ CITY: Buffalo
/ STATE: New York
/ COUNTRY: United States
/ ZIP: 14203-2391
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: MS-DOS/ Microsoft Windows 3.1
/ SOFTWARE: Wordperfect for Windows 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/306,871
/ FILING DATE: 20-SEP-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/129,719
/ FILING DATE: September 29, 1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Nelson, M. Bud
/ REGISTRATION NUMBER: 35,300
/ REFERENCE/DOCKET NUMBER: 11520.0053
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (716) 856-4000
/ TELEFAX: (716) 849-0349
/ INFORMATION FOR SEQ ID NO: 28:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 71 residues
/ TYPE: amino acid
/ TOPOLOGY: linear
/ ORGANISM: Branhamella catarrhalis
/ STRAIN: 25240
/ FEATURE:
/ LOCATION: CD amino acid positions 261-331
/ US-08-306-871-28
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Query Match 72.3%; Score 34; DB 1; Length 71;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 RVFFDY 8
DB 43 RVFFDY 48

RESULT 12
US-08-569-959-28
; Sequence 28, Application US/08569959
; Patent No. 5725862
; GENERAL INFORMATION:
; APPLICANT: Timothy F. Murphy
; TITLE OF INVENTION: Vaccine For Branhamella catarrhalis
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
; STREET: 1800 One Mt Plaza
; CITY: Buffalo
; STATE: New York
; COUNTRY: United States
; ZIP: 14203-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Dikette, 3.5 inch, 1.4 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS/ Microsoft Windows 3.1
; SOFTWARE: Wordperfect for Windows 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,959
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/129,719
; FILING DATE: September 29, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Nelson, M. Bud
; REGISTRATION NUMBER: 35,300
; REFERENCE/DOCKET NUMBER: 11520.0053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 856-4000
; TELEFAX: (716) 849-0349
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 71 residues
; TYPE: amino acid
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: Branhamella catarrhalis
; STRAIN: 25240
; FEATURE:
; LOCATION: CD amino acid positions 261-331
US-08-569-959-28

Query Match 72.3%; Score 34; DB 1; Length 71;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 RVFFDY 8
DB 43 RVFFDY 48

RESULT 13
US-08-270-767-61481
; Sequence 61481, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: .7326-094

; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 61481
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-61481

Query Match 72.3%; Score 34; DB 2; Length 92;
Best Local Similarity 62.5%; Pred. No. 38;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 YGRVFFDY 8
DB 84 FGKVFYDY 91

RESULT 14
US-09-027-449-50
; Sequence 50, Application US/09027449
; Patent No. 6025158
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania R.
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/027,449
; FILING DATE: 20-Feb-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/074,330
; FILING DATE: 22-Jan-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/038,664
; FILING DATE: 21-Feb-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R3-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-027-449-50

Query Match 72.3%; Score 34; DB 2; Length 116;
Best Local Similarity 62.5%; Pred. No. 48;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 YGRVFFDY 8
DB 104 YGTVFFDY 111

RESULT 15
US-08-804-444A-50
; Sequence 50, Application US/0880444A
; Patent No: 6117980
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania N
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/804,444A
; FILING DATE: 21-Feb-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-804-444A-50

Query Match 72.3%; Score 34; DB 2; Length 116;
Best Local Similarity 62.5%; Pred. NO. 48;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 YGRVFFDY 8
Db 104 YGTYFDY 111

Search completed: December 30, 2005, 13:37:19
Job time : 17.9355 secs

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OM protein - protein search, using sw model

Run on: December 30, 2005, 13:33:42 ; Search time 59.4839 Seconds
(without alignments)
56.194 Million cell updates/sec

Title: US-10-735-916A-12

Perfect score: 47

Sequence: 1 YGRVFFDY 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA_Main.*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	47	100.0	117	5	US-10-735-916A-75
4	47	100.0	117	5	US-10-735-916A-79
5	47	100.0	117	5	US-10-735-916A-83
6	47	100.0	127	5	US-10-735-916A-52
7	47	100.0	135	5	US-10-735-916A-77
8	47	100.0	135	5	US-10-735-916A-81
9	47	100.0	135	5	US-10-735-916A-85
10	37	78.7	101	4	US-10-424-599-232867
11	37	78.7	264	4	US-10-437-963-122750
12	37	78.7	331	4	US-10-156-761-10380
13	37	78.7	366	6	US-11-083-779-2
14	36	76.6	410	3	US-09-767-041-28
15	35	74.5	1425	6	US-11-097-143-42516
16	34	72.3	12	3	US-09-795-798-12
17	34	72.3	76	4	US-10-424-599-248530
18	34	72.3	116	3	US-09-726-258-50
19	34	72.3	121	3	US-09-795-798-4
20	34	72.3	121	3	US-09-795-798-5
21	34	72.3	121	3	US-09-795-798-24
22	34	72.3	121	4	US-10-727-737-4
23	34	72.3	121	4	US-10-727-737-5
24	34	72.3	121	4	US-10-727-737-17
25	34	72.3	121	5	US-10-877-532-6
26	34	72.3	126	4	US-10-041-860-25
27	34	72.3	126	4	US-10-041-860-210

Sequence 246, App
Sequence 306, App
Sequence 30, Appl
Sequence 190681, A
Sequence 51409, A
Sequence 61737, A
Sequence 7547, Ap
Sequence 331492,
Sequence 4, Appl
Sequence 39, Appl
Sequence 22, Appl
Sequence 196, App
Sequence 7151, Ap
Sequence 234979,
Sequence 191549,
Sequence 15, Appl
Sequence 6258, Ap
Sequence 6259, Ap

ALIGNMENTS

RESULT 1

US-10-735-916A-12
; Sequence 12, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 12
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-735-916A-12

Query Match 100.0%; Score 47; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YGRVFFDY 8
Db 1 YGRVFFDY 8

RESULT 2

US-10-735-916A-69
; Sequence 69, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier

; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10/735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 69
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-735-916A-69

Query Match 100.0%; Score 47; DB 5; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.78;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8
|||
DB 99 YGRVFFDY 106

RESULT 3
US-10-735-916A-75
; Sequence 75, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10/735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 75
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-735-916A-75

Query Match 100.0%; Score 47; DB 5; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.78;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8
|||
DB 99 YGRVFFDY 106

Db 99 YGRVFFDY 106
RESULT 4
US-10-735-916A-79
; Sequence 79, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10/735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-735-916A-79

Query Match 100.0%; Score 47; DB 5; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.78;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8
|||
DB 99 YGRVFFDY 106

RESULT 5
US-10-735-916A-83
; Sequence 83, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10/735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 83

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; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-735-916A-83

Query Match      100.0%; Score 47; DB 5; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.78;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YGRVFFDY 8
      |||||
Db      99 YGRVFFDY 106

RESULT 6
US-10-735-916A-52
; Sequence 52, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10/735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-735-916A-52

Query Match      100.0%; Score 47; DB 5; Length 127;
Best Local Similarity 100.0%; Pred. No. 0.84;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YGRVFFDY 8
      |||||
Db      109 YGRVFFDY 116

RESULT 7
US-10-735-916A-77
; Sequence 77, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10/735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-735-916A-77

Query Match      100.0%; Score 47; DB 5; Length 127;
Best Local Similarity 100.0%; Pred. No. 0.84;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YGRVFFDY 8
      |||||
Db      109 YGRVFFDY 116

RESULT 8
US-10-735-916A-81
; Sequence 81, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10/735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-735-916A-81

Query Match      100.0%; Score 47; DB 5; Length 135;
Best Local Similarity 100.0%; Pred. No. 0.89;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YGRVFFDY 8
      |||||
Db      117 YGRVFFDY 124

RESULT 9
US-10-735-916A-85
; Sequence 85, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
```

; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 01753-183
; CURRENT APPLICATION NUMBER: US/10/735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 85
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-735-916A-85

Query Match 100.0%; Score 47; DB 5; Length 135;
Best Local Similarity 100.0%; Pred. No. 0.89; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8
||| |||||
Db 117 YGRVFFDY 124

RESULT 10
US-10-424-599-232867
; Sequence 232867, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 232867
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(101)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_52303C.1.pep
US-10-424-599-232867

Query Match 78.7%; Score 37; DB 4; Length 101;
Best Local Similarity 75.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8
||| |||||
Db 77 YGRTLFY 84

RESULT 11

US-10-437-963-122750
; Sequence 122750, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 122750
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_2564C.1.pep
US-10-437-963-122750

Query Match 78.7%; Score 37; DB 4; Length 264;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8
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Db 111 YGRIFFIY 118

RESULT 12
US-10-156-761-10380
; Sequence 10380, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 10380
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-10380

Query Match 78.7%; Score 37; DB 4; Length 331;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8
||| |||||
Db 121 YGKGFFDY 128

RESULT 13
US-11-083-779-2

; Sequence 2, Application US/11083779
; Publication No. US20050227292A1
; GENERAL INFORMATION:
; APPLICANT: Malaysian Rubber Board
; APPLICANT: Sunderasan, Elumalai
; APPLICANT: Arif, Siti Ajuma Mad
; APPLICANT: Yeang, Hoong Vest
; TITLE OF INVENTION: AN ALLERGENIC PROTEIN COMPLEX OF NATURAL RUBBER LATEX
; FILE REFERENCE: SHP-PT086
; CURRENT APPLICATION NUMBER: US/11/083,779
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: P120040947
; PRIOR FILING DATE: 2004-03-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Hevea brasiliensis
US-11-083-779-2

Query Match 78.7%; Score 37; DB 6; Length 366;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YGRVFFDY 8
||| |||||
Db 59 YGTTFFDY 66

RESULT 14

US-09-767-041-28
; Sequence 28, Application US/09767041
; Patent No. US20020055168A1
; GENERAL INFORMATION:

; APPLICANT: Smith, Hilda
; TITLE OF INVENTION: STREPTOCOCCUS SUIS VACCINES AND DIAGNOSTIC TESTS
; FILE REFERENCE: 2183-4726
; CURRENT APPLICATION NUMBER: US/09/767,041
; CURRENT FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: PCT/NL99/00460
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: EP98202465.5
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: EP98202467.1
; PRIOR FILING DATE: 1998-07-22
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Streptococcus suis
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: CPS2T
US-09-767-041-28

Query Match 76.6%; Score 36; DB 3; Length 410;
Best Local Similarity 71.4%; Pred. No. 2.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GRVFFDY 8
||: |||
Db 219 GRVFFDY 225

RESULT 15

US-11-097-143-42516
; Sequence 42516, Application US/11097143
; Publication No. US2005020858A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.

; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728

; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42516
; LENGTH: 1425
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-42516

Query Match 74.5%; Score 35; DB 6; Length 1425;
Best Local Similarity 75.0%; Pred. No. 1.2e+03;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YGRVFFDY 8
||| |||
Db 514 YGRVFFDY 521

Search completed: December 30, 2005, 14:15:03
Job time : 64.4839 secs

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QM protein - protein search, using sw model

Run on: December 30, 2005, 13:35:07 ; Search time 2.96774 Seconds
(without alignments)
20.187 Million cell updates/sec

Title: US-10-735-916A-12

Perfect score: 47

Sequence: 1 YGRVFFDY 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 57103

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications AA New:*

- 1: /cgm2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgm2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 3: /cgm2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 4: /cgm2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 5: /cgm2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 6: /cgm2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 7: /cgm2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 8: /cgm2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	8	7	US-11-012-353-12
2	47	100.0	117	7	US-11-012-353-69
3	47	100.0	117	7	US-11-012-353-75
4	47	100.0	117	7	US-11-012-353-79
5	47	100.0	117	7	US-11-012-353-83
6	47	100.0	117	7	US-11-012-353-162
7	47	100.0	127	7	US-11-012-353-52
8	47	100.0	135	7	US-11-012-353-77
9	47	100.0	135	7	US-11-012-353-81
10	47	100.0	135	7	US-11-012-353-85
11	34	72.3	12	6	US-10-665-658-12
12	34	72.3	121	6	US-10-665-658-4
13	34	72.3	121	6	US-10-665-658-5
14	34	72.3	121	6	US-10-665-658-24
15	34	72.3	121	7	US-11-107-028-50
16	34	72.3	121	7	US-11-107-028-52
17	33	70.2	341	6	US-10-467-657-154
18	33	70.2	341	6	US-10-467-657-5822
19	33	70.2	341	6	US-10-467-657-7476
20	32	68.1	120	6	US-10-932-334-71
21	32	68.1	120	6	US-10-932-334-72
22	32	68.1	216	6	US-10-467-657-8102
23	31	66.0	161	6	US-10-467-657-8822
24	31	66.0	167	6	US-10-967-457-79
25	31	66.0	312	7	US-11-129-143-94

Sequence 1606, Ap
Sequence 54, Appl
Sequence 1097, Ap
Sequence 4, Appl
Sequence 2, Appl
Sequence 51, Appl
Sequence 10, Appl
Sequence 8, Appl
Sequence 2207, Ap
Sequence 2374, Ap
Sequence 3148, Ap
Sequence 1899, Ap
Sequence 199, App
Sequence 983, App
Sequence 950, App
Sequence 2608, Ap
Sequence 476, App
Sequence 1770, App
Sequence 208, App
Sequence 227, App

ALIGNMENTS

RESULT 1

US-11-012-353-12

; Sequence 12, Application US/11012353

; Publication No. US20050249730A1

; GENERAL INFORMATION:

; APPLICANT: GOETSCH, LILIANE

; APPLICANT: CORVAIA, NATHALIE

; APPLICANT: DUFLLOS, ALAIN

; APPLICANT: HAEUW, JEAN-FRANCOIS

; APPLICANT: LEGER, OLIVIER

; APPLICANT: BECK, ALAIN

; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF

; FILE REFERENCE: 017753-198

; CURRENT APPLICATION NUMBER: US/11/012,353

; CURRENT FILING DATE: 2004-12-16

; PRIOR APPLICATION NUMBER: 10/735,916

; PRIOR FILING DATE: 2003-12-16

; PRIOR APPLICATION NUMBER: FR 0308538

; PRIOR FILING DATE: 2003-07-11

; PRIOR APPLICATION NUMBER: PCT/FR03/00178

; PRIOR FILING DATE: 2003-01-20

; PRIOR APPLICATION NUMBER: FR 0205753

; PRIOR FILING DATE: 2002-05-07

; PRIOR APPLICATION NUMBER: FR 0200653

; PRIOR FILING DATE: 2002-01-18

; PRIOR APPLICATION NUMBER: FR 0200654

; PRIOR FILING DATE: 2002-01-18

; NUMBER OF SEQ ID NOS: 162

; SOFTWARE: PatentIn Ver. 3.3

; SEQ ID NO 12

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Mus musculus

US-11-012-353-12

Query Match 100.0%; Score 47; DB 7; Length 8;

Best Local Similarity 100.0%; Pred. No. 4.4e+04;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRVFFDY 8

Db 1 YGRVFFDY 8

RESULT 2

US-11-012-353-69

; Sequence 69, Application US/11012353

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; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETTSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 69
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-012-353-69

Query Match      100.0%; Score 47; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YGRVFFDY 8
Db      99 YGRVFFDY 106

RESULT 3
US-11-012-353-75
; Sequence 75, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETTSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 75
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-012-353-79

Query Match      100.0%; Score 47; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YGRVFFDY 8
Db      99 YGRVFFDY 106

RESULT 4
US-11-012-353-79
; Sequence 79, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETTSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 79
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-012-353-79

Query Match      100.0%; Score 47; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YGRVFFDY 8
Db      99 YGRVFFDY 106

RESULT 5
US-11-012-353-83
; Sequence 83, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETTSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-198
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; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 77
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-012-353-77

Query Match 100.0%; Score 47; DB 7; Length 135;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8
|||
Db 117 YGRVFFDY 124

RESULT 9

US-11-012-353-81
; Sequence 81, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN

; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16

; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 81
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-012-353-81

Query Match 100.0%; Score 47; DB 7; Length 135;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8
|||
Db 117 YGRVFFDY 124

RESULT 10

US-11-012-353-85
; Sequence 85, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN

; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 85
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-012-353-85

Query Match 100.0%; Score 47; DB 7; Length 135;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8
|||
Db 117 YGRVFFDY 124

RESULT 11

US-10-665-658-12
; Sequence 12, Application US/10665658
; Publication No. US20050276801A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 27-NOV-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001
ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.

REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-665-658-12

Query Match 72.3%; Score 34; DB 6; Length 12;
Best Local Similarity 62.5%; Pred. No. 0.74; 2; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YGRVFFDY 8
Db 5 YGTYFFDY 12

RESULT 12

US-10-665-658-4
; Sequence 4, Application US/10665658
; Publication No. US20050276801A1
; GENERAL INFORMATION:
; APPLICANT: Jardiou, Paula M.
; Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/665,658
; FILING DATE: 19-Sep-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 27-Nov-1996
; APPLICATION NUMBER: 08/974899
; FILING DATE: 20-Nov-1997
; APPLICATION NUMBER: 09/420745
; FILING DATE: 20-Oct-1999
; APPLICATION NUMBER: 09/975798
; FILING DATE: 28-Feb-2001
; ATTORNEY/AGENT INFORMATION:
; NAME: Tan, Lee K.
; REGISTRATION NUMBER: 39,447
; REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
; TELEPHONE: 650/225-4462
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-665-658-4

Query Match 72.3%; Score 34; DB 6; Length 121;
Best Local Similarity 62.5%; Pred. No. 5.7; 2; Indels 0; Gaps 0;

Qy 1 YGRVFFDY 8
Db 103 YGTYFFDY 110

RESULT 14

US-10-665-658-24
; Sequence 24, Application US/10665658
; Publication No. US20050276801A1
; GENERAL INFORMATION:
; APPLICANT: Jardiou, Paula M.
; Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YGRVFFDY 8
Db 103 YGTYFFDY 110

RESULT 13

US-10-665-658-5
; Sequence 5, Application US/10665658
; Publication No. US20050276801A1
; GENERAL INFORMATION:
; APPLICANT: Jardiou, Paula M.
; Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/665,658
; FILING DATE: 19-Sep-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 27-Nov-1996
; APPLICATION NUMBER: 08/974899
; FILING DATE: 20-Nov-1997
; APPLICATION NUMBER: 09/420745
; FILING DATE: 20-Oct-1999
; APPLICATION NUMBER: 09/975798
; FILING DATE: 28-Feb-2001
; ATTORNEY/AGENT INFORMATION:
; NAME: Tan, Lee K.
; REGISTRATION NUMBER: 39,447
; REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
; TELEPHONE: 650/225-4462
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-665-658-5

Query Match 72.3%; Score 34; DB 6; Length 121;
Best Local Similarity 62.5%; Pred. No. 5.7; 2; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YGRVFFDY 8
Db 103 YGTYFFDY 110

RESULT 14

US-10-665-658-24
; Sequence 24, Application US/10665658
; Publication No. US20050276801A1
; GENERAL INFORMATION:
; APPLICANT: Jardiou, Paula M.
; Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies

NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 27-NOV-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001
ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-665-658-24

Query Match 72.3%; Score 34; DB 6; Length 121;
Best Local Similarity 62.5%; Pred. No. 5.7;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8
||| :|||
Db 103 YGTTYFDY 110

RESULT 15
US-11-107-028-50
; Sequence 50, Application US/11107028
; Publication No. US20050276803A1
; GENERAL INFORMATION:
; APPLICANT: CHAN, ANDREW C.
; APPLICANT: GONG, QIAN
; APPLICANT: MARTIN, FLAVIUS
; TITLE OF INVENTION: Method for Augmenting B Cell Depletion
; FILE REFERENCE: P2112R1
; CURRENT APPLICATION NUMBER: US/11/107,028
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,263
; PRIOR FILING DATE: 2004-04-16
; NUMBER OF SEQ ID NOS: 52
; SEQ ID NO 50
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-107-028-50

Query Match 72.3%; Score 34; DB 7; Length 121;
Best Local Similarity 62.5%; Pred. No. 5.7;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8
||| :|||
Db 103 YGTTYFDY 110

Search completed: December 30, 2005, 14:15:22
Job time : 2.96774 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2005, 15:35:45 ; Search time 182 Seconds
(without alignments)
19.313 Million cell updates/sec

Title: US-10-735-916A-12
Perfect score: 47
Sequence: 1 YGRVFDY 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 49824

Minimum DB seq length: 8
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	8	7	ADJ76846
2	47	100.0	8	9	ADZ67016
3	28	59.6	8	2	AAR80018
4	28	59.6	8	2	AAR84899
5	28	59.6	8	2	AAW40865
6	28	59.6	8	2	AAW10595
7	28	59.6	8	2	AAW10107
8	28	59.6	8	5	ABG80278
9	28	59.6	8	5	ABG79790
10	28	59.6	8	8	ADK68717
11	28	59.6	8	8	ADK69224
12	28	59.6	8	8	ADJ84659
13	28	59.6	8	8	ADQ11023
14	28	59.6	8	8	ADQ10515
15	28	59.6	8	8	ADQ80395
16	28	59.6	8	8	ADS81503
17	26	55.3	8	5	ABP47168
18	26	55.3	8	7	ADG97995
19	25	53.2	8	3	AAV77587
20	25	53.2	8	4	ABW78856
21	25	53.2	8	5	ABG98099
22	25	53.2	8	5	AAE28157
23	25	53.2	8	6	ABP74517
24	25	53.2	8	7	ABR61876

25	25	53.2	8	7	ADC09376
26	25	53.2	8	8	ADL11879
27	25	53.2	8	8	ADP84864
28	25	53.2	8	8	ADQ31285
29	25	53.2	8	9	ADZ58521
30	25	53.2	8	9	AEA40143
31	25	53.2	8	9	AEA38763
32	25	53.2	8	9	AEA38795
33	25	53.2	8	9	AEA53829
34	25	53.2	8	9	AEA53800
35	25	53.2	8	9	AEA53496
36	25	53.2	8	9	AEA45972
37	24	51.1	8	5	AAU99851
38	24	51.1	8	7	AAO29925
39	24	51.1	8	8	ADJ87910
40	23	48.9	8	2	AAW29379
41	23	48.9	8	2	AAW28181
42	23	48.9	8	4	AAW98001
43	23	48.9	8	5	ABB76371
44	23	48.9	8	8	ADO05137
45	23	48.9	8	8	ADR04717

ALIGNMENTS

RESULT 1
ADJ76846
ID ADJ76846 standard; peptide; 8 AA.
XX
AC ADJ76846;
XX
DT 06-MAY-2004 (first entry)
XX
DE CDR sequence for anti-IGF-1R antibody.
XX
KW cytostatic; antipsoriatic; antibody;
KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;
KW or epidermal growth factor receptor; EGFR; signal transduction pathway;
KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;
KW CDR.
XX
OS Mus musculus.
XX
FN WO2003059951-A2.
XX
PD 24-JUL-2003.
XX
PF 20-JAN-2003; 2003WO-FR000178.
XX
18-JAN-2002; 2002FR-00000653.
PR 18-JAN-2002; 2002FR-00000654.
PR 07-MAY-2002; 2002FR-00005753.
XX
FA (FABR) FABRE MEDICAMENT SA PIERRE.
XX
PI Goetsch L, Corvaia N, Leger O;
XX
WPI; 2003-569653/53.
DR N-PSDB; ADJ76845.
XX
New antibodies that bind to human insulin-like growth factor receptor,
useful for treatment, prevention and diagnosis of cancers.
XX
Claim 1; SEQ ID NO 12; 164pp; French.
XX
The invention relates to an isolated antibody (Ab), and its functional
fragments, that bind to human insulin-like growth factor-1 receptor (IGF-
1R) and optionally: (i) inhibit natural binding of insulin-like growth
factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine
kinase activity of IGF-1R. Ab and its fragments are used to prevent or
treat diseases associated with overexpression and/or abnormal activity of
IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with

CC hyperactivity of signal transduction pathways mediated by interaction of
 CC these receptors with their ligands. Especially they inhibit
 CC transformation of normal cells to tumor cells, inhibit growth and/or
 CC proliferation of tumor cells, so are useful against cancers of the
 CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
 CC also for treating psoriasis. Ab are also used to diagnose diseases caused
 CC by abnormal expression of IGF-IR and/or EGFR. This sequence represents an
 CC CDR sequence used to generate the Ab of the invention.

XX SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 7; Length 8;

Best Local Similarity 100.0%; Pred. No. 2e+06; Indels 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8

Db 1 YGRVFFDY 8

RESULT 2

ID ADZ67016

AC ADZ67016 standard; peptide; 8 AA.

XX ADZ67016;

XX 30-JUN-2005 (first entry)

XX Murine insulin-like growth factor T receptor IGF-IR CDR SEQ ID NO:12.

XX Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
 XX neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;
 XX musculoskeletal disease; respiratory disease; lung tumor;
 XX endocrine disease; gynecology and obstetrics; breast tumor;
 XX endometrial carcinoma; gastrointestinal disease; colon tumor;
 XX antipsoriatic; psoriasis; dermatological disease; immune disorder.

OS Mus musculus.

XX US2005084906-A1.

XX 21-APR-2005.

XX 16-DEC-2003; 2003US-00735916.

XX 18-JAN-2002; 2002FR-00000653.

XX 18-JAN-2002; 2002FR-00000654.

XX 07-MAY-2002; 2002FR-00005753.

XX 20-JAN-2003; 2003WO-FR000178.

XX 11-JUL-2003; 2003FR-00008538.

XX (GOET/) GOETSCH L.

XX (CORV/) CORVAIA N.

XX (LEGE/) LEGER O.

XX (DUFLO/) DUFLOS A.

XX (HAEU/) HAEUW J.

XX (BECK/) BECK A.

XX Goetsch L, Corvaia N, Leger O, Duflos A, Haeuw J, Beck A;

XX WPI; 2005-321968/33.

XX N-PSDB; ADZ67015.

XX Novel isolated anti-insulin-like growth factor I receptor (IGF-IR)
 XX antibody or its functional fragment, being capable of binding human IGF-
 XX IR and specifically inhibiting tyrosine kinase activity of receptor,
 XX useful for treating cancer.

XX Claim 1; SEQ ID NO 12; 125pp; English.

XX The invention relates to a novel isolated anti-insulin-like growth factor
 XX I receptor (IGF-IR) antibody (I) or its functional fragment, being
 XX capable of binding to human IGF-IR and, if necessary, capable of

CC specifically inhibiting tyrosine kinase activity of the receptor,
 CC comprising a light or heavy chain having at least one complementary
 CC determining region (CDR) consisting of one of two fully defined 16 amino
 CC acids (ADZ67006 and ADZ67014). An antibody of the invention is useful in
 CC the preparation of a medicament intended for the prevention or treatment
 CC of an illness connected with an overexpression and/or an abnormal
 CC activation of the IGF-IR and/or EGFR, and/or connected with a
 CC hyperactivation of the transduction pathway of the signal mediated by the
 CC interaction of IGF1 or IGF2 with IGF-IR and/or of EGF with EGFR, where
 CC the administration of the medicament does not induce or only slightly
 CC induces secondary effects connected with inhibition of the insulin
 CC receptor. The antibody is useful for preparation of a medicament intended
 CC to inhibit the transformation of normal cells into cells with tumoral
 CC character, preferably IGF-dependent, especially IGF1 and/or IGF2-
 CC dependent and/or EGF-dependent and/or HER2/neu-dependent cells. (I) is
 CC useful for preparation of a medicament intended to inhibit the growth
 CC and/or the proliferation of tumor cells, preferably IGF-dependent,
 CC especially IGF1-and/or IGF2-dependent and/or EGF-dependent and/or
 CC HER2/neu-dependent cells. (I) is useful in the preparation of a
 CC medicament intended for prevention or for the treatment of cancer, where
 CC the cancer is chosen from prostate cancer, osteosarcoma, lung cancer,
 CC breast cancer, endometrial cancer or colon cancer. (I) is useful in the
 CC preparation of a medicament intended for the prevention or for the
 CC treatment of psoriasis. (I) is useful in preparation of a medicament
 CC intended for the specific targeting of the IGF-IR and/or EGFR receptor. (I)
 CC cells expressing or overexpressing the IGF-IR and/or EGFR receptor. (I)
 CC is useful for in vitro diagnosis of illnesses induced by an
 CC overexpression or an underexpression of the IGF-IR and/or EGFR receptor
 CC starting from a biological sample in which the abnormal presence, of IGF-
 CC IR and/or EGFR receptor is suspected, which involves contacting the
 CC biological sample with (I), which is optionally labeled. The present
 CC sequence is used in the exemplification of the invention.

XX SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 9; Length 8;

Best Local Similarity 100.0%; Pred. No. 2e+06; Indels 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8

Db 1 YGRVFFDY 8

RESULT 3

AA80018

ID AA80018 standard; peptide; 8 AA.

XX AA80018;

XX 16-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 24-APR-1996 (first entry)

XX Cytotoxic Epstein-Barr virus T-cell epitope.

XX Epitope; EBV; cytotoxic T cell; lymphocyte; vaccine; immunisation; CD8+.

XX Human herpesvirus 4.

XX WO9524925-A1.

XX 21-SEP-1995.

XX 16-MAR-1995; 95WO-AU000140.

XX 16-MAR-1994; 94AU-00004465.

XX (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.

XX (CSIR) COMMONWEALTH SCI & IND RES ORG.

XX (UYME) UNIV MELBOURNE.

XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.

XX (BIOT-) BIOTECH AUSTRALIA PTY LTD.

PA (CSLC-) CSL LTD.
 XX Moss DJ, Burrows SR, Khanna R, Kerr BM, Burrows JM, Suhribier A;
 XX WPI; 1995-336817/43.
 XX New cytotoxic T-cell epitope(s) of Epstein Barr virus - useful in sub-
 XX unit vaccines to induce cytotoxic T cells.
 XX Claim 1; Page 15; 23pp; English.
 XX PS
 XX New cytotoxic T-cell epitopes of Epstein-Barr virus have been isolated
 XX and purified (AAR80017-R80028). Variants of these epitopes have also been
 XX identified (AAR80029-R80033). The epitopes are small, stable peptides
 XX whose manufacture does not involve use of any infectious material. The
 XX epitopes may be used as components of subunit vaccines to induce
 XX cytotoxic T lymphocytes in a subject. The vaccines are partic. useful
 XX against viral infections where CD8+ cytotoxic T lymphocytes are
 XX protective. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 16-
 XX OCT-2003 to standardise OS field)
 XX SQ Sequence 8 AA;
 Query Match 59.6%; Score 28; DB 2; Length 8;
 Best Local Similarity 80.0%; Pred. No. 2e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 4 VFDDY 8
 Db :|||
 4 IFDDY 8
 RESULT 4
 ID AAR84899 standard; peptide; 8 AA.
 XX AAR84899;
 AC
 XX 27-AUG-2003 (revised)
 DT 25-APR-1996 (first entry)
 XX Epstein-Barr virus derived cytotoxic T cell epitope.
 DE
 XX Cytotoxic T cell; epitope; vaccine; antigen; tetanus; toxoid; helper;
 KW poliovirus; diphtheria.
 XX Human herpesvirus 4.
 OS
 XX WO9524926-A1.
 PN
 XX 21-SEP-1995.
 PD
 XX 16-MAR-1995; 95WO-AU000141.
 PF
 XX 16-MAR-1994; 94AU-00004465.
 PR
 XX (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
 PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
 PA (UYME) UNIV MELBOURNE.
 PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 PA (BIOT-) BIOTECH AUSTRALIA PTY LTD.
 PA (CSLC-) CSL LTD.
 XX Cox JC, Suhribier A, Elliott SL;
 PI
 XX WPI; 1995-336818/43.
 DR
 XX Compsn. for induction of cytotoxic T cells - comprising CTL epitope and
 PT at least one antigen, in a water in oil formulation.
 XX Claim 6; Page 23; 35pp; English.
 XX A water in oil compsn. comprising at least 1 antigen to which an

CC individual will mount an anamnestic response, and at least one cytotoxic
 CC T cell (CTL) epitope can be used to induce CD8+ CTL cells in a vaccine,
 CC where the CTL epitope is known. The antigen is a diphtheria toxoid, a
 CC pertussis or poliovirus antigen, a helper epitope or esp. a tetanus
 CC toxoid, and the CTL epitope is 1 of the Epstein-Barr virus derived
 CC peptides AAR84898-910. (Updated on 27-AUG-2003 to correct OS field.)
 XX SQ Sequence 8 AA;
 Query Match 59.6%; Score 28; DB 2; Length 8;
 Best Local Similarity 80.0%; Pred. No. 2e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 4 VFDDY 8
 Db :|||
 4 IFDDY 8
 RESULT 5
 ID AAW40865 standard; peptide; 8 AA.
 XX AAW40865;
 AC
 XX 09-JUN-1998 (first entry)
 DT
 XX Cytotoxic Epstein-Barr T-cell epitope 38.
 DE
 XX Herpes simplex virus type 4; Epstein-Barr virus; EBV; cytotoxic;
 KW T-cell epitope; nuclear antigen; human leukocyte antigen; HLA; vaccine;
 KW tetanus toxoid; diphtheria toxoid; Bordetella pertussis;
 KW poliovirus antigen.
 XX Herpes simplex virus 4.
 OS
 XX WO9745444-A1.
 PN
 XX 04-DEC-1997.
 PD
 XX 23-MAY-1997; 97WO-AU000328.
 PF
 XX 24-MAY-1996; 96AU-00000073.
 PR
 XX (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
 PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
 PA (UYME) UNIV MELBOURNE.
 PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 PA (BIOT-) BIOTECH AUSTRALIA PTY LTD.
 PA (CSLC-) CSL LTD.
 XX Khanna R, Kerr BM, Misko IS, Moss DJ, Burrows SR;
 FI
 XX WPI; 1998-032576/03.
 DR
 XX Cytotoxic Epstein-Barr virus T cell epitope - useful to prepare vaccine
 PT to prevent and treat infection.
 XX Claim 3; Page 32; 41pp; English.
 PS
 XX This amino acid sequence is a cytotoxic Epstein-Barr virus (EBV) T-cell
 XX epitope of the EBV nuclear antigen 3A (EBNA3A), which binds the human
 XX leukocyte antigen acceptor 24 (HLA 24). It is used to prepare a vaccine
 XX which may include the cytotoxic EBV T-cell epitope (AAW40828- AAW40846),
 XX or a nucleic acid sequence encoding it. The vaccine produced comprises or
 XX encode at least one antigen (AAW40847-W40876) to which the individual
 XX will mount an anamnestic response, e.g. a tetanus toxoid, diphtheria
 XX toxoid, Bordetella pertussis antigen, poliovirus antigen, purified
 XX protein derivative, glycoprotein 350 protein, and/or helper epitope
 XX SQ Sequence 8 AA;
 Query Match 59.6%; Score 28; DB 2; Length 8;
 Best Local Similarity 80.0%; Pred. No. 2e+06;

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Matches      4;  Conservative      1;  Mismatches      0;  Indels      0;  Gaps      0;

QY      4 VFPDY 8
      :||||
Db      4 IFPDY 8

RESULT 6
AAY10595
ID      AAY10595 standard; peptide; 8 AA.
AC      AAY10595;
XX
DT      12-MAY-1999 (first entry)
XX
DE      HLA Class I motif peptide SEQ ID NO:525.
XX
KW      Cytotoxic T-lymphocyte response; CTL; antigen; lymphatic system;
KW      immunisation; tumour; infectious disease; immunotherapy; cancer;
KW      malignant melanoma; viral disease; hepatitis; AIDS.
XX
OS      Synthetic.
OS      Human herpesvirus 4.
XX
PN      WO9902183-A2.
XX
PD      21-JAN-1999.
XX
PF      10-JUL-1998; 98WO-US014289.
XX
PR      10-JUL-1997; 97CA-02209815.
PR      10-DEC-1997; 97US-00988320.
XX
PA      (CTLI-) CTL IMMUNOTHERAPIES CORP.
XX
PI      Kuendig TM, Simard JUL;
XX
DR      WPI; 1999-120514/10.
XX
PT      Inducing a cytotoxic T lymphocyte response - by maintaining a level of
PT      antigen in the lymphatic system of a mammal so as to provide a sustained
PT      CTL response, used to treat, e.g. AIDS.
XX
PS      Disclosure; Page 49; 199pp; English.
XX
CC      The present invention describes a method of inducing and/or sustaining an
CC      immunological cytotoxic T lymphocyte (CTL) response in a mammal. The
CC      method comprises: (a) delivering an antigen to the mammal at a level to
CC      induce an immunological CTL response in the mammal; and (b) maintaining
CC      the level of the antigen in the mammal's lymphatic system to maintain the
CC      immunologic CTL response. The method can be used for the delivery of e.g.
CC      a differentiation antigen, a tumour-specific multilineage antigen, an
CC      embryonic antigen, an oncogene antigen, a mutated tumour-suppressor gene
CC      antigen, or a viral antigen. They can be used for the treatment of
CC      disease such as cancer, e.g. malignant melanoma or infectious disease,
CC      e.g. viral disease such as hepatitis or AIDS. Sustained antigen delivery
CC      to the lymphatic system provides for potent CTL stimulation that takes
CC      place in the milieu of the lymphoid organ, and it sustains stimulation
CC      that is necessary to keep CTL active, cytotoxic and recirculating through
CC      the body. AAY10071 to AAY10639 represent examples of peptide antigens
CC      given in the present invention
XX
SQ      Sequence 8 AA;

Query Match      59.6%; Score 28; DB 2; Length 8;
Best Local Similarity 80.0%; Pred. No. 2e+06;
Matches      4;  Conservative      1;  Mismatches      0;  Indels      0;  Gaps      0;

QY      4 VFPDY 8
      :||||
Db      4 IFPDY 8

RESULT 8
ABG80278
ID      ABG80278 standard; peptide; 8 AA.
XX
AC      ABG80278;
XX
DT      29-AUG-2003 (revised)

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RESULT 7
AAY10107
ID      AAY10107 standard; peptide; 8 AA.
XX
AC      AAY10107;
XX
DT      12-MAY-1999 (first entry)
XX
DE      T cell epitope/MHC ligand SEQ ID NO:37.
XX
KW      Cytotoxic T-lymphocyte response; CTL; antigen; lymphatic system;
KW      immunisation; tumour; infectious disease; immunotherapy; cancer;
KW      malignant melanoma; viral disease; hepatitis; AIDS.
XX
OS      Synthetic.
OS      Human herpesvirus 4.
XX
PN      WO9902183-A2.
XX
PD      21-JAN-1999.
XX
PF      10-JUL-1998; 98WO-US014289.
XX
PR      10-JUL-1997; 97CA-02209815.
PR      10-DEC-1997; 97US-00988320.
XX
PA      (CTLI-) CTL IMMUNOTHERAPIES CORP.
XX
PI      Kuendig TM, Simard JUL;
XX
DR      WPI; 1999-120514/10.
XX
PT      Inducing a cytotoxic T lymphocyte response - by maintaining a level of
PT      antigen in the lymphatic system of a mammal so as to provide a sustained
PT      CTL response, used to treat, e.g. AIDS.
XX
PS      Disclosure; Page 24; 199pp; English.
XX
CC      The present invention describes a method of inducing and/or sustaining an
CC      immunological cytotoxic T lymphocyte (CTL) response in a mammal. The
CC      method comprises: (a) delivering an antigen to the mammal at a level to
CC      induce an immunological CTL response in the mammal; and (b) maintaining
CC      the level of the antigen in the mammal's lymphatic system to maintain the
CC      immunologic CTL response. The method can be used for the delivery of e.g.
CC      a differentiation antigen, a tumour-specific multilineage antigen, an
CC      embryonic antigen, an oncogene antigen, a mutated tumour-suppressor gene
CC      antigen, or a viral antigen. They can be used for the treatment of
CC      disease such as cancer, e.g. malignant melanoma or infectious disease,
CC      e.g. viral disease such as hepatitis or AIDS. Sustained antigen delivery
CC      to the lymphatic system provides for potent CTL stimulation that takes
CC      place in the milieu of the lymphoid organ, and it sustains stimulation
CC      that is necessary to keep CTL active, cytotoxic and recirculating through
CC      the body. AAY10071 to AAY10639 represent examples of peptide antigens
CC      given in the present invention
XX
SQ      Sequence 8 AA;

Query Match      59.6%; Score 28; DB 2; Length 8;
Best Local Similarity 80.0%; Pred. No. 2e+06;
Matches      4;  Conservative      1;  Mismatches      0;  Indels      0;  Gaps      0;

QY      4 VFPDY 8
      :||||
Db      4 IFPDY 8

RESULT 8
ABG80278
ID      ABG80278 standard; peptide; 8 AA.
XX
AC      ABG80278;
XX
DT      29-AUG-2003 (revised)

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DT 15-NOV-2002 (first entry)
 XX MHC class I molecule, viral epitope #526.
 DE
 XX Major histocompatibility complex; MHC; MHC class I molecule; virus;
 KW epitope; cytotoxic T lymphocyte response; CTL response; lymphatic system;
 KW antigen; immunogenic; malignant tumour; carcinoma; melanoma; leukaemia;
 KW lymphoma; infectious disease; hepatitis; malaria; measles; tuberculosis;
 KW acquired immune deficiency syndrome; AIDS.
 XX
 OS Viruses.
 XX WO200262368-A2.
 XX 15-AUG-2002.
 XX 22-JAN-2002; 2002WO-US002033.
 XX 02-FEB-2001; 2001US-00776232.
 XX (CTLI-) CTL IMMUNOTHERAPIES CORP.
 XX Kundig TM, Simard JLL;
 XX WPI; 2002-657506/70.
 XX Inducing or sustaining immunological cytotoxic T lymphocyte response in a
 PT mammal, useful for treating a mammal with malignant tumor or infectious
 PT disease, by directly administering an antigen to the lymphatic system of
 PT the mammal.
 XX
 PS Disclosure; Page 42; 73pp; English.
 XX The invention relates to a method of inducing and/or sustaining an
 CC immunological cytotoxic T lymphocyte (CTL) response in a mammal
 CC comprising administering directly to the lymphatic system of the mammal:
 CC (a) an antigen in the form of a polypeptide; (b) a vector comprising a
 CC nucleic acid encoding the antigen; or (c) a non-peptide antigen. The
 CC method is useful for inducing and/or sustaining CTL response in a mammal.
 CC This is particularly useful for treating a mammal having a malignant
 CC tumour (e.g. carcinoma, melanoma, leukaemia or lymphoma) or infectious
 CC disease (e.g. hepatitis, acquired immune deficiency syndrome (AIDS),
 CC malaria, measles or tuberculosis), or in an animal having a
 CC predilection to these diseases. The mammal may be dogs, cats, mice,
 CC cattle, sheep, pigs, goats, rabbits, or preferably humans. ABG79753-
 CC ABG80319 represent viral epitopes on major histocompatibility complex
 CC (MHC) class I molecules, used in the method of the invention. (Updated on
 CC 29-AUG-2003 to standardise OS field)
 XX
 SQ Sequence 8 AA;
 Query Match 59.6%; Score 28; DB 5; Length 8;
 Best Local Similarity 80.0%; Pred. No. 2e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 4 VFFDY 8
 :|||
 Db 4 IFFDY 8
 RESULT 9
 ABG79790
 ID ABG79790 standard; peptide; 8 AA.
 XX
 AC ABG79790;
 XX
 DT 06-AUG-2003 (revised)
 DT 15-NOV-2002 (first entry)
 XX
 DE MHC class I molecule, viral epitope #38.
 XX Major histocompatibility complex; MHC; MHC class I molecule; virus;
 KW epitope; cytotoxic T lymphocyte response; CTL response; lymphatic system;
 KW

KW antigen; immunogenic; malignant tumour; carcinoma; melanoma; leukaemia;
 KW lymphoma; infectious disease; hepatitis; malaria; measles; tuberculosis;
 XX acquired immune deficiency syndrome; AIDS.
 OS Cercopithecine herpesvirus 15.
 XX WO200262368-A2.
 XX 15-AUG-2002.
 XX 22-JAN-2002; 2002WO-US002033.
 XX 02-FEB-2001; 2001US-00776232.
 XX (CTLI-) CTL IMMUNOTHERAPIES CORP.
 XX Kundig TM, Simard JLL;
 XX WPI; 2002-657506/70.
 XX Inducing or sustaining immunological cytotoxic T lymphocyte response in a
 PT mammal, useful for treating a mammal with malignant tumor or infectious
 PT disease, by directly administering an antigen to the lymphatic system of
 PT the mammal.
 XX
 PS Disclosure; Page 18; 73pp; English.
 XX The invention relates to a method of inducing and/or sustaining an
 CC immunological cytotoxic T lymphocyte (CTL) response in a mammal
 CC comprising administering directly to the lymphatic system of the mammal:
 CC (a) an antigen in the form of a polypeptide; (b) a vector comprising a
 CC nucleic acid encoding the antigen; or (c) a non-peptide antigen. The
 CC method is useful for inducing and/or sustaining CTL response in a mammal.
 CC This is particularly useful for treating a mammal having a malignant
 CC tumour (e.g. carcinoma, melanoma, leukaemia or lymphoma) or infectious
 CC disease (e.g. hepatitis, acquired immune deficiency syndrome (AIDS),
 CC malaria, measles or tuberculosis), or in an animal having a
 CC predilection to these diseases. The mammal may be dogs, cats, mice,
 CC cattle, sheep, pigs, goats, rabbits, or preferably humans. ABG79753-
 CC ABG80319 represent viral epitopes on major histocompatibility complex
 CC (MHC) class I molecules, used in the method of the invention. (Updated on
 CC 06-AUG-2003 to correct OS field)
 XX
 SQ Sequence 8 AA;
 Query Match 59.6%; Score 28; DB 5; Length 8;
 Best Local Similarity 80.0%; Pred. No. 2e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 4 VFFDY 8
 :|||
 Db 4 IFFDY 8
 RESULT 10
 ADK68717
 ID ADK68717 standard; peptide; 8 AA.
 XX
 AC ADK68717;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Epitope liberation-related peptide SeqID80.
 XX
 DE epitope liberation; substrate; proteasome; cytostatic; antibacterial;
 KW protozoacide; fungicide; T-cell activator; vaccine; housekeeping epitope;
 KW cytotoxic T lymphocyte; CTL; adoptive immunotherapy; neoplastic cell;
 KW virus; bacterium; protozoan; fungus; housekeeping proteasome system.
 XX
 OS Human herpesvirus 4.
 XX
 PN US2003228634-A1.
 XX

PD 11-DEC-2003.
 XX
 PF 07-NOV-2002; 2002US-00292413.
 XX
 PR 07-NOV-2001; 2001US-0336968P.
 XX
 PR (SIMA/) SIMARD J J L.
 PA (DIAM/) DIAMOND D C.
 PA (QIUZ/) QIU Z.
 PA (LEIX/) LEI X.
 XX
 PI Simard J J L, Diamond DC, Qiu Z, Lei X;
 XX
 DR WPI; 2004-167209/16.
 XX
 XX Identifying polypeptide suitable for epitope e.g., housekeeping epitope,
 PT liberation by contacting substrate polypeptide comprising epitope of
 PT interest, with proteasome, and assaying for liberation of epitope.
 XX
 PS Disclosure; SEQ ID NO 80; 67pp; English.
 XX
 CC This invention relates to a novel method of identifying a polypeptide
 CC suitable for epitope liberation, including the steps of identifying an
 CC epitope of interest; providing substrate polypeptide sequence including
 CC the epitope, wherein the substrate permits processing by a proteasome;
 CC contacting the substrate with a composition including the proteasome;
 CC under conditions that support processing of the substrate by proteasome;
 CC and assaying for liberation of epitope. The invention may be useful for
 CC the development of compounds with a cytostatic, antibacterial,
 CC protozoacide or fungicide activity acting as T-cell activators. In
 CC addition, the invention may allow development of a vaccine. The invention
 CC is useful for identifying a polypeptide suitable for epitope liberation,
 CC where the epitope is a housekeeping epitope. The compositions comprising
 CC the identified housekeeping epitopes are useful in vitro in vaccine
 CC development or in the generation or expansion of cytotoxic T lymphocyte
 CC (CTL) to be used in adoptive immunotherapy. The invention is also useful
 CC for activating T-cells against neoplastic cells, and cells infected with
 CC virus, bacterium, protozoan or fungus. CTL epitopes are identified based
 CC on the knowledge that such epitopes are, in fact, produced by the
 CC housekeeping proteasome system. Once identified, these epitopes, embodied
 CC as peptides, can be used to successfully immunise or induce therapeutic
 CC CTL responses against housekeeping proteasome expressing target cells in
 CC the host. The present sequence is that of a peptide which is related to
 CC the method of the invention.
 XX
 SQ Sequence 8 AA;
 Query Match 59.6%; Score 28; DB 8; Length 8;
 Best Local Similarity 80.0%; Pred. No. 2e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 4 VFFDY 8
 :|||
 Db 4 IFPDY 8
 :|||
 RESULT 11
 ID ADK69224
 XX ADK69224 standard; peptide; 8 AA.
 AC ADK69224;
 XX
 XX 06-MAY-2004 (first entry)
 DT
 XX Epitope liberation-related peptide #587.
 DE
 XX epitope liberation; substrate; proteasome; cytostatic; antibacterial;
 KW protozoacide; fungicide; T-cell activator; vaccine; housekeeping epitope;
 KW cytotoxic T lymphocyte; CTL; adoptive immunotherapy; neoplastic cell;
 KW virus; bacterium; protozoan; fungus; housekeeping proteasome system.
 XX Unidentified.
 OS
 XX

PN US2003228634-A1.
 XX
 PD 11-DEC-2003.
 XX
 PF 07-NOV-2002; 2002US-00292413.
 XX
 PR 07-NOV-2001; 2001US-0336968P.
 XX
 PR (SIMA/) SIMARD J J L.
 PA (DIAM/) DIAMOND D C.
 PA (QIUZ/) QIU Z.
 PA (LEIX/) LEI X.
 XX
 PI Simard J J L, Diamond DC, Qiu Z, Lei X;
 XX
 DR WPI; 2004-167209/16.
 XX
 XX Identifying polypeptide suitable for epitope e.g., housekeeping epitope,
 PT liberation by contacting substrate polypeptide comprising epitope of
 PT interest, with proteasome, and assaying for liberation of epitope.
 XX
 PS Disclosure; Page 22; 67pp; English.
 XX
 CC This invention relates to a novel method of identifying a polypeptide
 CC suitable for epitope liberation, including the steps of identifying an
 CC epitope of interest; providing substrate polypeptide sequence including
 CC the epitope, wherein the substrate permits processing by a proteasome;
 CC contacting the substrate with a composition including the proteasome;
 CC under conditions that support processing of the substrate by proteasome;
 CC and assaying for liberation of epitope. The invention may be useful for
 CC the development of compounds with a cytostatic, antibacterial,
 CC protozoacide or fungicide activity acting as T-cell activators. In
 CC addition, the invention may allow development of a vaccine. The invention
 CC is useful for identifying a polypeptide suitable for epitope liberation,
 CC where the epitope is a housekeeping epitope. The compositions comprising
 CC the identified housekeeping epitopes are useful in vitro in vaccine
 CC development or in the generation or expansion of cytotoxic T lymphocyte
 CC (CTL) to be used in adoptive immunotherapy. The invention is also useful
 CC for activating T-cells against neoplastic cells, and cells infected with
 CC virus, bacterium, protozoan or fungus. CTL epitopes are identified based
 CC on the knowledge that such epitopes are, in fact, produced by the
 CC housekeeping proteasome system. Once identified, these epitopes, embodied
 CC as peptides, can be used to successfully immunise or induce therapeutic
 CC CTL responses against housekeeping proteasome expressing target cells in
 CC the host. The present sequence is that of a peptide which is related to
 CC the method of the invention.
 XX
 SQ Sequence 8 AA;
 Query Match 59.6%; Score 28; DB 8; Length 8;
 Best Local Similarity 80.0%; Pred. No. 2e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 4 VFFDY 8
 :|||
 Db 4 IFPDY 8
 :|||
 RESULT 12
 ADJ84659
 ID ADJ84659 standard; peptide; 8 AA.
 XX
 AC ADJ84659;
 XX
 XX 06-MAY-2004 (first entry)
 DT
 XX CTL epitope peptide SEQ ID NO:117.
 DE
 XX lipopeptide; lipid moiety; T helper cell epitope; Th epitope;
 KW cytotoxic T cell epitope; CTL epitope; immune response; immunisation;
 KW influenza; hepatitis C virus; Listeria monocytogenes; vaccine; cancer;
 KW cytostatic; virucide.
 KW

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OM protein - protein search, using sw model

Run on: December 30, 2005, 15:45:25 ; Search time 36 Seconds

(without alignments)
21.382 Million cell updates/sec

Title: US-10-735-916A-12

Perfect score: 47

Sequence: 1 YGRVFFDY 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 149

Minimum DB seq length: 8

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 80.*

1: Pirl.*

2: Pirl.*

3: Pirl.*

4: Pirl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	31.9	8	2 PC4373	telomeric and tetra
2	14	29.8	8	2 PT0311	Ig heavy chain CRD
3	14	29.8	8	2 PT0030	inulinase (EC 3.2.
4	14	29.8	8	2 T13818	cytochrome oxidase
5	13	27.7	8	2 PQ0012	cholecystokinin -
6	13	27.7	8	2 A43001	cholecystokinin -
7	13	27.7	8	2 PH1618	Ig H chain V-D-J r
8	13	27.7	8	2 PQ0701	unidentified 6.5/3
9	13	27.7	8	2 JS0318	leucokinin VIII -
10	13	27.7	8	2 S68325	blood cell protein
11	12	25.5	8	2 B33099	158K exoantigen -
12	12	25.5	8	2 B47393	neuropeptide calla
13	11	23.4	8	2 PT0279	Ig heavy chain CRD
14	11	23.4	8	2 B27867	homeotic protein U
15	11	23.4	8	2 A61467	penalbumin - Adeli
16	11	23.4	8	2 A25836	L-serine ammonia-1
17	11	23.4	8	2 T48890	hypothetical prote
18	10	21.3	8	2 S66646	cardioacceleratory
19	9	19.1	8	2 PH1407	Ig heavy chain V r
20	9	19.1	8	2 S16324	hypothetical prote
21	9	19.1	8	2 PT0298	Ig heavy chain CRD
22	9	19.1	8	2 B45800	serum albumin - do
23	9	19.1	8	2 PH0803	T-cell receptor al
24	9	19.1	8	2 S66296	Na+-transporting A
25	9	19.1	8	2 S11078	glucose-6-phosphat
26	9	19.1	8	2 H41978	calliFMRamide 8 -
27	9	19.1	8	2 D47393	neuropeptide calla
28	9	19.1	8	2 S65381	cytochrome-c oxida
29	9	19.1	8	2 A59028	MHC class I histoc

ALIGNMENTS

RESULT 1

PC4373

telomeric and tetraplex DNA binding protein qTBP42 III - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 09-Jul-2004

C;Accession: PC4373

R;Sarig, G.; Weisman-Shomer, P.; Fry, M.

Biochem. Biophys. Res. Commun. 237, 617-623, 1997

A;Title: Telomeric and tetraplex DNA binding properties of qTBP42: A homologue of the CAI

A;Reference number: PC4371; MUID:97445086; PMID:9299414

A;Accession: PC4373

A;Molecule type: protein

A;Residues: 1-8 <SAR>

A;Cross-references: UNIPROT:Q7M032; UNIPARC:UPI000017CA04

C;Comment: This protein binds either strand of the telomeric DNA as well as unimolecular

F;1-4/Domain: RNPI #status predicted <RNP>

Query Match 31.9%; Score 15; DB 2; Length 8;

Best Local Similarity 33.3%; Pred. No. 2.8e+05;

Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGRVFF 6

Db 2 FGFLF 7

RESULT 2

PT0311

Ig heavy chain CRD3 region (clone 6-100) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C;Accession: PT0311

R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j

A;Reference number: PT0222; MUID:91108337; PMID:1899102

A;Accession: PT0311

A;Molecule type: DNA

A;Residues: 1-8 <YAM>

A;Cross-references: UNIPARC:UPI000017C20F

A;Experimental source: B lymphocyte

C;Keywords: heterotetramer; immunoglobulin

Query Match 29.8%; Score 14; DB 2; Length 8;

Best Local Similarity 50.0%; Pred. No. 2.8e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 YGRVFFDY 8

Db 4 YG----DY 7

neuropeptide led-C
adipokinetic hormo
adipokinetic hormo
adipokinetic hormo
adipokinetic hormo
hypertrehaolosemic
adipokinetic hormo
adipokinetic hormo
adipokinetic hormo
adipokinetic hormo
ipgf protein - Shi
disseminatory sulf
phosphatidylethano
T-cell receptor be
acylase - Kluyvera
variant surface gl

30 8 17.0 8 2 A44960
31 8 17.0 8 2 A58620
32 8 17.0 8 2 S11545
33 8 17.0 8 2 S5310
34 8 17.0 8 2 S10596
35 8 17.0 8 2 S08995
36 8 17.0 8 2 A49823
37 8 17.0 8 2 A28004
38 8 17.0 8 2 S15422
39 8 17.0 8 2 A58641
40 8 17.0 8 2 S70727
41 8 17.0 8 2 S63493
42 8 17.0 8 2 PN0043
43 8 17.0 8 2 PT0724
44 8 17.0 8 2 S19288
45 8 17.0 8 2 A21440

RESULT 3
PT0030
inulinase (EC 3.2.1.7) - Aspergillus ficuum (fragment)
N/Alternate names: inulase
C/Species: Aspergillus ficuum
C/Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C/Accession: PT0030
R/Ettalibi, M.; Baratti, J.C.
Agric. Biol. Chem. 54, 61-68, 1990
A/Title: Molecular and kinetic properties of Aspergillus ficuum inulinases.
A/Reference number: PT0030; MUID:90344234; PMID:1368526
A/Accession: PT0030
A/Molecule type: protein
A/Residues: 1-8 <ETT>
A/Cross-references: UNIPROT:Q7M4U4; UNIPARC:UPI00001783B3
C/Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 29.8%; Score 14; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 FDY 8
|:
Db 1 FNY 3

RESULT 4
T13818
cytochrome oxidase subunit I - Atlantic hagfish mitochondrion (fragment)
C/Species: mitochondrion Myxine glutinosa (Atlantic hagfish)
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T13818
R/Delabarre, C.; Barriol, V.; Tillier, S.; Janvier, P.; Gachalin, G.
Mol. Biol. Evol. 14, 807-813, 1997
A/Title: The main features of the cranial mitochondrial DNA between the ND1 and the COI
A/Reference number: Z17775; MUID:97398704; PMID:9254918
A/Accession: T13818
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-8
A/Cross-references: UNIPROT:O21079; UNIPARC:UPI000016D463; EMBL:Y09527; NID:g2340019; PI
C/Genetics:
A/Genome: mitochondrion
A/Note: COI
C/Keywords: mitochondrion

Query Match 29.8%; Score 14; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 RVFF 6
|:
Db 5 RWFF 8

RESULT 5
PQ0012
cholecystokinin - southeastern quoll
N/Alternate names: CCK
C/Species: Dasyurus viverrinus (southeastern quoll)
C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C/Accession: PQ0012
R/Fan, Z.W.; Eng, J.; Shaw, R.S.
Peptides 9, 429-431, 1988
A/Title: Cholecystokinin octapeptide purified from brains of Australian marsupials.
A/Reference number: PQ0012; MUID:88234141; PMID:3375140
A/Accession: PQ0012
A/Molecule type: protein
A/Residues: 1-8 <FAN>
A/Cross-references: UNIPROT:P30369; UNIPARC:UPI000002CDD4
C/Suprafamily: gastrin
C/Keywords: amidated carboxyl end; hormone; neuropeptide; sulfoprotein
P/2/Binding site: sulfate (Tyr) (covalent) #status predicted

Query Match 27.7%; Score 13; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YG 2
|:
Db 6 YG 7

RESULT 8
PQ0701
unidentified 6.5/31K protein [imported] - rice (fragment)
C/Species: Oryza sativa (rice)
C/Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C/Accession: PQ0701
R/Komatsu, S.; Kajiwara, H.; Hirano, H.

F/8/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 27.7%; Score 13; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DY 8
|:
Db 1 DY 2

RESULT 6
A43001
cholecystokinin - tammar wallaby
N/Alternate names: CCK
C/Species: Macropus eugenii (tammar wallaby)
C/Date: 30-Oct-1992 #sequence_revision 30-Oct-1992 #text_change 09-Jul-2004
C/Accession: A43001; PQ0012
R/Fan, Z.W.; Eng, J.; Shaw, G.; Yalow, R.S.
Peptides 9, 429-431, 1988
A/Title: Cholecystokinin octapeptide purified from brains of Australian marsupials.
A/Reference number: PQ0012; MUID:88234141; PMID:3375140
A/Accession: A43001
A/Molecule type: protein
A/Residues: 1-8 <FAN>
A/Cross-references: UNIPROT:P30369; UNIPARC:UPI000002CDD4
C/Suprafamily: gastrin
C/Keywords: amidated carboxyl end; hormone; neuropeptide; sulfoprotein
P/2/Binding site: sulfate (Tyr) (covalent) #status predicted
F/8/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 27.7%; Score 13; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DY 8
|:
Db 1 DY 2

RESULT 7
PH1618
Ig H chain V-D-J region (clone B-less 33) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C/Accession: PH1618
R/Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A/Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A/Reference number: PH1580; MUID:93301609; PMID:8315387
A/Accession: PH1618
A/Molecule type: DNA
A/Residues: 1-8 <LEV>
A/Cross-references: UNIPARC:UPI000017C6A7
A/Experimental source: bone marrow pre-B lymphocyte
C/Keywords: immunoglobulin

Query Match 27.7%; Score 13; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YG 2
|:
Db 6 YG 7

RESULT 8
PQ0701
unidentified 6.5/31K protein [imported] - rice (fragment)
C/Species: Oryza sativa (rice)
C/Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C/Accession: PQ0701
R/Komatsu, S.; Kajiwara, H.; Hirano, H.

Theor. Appl. Genet. 86, 935-942, 1993
A;Title: A rice protein library; a data-file of rice proteins separated by two-dimension
A;Reference number: PQ0696

A;Accession: PQ0701

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-8 <KOW>

A;Cross-references: UNIPROT:Q7M1U0; UNIPARC:UPI0000017B129

Query Match 27.7%; Score 13; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YG 2

Db 1 YG 2

RESULT 9

JS0318

leucokinin VIII - Madeira cockroach

C;Species: Leucophaea maderae (Madeira cockroach)

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004

A;Accession: JS0318

R;Holman, G.M.; Cook, B.J.; Nachman, R.J.

Comp. Biochem. Physiol. C 88, 31-34, 1987

A;Title: Isolation, primary structure and synthesis of leucokinins VII and VIII: the first

A;Reference number: JS0317

A;Accession: JS0318

A;Molecule type: protein

A;Residues: 1-8 <HOL>

A;Cross-references: UNIPROT:P19990; UNIPARC:UPI000012E29F

C;Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile act

C;Keywords: amidated carboxyl end; cephalomyotropic peptide

F;8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 27.7%; Score 13; DB 2; Length 8;

Best Local Similarity 28.6%; Pred. No. 2.8e+05;

Matches 2; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GRVFFDY 8

Db 1 GADFYSW 7

RESULT 10

S68325

blood cell protein A8 - Ascidia ceratodes (fragment)

N;Alternate names: Abcp-A

C;Species: Ascidia ceratodes

C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004

A;Accession: S68325

R;Taylor, S.W.; Ross, M.M.; Waite, J.H.

Arch. Biochem. Biophys. 324, 228-240, 1995

A;Title: Novel 3,4-di- and 3,4,5-trihydroxyphenylalanine-containing polypeptides from th

A;Reference number: S68325; MUID:96132650; PMID:8554314

A;Accession: S68325

A;Molecule type: protein

A;Residues: 1-8 <TAY>

A;Cross-references: UNIPROT:Q7M3L7; UNIPARC:UPI000017CA56

F;2,3,4/Modified site: 3',4',5'-trihydroxyphenylalanine (Tyr) #status experimental

Query Match 27.7%; Score 13; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DY 8

Db 1 DY 2

RESULT 11

B33099

158K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)

C;Species: Plasmodium falciparum

C;Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000

A;Accession: B33099

R;Nichols, J.H.; Hager, L.P.

submitted to the Protein Sequence Database, May 1990

A;Reference number: A33098

A;Accession: B33099

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-8 <NIC>

A;Cross-references: UNIPARC:UPI000017B5DF

Query Match 25.5%; Score 12; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FD 7

Db 2 FD 3

RESULT 12

E47393

neuropeptide callatostatin 5 - bluebottle fly (Calliphora vomitoria)

C;Species: Calliphora vomitoria

C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

A;Accession: E47393

R;Duve, H.; Johnsen, A.H.; Scott, A.G.; Yu, C.G.; Yagi, K.J.; Tobe, S.S.; Thorpe, A.

Proc. Natl. Acad. Sci. U.S.A. 90, 2456-2460, 1993

A;Title: Callatostatins: neuropeptides from the blowfly Calliphora vomitoria with sequen

A;Reference number: A47393; MUID:93211980; PMID:8460157

A;Accession: E47393

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-8 <DUV>

A;Cross-references: UNIPROT:P41841; UNIPARC:UPI000002EAB5

A;Experimental source: whole flies

A;Note: sequence extracted from NCBI backbone (NCBIP:128482)

Query Match 25.5%; Score 12; DB 2; Length 8;

Best Local Similarity 33.3%; Pred. No. 2.8e+05;

Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FDY 8

Db 4 YDF 6

RESULT 13

PT0279

Ig heavy chain CRD3 region (clone 4-91A) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

A;Accession: PT0279

R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j

A;Reference number: PT0222; MUID:91108337; PMID:1899102

A;Accession: PT0279

A;Molecule type: DNA

A;Residues: 1-8 <YAM>

A;Cross-references: UNIPARC:UPI0000017C203

A;Experimental source: B lymphocyte

C;Keywords: heterotetramer; immunoglobulin

Query Match 23.4%; Score 11; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GR 3

Db 5 GR 6

RESULT 14

B27867
homeotic protein Ultrabithorax - fruit fly (Drosophila melanogaster) (fragment)
C:Species: Drosophila melanogaster
C>Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 09-Jul-2004
C:Accession: B27867
R:Saari, G.; Bienz, M.
EMBO J. 6, 1775-1779, 1987
A:Title: The structure of the ultrabithorax promoter of Drosophila melanogaster.
A:Reference number: A91072
A:Accession: B27867
A:Molecule type: mRNA
A:Residues: 1-8 <SAA>
A:Cross-references: UNIPROT:P83949; UNIPARC:UPI000016BDEE
C:Genetics:
A:Gene: FlyBase:Ubx
A:Cross-references: FlyBase:FBgn0003944
C:Keywords: DNA binding; nucleus; transcription regulation

Query Match 23.4%; Score 11; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 FFD 7
:|:
Db 4 YFE 6

RESULT 15

A61467
penalbumin - Adelie penguin (fragment)
C:Species: Pygoscelis adeliae (Adelie penguin)
C>Date: 07-Oct-1994 #sequence_revision 04-Nov-1994 #text_change 09-Jul-2004
C:Accession: A61467
R:Osuga, D.T.; Amlinari, M.; Ho, C.Y.K.; Allison, R.G.; Feeney, R.E.
J. Protein Chem. 2, 43-62, 1983
A:Title: Sulfhydryl proteins of penguin egg white: ovalbumin and penalbumin. Comparisons
A:Reference number: A61467
A:Accession: A61467
A:Molecule type: protein
A:Residues: 1-8 <OSU>
A:Cross-references: UNIPROT:Q7L2I8; UNIPARC:UPI000017C04A
C:Comment: Penalbumin is a major protein component of egg whites from penguins but not f
C:Keywords: egg white; glycoprotein

Query Match 23.4%; Score 11; DB 2; Length 8;
Best Local Similarity 25.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GRVF 5
:|:
Db 1 GSIY 4

Search completed: December 30, 2005, 15:56:00
Job time : 37 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2005, 15:36:05 ; Search time 224 Seconds
(without alignments)
25.197 Million cell updates/sec

Title: US-10-735-916A-12
Perfect score: 47
Sequence: 1 YGRVFFDY 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 707

Minimum DB seq length: 8
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	38.3	8	2	Q6EX60_9LAMI
2	17	36.2	8	2	Q4X617_PLACH
3	16	34.0	8	2	O13591_YEAST
4	15	31.9	8	2	Q56759_XANTHOBACTE
5	15	31.9	8	2	Q7M032_RAT
6	15	31.9	8	2	Q80H91_9PARA
7	14	29.8	8	2	Q7M4U4_ASPFI
8	14	29.8	8	2	Q40530_TOBAC
9	14	29.8	8	2	Q99NX9_HYDHY
10	14	29.8	8	2	Q9TD02_9SMEG
11	13	27.7	8	1	ALL16_CARMA
12	13	27.7	8	1	CKKN_DASVI
13	13	27.7	8	1	CKKN_MACEU
14	13	27.7	8	1	LCK8_LEUMA
15	13	27.7	8	2	Q35792_YEAST
16	13	27.7	8	2	Q6BC29_HUMAN
17	13	27.7	8	2	Q9UDZ4_HUMAN
18	13	27.7	8	2	Q9UMH9_HUMAN
19	13	27.7	8	2	Q7M317_PASCI
20	13	27.7	8	2	Q5RLS1_PIG
21	13	27.7	8	2	Q7M1U0_ORYSA
22	13	27.7	8	2	Q6DQ21_CLOBE
23	13	27.7	8	2	Q09258_SYNP8
24	13	27.7	8	2	O85406_COXBU
25	13	27.7	8	2	Q5Y8D4_ONCMY
26	13	27.7	8	2	Q5YDW3_9PERC
27	13	27.7	8	2	Q68LFI_9PASS
28	13	27.7	8	2	Q68LGI_9PASS
29	12	25.5	8	1	ALL5_CALVO
30	12	25.5	8	1	ALL5_CVDPO
31	12	25.5	8	1	ANGT2_BOTPA

32	12	25.5	8	1	ORMY_ORCLI
33	12	25.5	8	2	O15899_BABOV
34	12	25.5	8	2	Q8MC18_QUIIN
35	12	25.5	8	2	Q8MC20_5MYRT
36	12	25.5	8	2	Q7X139_9STAP
37	12	25.5	8	2	Q7X145_STASA
38	12	25.5	8	2	Q9RQ49_9ENTR
39	12	25.5	8	2	Q9RQ57_9ENTR
40	12	25.5	8	2	Q8JFN8_CHICK
41	11	23.4	8	2	Q6SE42_DROSI
42	11	23.4	8	2	Q9TWH6_9ANNE
43	11	23.4	8	2	Q28866_MEGNO
44	11	23.4	8	2	Q6R4Q8_BUBBU
45	11	23.4	8	2	Q9GWH3_LAGOB

ALIGNMENTS

RESULT 1
Q6EX60_9LAMI
ID Q6EX60_9LAMI PRELIMINARY; PRT; 8 AA.
AC Q6EX60;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DB Ribosomal protein (fragment).
GN Name: rps16;
OS Isodon pharicus.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Isodon.
OX NCBI_TaxID=204134;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Willis F.,
RA Powell M.P., Savolainen V.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ505344; CAD45467.1; -; Genomic_DNA.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
KW Chloroplast; Ribosomal protein.
FT NON TER 1 1
FT NON TER 8 8
SQ SEQUENCE 8 AA; 881 MW; 175059C732C87877 CRC64;
Query Match 38.3%; Score 18; DB 2; Length 8;
Best Local Similarity 57.1%; Pred. No. 2.2e+06;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GRVFFDY 8
Db 2 GGVLFY 8
RESULT 2
Q4X617_PLACH
ID Q4X617_PLACH PRELIMINARY; PRT; 8 AA.
AC Q4X617;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=PC405959.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,

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RA Quail M.A.; Ormond D.; Doggett J.; Trueman H.E.; Mendoza J.;
RA Bidwell S.L.; Rajandream M.A.; Carucci D.J.; Yates J.R.; Kafatos F.C.;
RA Janse C.J.; Barrell B.; Turner C.M.R.; Waters A.P.; Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RL transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; CAJ01009638; CAH87659.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 8 AA; 1098 MW; E24B4B5449D2D2C6 CRC64;

Query Match 36.2%; Score 17; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 VFFDY 8
Db | | |
2 VFFNY 6

RESULT 3
O13591_YEAST PRELIMINARY; PRT; 8 AA.
ID O13591_YEAST
AC O13591;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE ORF YNL337w (Fragment).
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Obermaier B., Piravandi E., Rinke M.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA MIPS;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z71612; CAA96271.2; -; Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 8 AA; 1005 MW; 5CA441B449C9C720 CRC64;

Query Match 34.0%; Score 16; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 VFFDY 8
Db | | |
2 LFFNH 6

RESULT 4
Q56759_XANAU PRELIMINARY; PRT; 8 AA.
ID Q56759_XANAU
AC Q56759;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Halocid dehalogenase (Fragment).
GN Names-dhlB;
OS Xanthobacter autotrophicus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Hyphomicrobiaceae; Xanthobacter.
OX NCBI_TaxID=280;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC SFRATN=G310;
RX MEDLINE=95173113; PubMed=7868610;
RA Van der Ploeg J., Willemse M., van Hall G., Janssen D.B.;
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RT "Adaptation of Xanthobacter autotrophicus G310 to bromoacetate due to
RT activation and mobilization of the haloacetate dehalogenase gene by
RT insertion element IS1247.";
RL J. Bacteriol. 177:1348-1356(1995).
DR EMBL; X84038; CAA58857.1; -; Genomic_DNA.
FT NON_TER 8
SQ SEQUENCE 8 AA; 922 MW; F3A9D2D2CDD33056 CRC64;

Query Match 31.9%; Score 15; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 VFFD 7
Db | | |
5 VVFD 8

RESULT 5
Q7M032_RAT PRELIMINARY; PRT; 8 AA.
ID Q7M032_RAT
AC Q7M032;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Telomeric and tetraplex DNA binding protein qTBP42 III
DE (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=97445086; PubMed=92999414; DOI=10.1006/bbrc.1997.7198;
RA Sarig G., Weisman-Shomer P., Fry M.;
RT "Telomeric and tetraplex DNA binding properties of qTBP42: A homologue
RL of the CARG box binding protein CBP-A.";
RL Biochem. Biophys. Res. Commun. 237:617-623(1997).
DR PIR; PC4373; PC4373.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 928 MW; 7839C72059C879C8 CRC64;

Query Match 31.9%; Score 15; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 2.2e+06;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGRVFF 6
Db | | |
2 FGFIIF 7

RESULT 6
Q80H91_9PARA PRELIMINARY; PRT; 8 AA.
ID Q80H91_9PARA
AC Q80H91;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE HN/HNO (Fragment).
GN Name=HN/HNO;
OS Newcastle disease virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Avulavirus.
OX NCBI_TaxID=11176;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94175786; PubMed=8129624;
RA Collins M.S., Strong I., Alexander D.J.;
RT "Evaluation of the molecular basis of pathogenicity of the variant
RL Arch. Virol. 134:403-411(1994).
DR EMBL; S69419; AAP19628.1; -; Genomic_DNA.
```

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FT NON TER 1
SQ SEQUENCE 8 AA; 929 MW; 33D4087AA337205B CRC64;

Query Match 31.9%; Score 15; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GRV 4
Db |||
6 GRV 8

RESULT 7
Q7M4U4 ASPFI
ID Q7M4U4_ASPP1 PRELIMINARY; PRT; 8 AA.
AC Q7M4U4;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE Inulinase (EC 3.2.1.7) (Fragment).
OS Aspergillus ficum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Euryotales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5058;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=90344234; PubMed=1368526;
RA Etalibi M., Baratti J.C.;
RT "Molecular and kinetic properties of Aspergillus ficum inulinases.";
RL Agric. Biol. Chem. 54:61-68(1990).
DR PIR: P00030; PT0030.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 1102 MW; 9A1B4776DAB5449 CRC64;

Query Match 29.8%; Score 14; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.2e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FDY 8
Db |||
1 FNY 3

RESULT 8
Q40530 TOBAC
ID Q40530_TOBAC PRELIMINARY; PRT; 8 AA.
AC Q40530;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE N.tabacum P20 with a leader peptide.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=87089808; PubMed=3540612;
RA Herman L.M.F., Montagu M.C.V., Depicker A.G.;
RT "Isolation of tobacco DNA segments with plant promoter activity.";
RL Mol. Cell. Biol. 6:4486-4492(1986).
DR EMBL; M14685; AAA34090.1; -; Genomic DNA.
SQ SEQUENCE 8 AA; 1109 MW; E257205B19C9C6 CRC64;

Query Match 29.8%; Score 14; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.2e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FPD 7
Db |||
3 FFE 5

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RESULT 9
Q99NX9 HYDHY
ID Q99NX9_HYDHY PRELIMINARY; PRT; 8 AA.
AC Q99NX9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Amyloid beta protein (Fragment).
DE Name=APP;
GN Name=APP;
OS Hydrochoerus hydrochaeris (Capybara) (Carpincho).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC Hystricognathi; Hydrochaeridae; Hydrochaeris.
OX NCBI_TaxID=10149;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21082082; PubMed=11214319; DOI=10.1038/35054550;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011342; AAG47377.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 1071 MW; 1356D686DB19C93 CRC64;

Query Match 29.8%; Score 14; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.2e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FPD 7
Db |||
2 FFE 4

RESULT 10
Q9TD02 9SMEG
ID Q9TD02_9SMEG PRELIMINARY; PRT; 8 AA.
AC Q9TD02;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Cytochrome c oxidase subunit I (Fragment).
DE Terranatos dolichopterus.
OS Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Cyprinodontiformes; Aplocheilidae; Rivulinae; Terranatos.
OX NCBI_TaxID=61836;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hrbek T., Larson A.;
RT "The evolution of diapause in the killifish family Rivulidae
RT (Atherinomorpha, Cyprinodontiformes): A molecular phylogenetic and
RT biogeographic perspective.";
RL Evolution 53:1200-1216(1999).
DR EMBL; AF092421; AAF03041.1; -; Genomic_DNA.
DR GO; GO:0005739; C:mitochondrion; IEA.
FT NON_TER 8
FT NON_TER 8
SQ SEQUENCE 8 AA; 1084 MW; F0C9D3640DD44056 CRC64;

Query Match 29.8%; Score 14; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 RVFF 6
Db |||
5 RWFF 8

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RESULT 11
AL16_CARMA
ID ALL16_CARMA STANDARD; PRT; 8 AA.
AC P81819;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Carcinus maenas (Common shore crab) (Green crab).
OS Carcinus maenas (Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidea; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -I- FUNCTION: May act as a neurotransmitter or neuromodulator.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- SIMILARITY: Belongs to the allatostatin family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC Anidation; Direct protein sequencing; Multigene family; Neuropeptide.
KW MOD_RES 8 Leucine amide.
FT MOD_RES 8 AA; 813 MW; 7C286B45AB476878 CRC64;
SQ SEQUENCE 8 AA; 813 MW; 7C286B45AB476878 CRC64;

Query Match 27.7%; Score 13; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YG 2
DB 6 YG 7

RESULT 12
CCKN_DASVI
ID CCKN_DASVI STANDARD; PRT; 8 AA.
AC P68125; P30369;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Cholecystokinin (CCK).
GN Name=CCK;
OS Dasyurus viverrinus (Southeastern quoll).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Dasyurus.
OX NCBI_TaxID=9279;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=88234141; PubMed=3375140; DOI=10.1016/0196-9781(88)90280-X;
RA Fan Z.W., Eng J., Shaw G., Yalow R.S.;
RT "Cholecystokinin octapeptide purified from brains of Australian
RT marsupials.";
RL Peptides 9:429-431(1988).
CC -I- FUNCTION: This peptide hormone induces gall bladder contraction
CC and the release of pancreatic enzymes in the gut. Its function in
CC the brain is not clear.
CC -I- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
CC
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CC removed.
CC
CC PIR; A43001; A43001.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Anidation; Direct protein sequencing; Hormone; Sulfation.
FT MOD_RES 2 2 Sulfotyrosine.
FT MOD_RES 8 8 Phenylalanine amide.
SQ SEQUENCE 8 AA; 1064 MW; DDCAA68378768B5A CRC64;

Query Match 27.7%; Score 13; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DY 8
DB 1 DY 2

RESULT 14
LCK8_LEUMA
ID LCK8_LEUMA STANDARD; PRT; 8 AA.

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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC PIR; PQ0012; PQ0012.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Anidation; Direct protein sequencing; Hormone; Sulfation.
FT MOD_RES 2 2 Sulfotyrosine.
FT MOD_RES 8 8 Phenylalanine amide.
SQ SEQUENCE 8 AA; 1064 MW; DDCAA68378768B5A CRC64;

Query Match 27.7%; Score 13; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DY 8
DB 1 DY 2

RESULT 13
CCKN_MACEU
ID CCKN_MACEU STANDARD; PRT; 8 AA.
AC P68126; P30369;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Cholecystokinin (CCK).
GN Name=CCK;
OS Macropus eugenii (Tamar wallaby).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=9315;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=88234141; PubMed=3375140; DOI=10.1016/0196-9781(88)90280-X;
RA Fan Z.W., Eng J., Shaw G., Yalow R.S.;
RT "Cholecystokinin octapeptide purified from brains of Australian
RT marsupials.";
RL Peptides 9:429-431(1988).
CC -I- FUNCTION: This peptide hormone induces gall bladder contraction
CC and the release of pancreatic enzymes in the gut. Its function in
CC the brain is not clear.
CC -I- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC PIR; A43001; A43001.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Anidation; Direct protein sequencing; Hormone; Sulfation.
FT MOD_RES 2 2 Sulfotyrosine.
FT MOD_RES 8 8 Phenylalanine amide.
SQ SEQUENCE 8 AA; 1064 MW; DDCAA68378768B5A CRC64;

Query Match 27.7%; Score 13; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DY 8
DB 1 DY 2

RESULT 14
LCK8_LEUMA
ID LCK8_LEUMA STANDARD; PRT; 8 AA.

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Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DY 8
Db 3 DY 4

Search completed: December 30, 2005, 15:55:19
Job time : 226 secs

AC P19990;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Leucokinin-8 (Leucokinin VIII) (L-VIII).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of leucokinin VII and
RT VIII: the final members of this new family of cephalomyotropic
RT peptides isolated from head extracts of Leucophaea maderae.";
RL Comp. Biochem. Physiol. 89C:31-34(1987).
CC -1- FUNCTION: This cephalomyotropic peptide stimulates contractile
CC activity of cockroach prothodaeum (hindgut).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; JS0318; JS0318.
DR Amidation; Direct protein sequencing; Neuropeptide.
KW MOD RES 8 Glycine amide.
FT MOD RES 8
SQ SEQUENCE 8 AA; 902 MW; 736365AB59CAADD8 CRC64;

Query Match 27.7%; Score 13; DB 1; Length 8;
Best Local Similarity 28.6%; Pred. No. 2.2e+06;
Matches 2; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GRVFFDY 8
Db 1 GADFYW 7

RESULT 15
Q35792 YEAST
ID Q35792 YEAST PRELIMINARY; PRT; 8 AA.
AC Q35792;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Inside intron 3 (Fragment).
OS Saccharomyces cerevisiae (Baker's yeast).
OC Mitochondrion.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=D273-10B;
RX MEDLINE=81069885; PubMed=6254986;
RA Bonitz S.G., Coruzzi G., Thalenfeld B.E., Tzagoloff A., Macino G.;
RT "Assembly of the mitochondrial membrane system. Structure and
RT nucleotide sequence of the gene coding for subunit 1 of yeast
RT cytochrome oxidase.";
RL J. Biol. Chem. 255:11927-11941(1980).
RL EMBL; V00694; CAA24063.1; -; Genomic DNA.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 1025 MW; 084693345B5AA337 CRC64;

Query Match 27.7%; Score 13; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 30, 2005, 15:48:10 ; Search time 45 Seconds

(without alignments)
14.698 Million cell updates/sec

Title: US-10-735-916A-12

Perfect score: 47

Sequence: 1 YGRVFFDY 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 18170

Minimum DB seq length: 8

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*

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2: /cgm2_6/ptodata/1/iaa/6 COMB.pap.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	59.6	8	1	US-08-704-655-13
2	28	59.6	8	2	US-09-920-174-19
3	28	59.6	8	2	US-09-920-195A-19
4	25	53.2	8	1	US-08-350-260A-423
5	25	53.2	8	1	US-08-350-260A-486
6	25	53.2	8	2	US-09-104-337A-423
7	25	53.2	8	2	US-09-104-337A-486
8	23	48.9	8	2	US-09-211-715-206
9	22	46.8	8	1	US-08-350-260A-380
10	22	46.8	8	1	US-08-350-260A-391
11	22	46.8	8	1	US-08-350-260A-487
12	22	46.8	8	2	US-08-649-100-23
13	22	46.8	8	2	US-08-649-100-39
14	22	46.8	8	2	US-09-104-337A-380
15	22	46.8	8	2	US-09-104-337A-391
16	22	46.8	8	2	US-09-104-337A-487
17	22	46.8	8	2	US-09-802-083-9
18	21.5	45.7	8	1	US-08-350-260A-471
19	21.5	45.7	8	1	US-09-104-337A-471
20	21	44.7	8	1	US-08-350-260A-463
21	21	44.7	8	2	US-09-104-337A-463
22	20	42.6	8	1	US-08-279-906A-6
23	20	42.6	8	1	US-08-279-906A-7
24	20	42.6	8	1	US-08-279-906A-8
25	20	42.6	8	1	US-08-279-906A-9
26	20	42.6	8	1	US-08-713-254-4
27	20	42.6	8	1	US-08-487-860-61

28	20	42.6	8	1	US-08-350-260A-465	Sequence 465, App
29	20	42.6	8	2	US-08-855-767-4	Sequence 4, Appli
30	20	42.6	8	2	US-09-104-337A-465	Sequence 465, App
31	20	42.6	8	6	5164366-14	Patent No. 5164366
32	19.5	41.5	8	2	US-08-479-089A-9	Sequence 9, Appli
33	19.5	41.5	8	2	US-07-669-545B-9	Sequence 9, Appli
34	19	40.4	8	1	US-08-233-558-1	Sequence 1, Appli
35	19	40.4	8	1	US-08-233-558-10	Sequence 10, Appl
36	19	40.4	8	1	US-08-233-558-25	Sequence 25, Appl
37	19	40.4	8	1	US-08-233-558-26	Sequence 26, Appl
38	19	40.4	8	1	US-08-233-558-27	Sequence 27, Appl
39	19	40.4	8	1	US-08-310-429A-13	Sequence 13, Appl
40	19	40.4	8	1	US-08-704-170-69	Sequence 69, Appl
41	19	40.4	8	1	US-08-690-734A-12	Sequence 12, Appl
42	19	40.4	8	1	US-08-350-260A-379	Sequence 379, App
43	19	40.4	8	1	US-08-350-260A-381	Sequence 381, App
44	19	40.4	8	1	US-08-350-260A-382	Sequence 382, App
45	19	40.4	8	1	US-08-350-260A-464	Sequence 464, App

ALIGNMENTS

RESULT 1
US-08-704-655-13
; Sequence 13, Application US/08704655
; Patent No. 5869453
; GENERAL INFORMATION:
; APPLICANT: Moss, Denis J.
; APPLICANT: Burrows, Scott R.
; APPLICANT: Khanna, Rajiv
; APPLICANT: Kerr, Veerly M.
; APPLICANT: Burrows, Jacqueline M.
; APPLICANT: Suhrbier, Andreas
; TITLE OF INVENTION: Cytotoxic T Cell Epitopes
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,655
; FILING DATE: 13-SEP-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU95/00140
; FILING DATE: 16-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: FBRC002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (712) 789-2679
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-704-655-13

Query Match 59.6%; Score 28; DB 1; Length 8;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 VFFDY 8
:||||
Db 4 IFFDY 8

RESULT 2

US-09-920-174-19
; Sequence 19, Application US/09920174
; Patent No. 6699477
; GENERAL INFORMATION:
; APPLICANT: KHANNA, RAJIV
; APPLICANT: KERR, BEVERLEY M.
; APPLICANT: MISKO, IHOR S.
; APPLICANT: MOSS, DENIS J.
; APPLICANT: BURROWS, SCOTT R.
; TITLE OF INVENTION: EBV CTL EPITOPES
; FILE REFERENCE: FERC:008USC2
; CURRENT APPLICATION NUMBER: US/09/920,174
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 09/920,175
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 09/194,450
; PRIOR FILING DATE: 1998-11-23
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-920-174-19

Query Match 59.6%; Score 28; DB 2; Length 8;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 VFFDY 8
:||||
Db 4 IFFDY 8

RESULT 3

US-09-920-195A-19
; Sequence 19, Application US/09920195A
; Patent No. 6703024
; GENERAL INFORMATION:
; APPLICANT: KHANNA, RAJIV
; APPLICANT: KERR, BEVERLEY M.
; APPLICANT: MISKO, IHOR S.
; APPLICANT: MOSS, DENIS J.
; APPLICANT: BURROWS, SCOTT R.
; TITLE OF INVENTION: EBV CTL EPITOPES
; FILE REFERENCE: FERC:008USC1
; CURRENT APPLICATION NUMBER: US/09/920,195A
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 09/194,450
; PRIOR FILING DATE: 1998-11-23
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-920-195A-19

Query Match 59.6%; Score 28; DB 2; Length 8;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;

QY 4 VFFDY 8
:||||
Db 4 IFFDY 8

RESULT 4

US-08-350-260A-423
; Sequence 423, Application US/08350260A
; Patent No. 5962255
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; TITLE OF INVENTION: binding pairs
; NUMBER OF SEQUENCES: 602
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,260A
; FILING DATE: 05-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01134
; FILING DATE: 10-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/32372
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 423:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-350-260A-423

Query Match 53.2%; Score 25; DB 1; Length 8;
 Best Local Similarity 66.7%; Pred. No. 4.6e+05;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 RVPDFY 8
 Db 3 RKYFDY 8

RESULT 5
 US-08-350-260A-486
 ; Sequence 486, Application US/08350260A
 ; Patent No. 5962255
 ; GENERAL INFORMATION:
 ; APPLICANT: Winter, Gregory Paul
 ; APPLICANT: Griffiths, Andrew David
 ; APPLICANT: Williams, Samuel Cameron
 ; APPLICANT: Waterhouse, Peter
 ; APPLICANT: Nissim, Ahuva
 ; APPLICANT: Johnson, Kevin Stuart
 ; APPLICANT: Smith, Andrew John Hammond
 ; TITLE OF INVENTION: Methods for producing members of specific
 ; binding pairs
 ; NUMBER OF SEQUENCES: 602
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: David W. Clough
 ; STREET: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/350,260A
 ; FILING DATE: 05-DEC-1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB 9110549.4
 ; FILING DATE: 15-MAY-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB 9206318.9
 ; FILING DATE: 24-MAR-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/GB91/01134
 ; FILING DATE: 10-JUL-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/GB92/00883
 ; FILING DATE: 15-MAY-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/GB93/00605
 ; FILING DATE: 24-MAR-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/150,002
 ; FILING DATE: 31-MAR-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/307,619
 ; FILING DATE: 16-SEP-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Clough, David W
 ; REGISTRATION NUMBER: 36,107
 ; REFERENCE/DOCKET NUMBER: 28111/32372
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312-474-6300
 ; INFORMATION FOR SEQ ID NO: 486:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 8 amino acids
 ; TYPE: amino acid

; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-350-260A-486
 ; Query Match 53.2%; Score 25; DB 1; Length 8;
 ; Best Local Similarity 100.0%; Pred. No. 4.6e+05;
 ; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 ; QY 5 FFDY 8
 ; Db 5 FFDY 8
 ; RESULT 6
 ; US-09-104-337A-423
 ; Sequence 423, Application US/09104337A
 ; Patent No. 6492160
 ; GENERAL INFORMATION:
 ; APPLICANT: Winter, Gregory Paul
 ; APPLICANT: Griffiths, Andrew David
 ; APPLICANT: Williams, Samuel Cameron
 ; APPLICANT: Waterhouse, Peter
 ; APPLICANT: Nissim, Ahuva
 ; APPLICANT: Johnson, Kevin Stuart
 ; APPLICANT: Smith, Andrew John Hammond
 ; TITLE OF INVENTION: Methods for producing members of specific
 ; binding pairs
 ; NUMBER OF SEQUENCES: 600
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Audrey L. Bartnicki
 ; STREET: Marshall, Gerstein & Borun
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/104,337A
 ; FILING DATE: 25-Jun-1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/350,260
 ; FILING DATE: 05-DEC-1994
 ; APPLICATION NUMBER: GB 9110549.4
 ; FILING DATE: 15-MAY-1991
 ; APPLICATION NUMBER: GB 9206318.9
 ; FILING DATE: 24-MAR-1992
 ; APPLICATION NUMBER: PCT/GB92/00883
 ; FILING DATE: 15-MAY-1992
 ; APPLICATION NUMBER: PCT/GB93/00605
 ; FILING DATE: 24-MAR-1993
 ; APPLICATION NUMBER: US 08/150,002
 ; FILING DATE: 31-MAR-1994
 ; APPLICATION NUMBER: US 08/307,619
 ; FILING DATE: 16-SEP-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Bartnicki, Audrey L.
 ; REGISTRATION NUMBER: 40,499
 ; REFERENCE/DOCKET NUMBER: 28111/32372A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312-474-6300
 ; INFORMATION FOR SEQ ID NO: 423:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 8 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 423:
 ; US-09-104-337A-423

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Query Match      53.2%; Score 25; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 RVFFDY 8
Db      3 RKYFDY 8

RESULT 7
US-09-104-337A-486
; Sequence 486, Application US/09104337A
; Patent No. 6492160
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; Griffiths, Andrew David
; Williams, Samuel Cameron
; Waterhouse, Peter
; Nissim, Ahuva
; Johnson, Kevin Stuart
; Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; binding pairs
; NUMBER OF SEQUENCES: 600
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Audrey L. Bartnicki
; STREET: Marshall, Gerstein & Borun
; 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/104,337A
; FILING DATE: 25-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/350,260
; FILING DATE: 05-DEC-1994
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bartnicki, Audrey L.
; REGISTRATION NUMBER: 40,499
; REFERENCE/DOCKET NUMBER: 28111/33372A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 486:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 486:

US-09-104-337A-486

Query Match      53.2%; Score 25; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 FFYD 8
Db      5 FFYD 8

RESULT 8
US-09-211-715-206
; Sequence 206, Application US/09211715
; Patent No. 6759384
; GENERAL INFORMATION:
; APPLICANT: Al-Obeidi, Fahad
; APPLICANT: Lebl, Michal
; APPLICANT: Ostrem, James A.
; APPLICANT: Safar, Pavel
; APPLICANT: Stierandova, Alena
; APPLICANT: Strop, Peter
; APPLICANT: Walser, Armin
; TITLE OF INVENTION: Factor Xa Inhibitors
; FILE REFERENCE: P-SE3243
; CURRENT APPLICATION NUMBER: US/09/211,715
; CURRENT FILING DATE: 1998-12-14
; EARLIER APPLICATION NUMBER: 08/233,054
; EARLIER FILING DATE: 1994-04-26
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 206
; LENGTH: 8
; TYPE: PRT
; ORGANISM: synthetic construct
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (8)-
; OTHER INFORMATION: AMIDATION

US-09-211-715-206

Query Match      48.9%; Score 23; DB 2; Length 8;
Best Local Similarity 62.5%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 YGRVFYD 8
Db      1 YIRFSDY 8

RESULT 9
US-08-350-260A-380
; Sequence 380, Application US/08350260A
; Patent No. 5962255
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; binding pairs
; NUMBER OF SEQUENCES: 602
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: David W. Clough
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun
; 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,260A
; FILING DATE: 05-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01134
; FILING DATE: 10-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/32372
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 380:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-350-260A-380

Query Match 46.8%; Score 22; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 RVFFDY 8
Db 3 RTSFDY 8

RESULT 10
US-08-350-260A-391
; Sequence 391, Application US/08350260A
; Patent No. 5962255
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; TITLE OF INVENTION: Methods for producing members of specific
; TITLE OF INVENTION: binding pairs
; NUMBER OF SEQUENCES: 602
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,260A
; FILING DATE: 05-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01134
; FILING DATE: 10-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/32372
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 391:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-350-260A-391

Query Match 46.8%; Score 22; DB 1; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8
Db 1 YKSLSFY 8

RESULT 11
US-08-350-260A-487
; Sequence 487, Application US/08350260A
; Patent No. 5962255
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; TITLE OF INVENTION: binding pairs
; NUMBER OF SEQUENCES: 602
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:

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COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350,260A
FILING DATE: 05-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB91/01134
FILING DATE: 10-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/32372
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 487:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-350-260A-487

Query Match 46.8%; Score 22; DB 1; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 FPDY 8
Db 5 YFDY 8

RESULT 12
US-08-649-100-23
Sequence 23, Application US/08649100
Patent No. 6114507
GENERAL INFORMATION:
APPLICANT: SHIRAKAWA, KAMON
APPLICANT: MATSUE, TOMOKAZU
APPLICANT: NAGATA, SHIGEKAZU
APPLICANT: CO, MAN SUNG
APPLICANT: VASQUEZ, MAXIMILIANO
TITLE OF INVENTION: ANTI-FAS LIGAND ANTIBODY AND ASSAY
TITLE OF INVENTION: METHOD USING THE ANTI-FAS LIGAND ANTIBODY
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA

COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/649,100
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1110-160
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLSCULE TYPE: peptide
US-08-649-100-23

Query Match 46.8%; Score 22; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 FPDY 8
Db 5 YFDY 8

RESULT 13
US-08-649-100-39
Sequence 39, Application US/08649100
Patent No. 6114507
GENERAL INFORMATION:
APPLICANT: SHIRAKAWA, KAMON
APPLICANT: MATSUE, TOMOKAZU
APPLICANT: NAGATA, SHIGEKAZU
APPLICANT: CO, MAN SUNG
APPLICANT: VASQUEZ, MAXIMILIANO
TITLE OF INVENTION: ANTI-FAS LIGAND ANTIBODY AND ASSAY
TITLE OF INVENTION: METHOD USING THE ANTI-FAS LIGAND ANTIBODY
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/649,100
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1110-160
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 39:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-649-100-39

Query Match 46.8%; Score 22; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FFYD 8
Db 5 YFDY 8

RESULT 14

US-09-104-337A-380
; Sequence 380, Application US/09104337A
; Patent No. 6492160
; GENERAL INFORMATION:

APPLICANT: Winter, Gregory Paul
Griffiths, Andrew David
Williams, Samuel Cameron
Waterhouse, Peter
Nissim, Ahuva
Johnson, Kevin Stuart
Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
binding pairs

NUMBER OF SEQUENCES: 600
CORRESPONDENCE ADDRESS:

ADDRESSEE: Audrey L. Bartnicki
STREET: Marshall, Gerstein & Borun
6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/104,337A
FILING DATE: 25-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/350,260
FILING DATE: 05-DEC-1994
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994

ATTORNEY/AGENT INFORMATION:

NAME: Bartnicki, Audrey L.
REGISTRATION NUMBER: 40,499
REFERENCE/DOCKET NUMBER: 28111/32372A
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 380:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid

; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 380:
US-09-104-337A-380

Query Match 46.8%; Score 22; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 RVFFDY 8
Db 3 RTSFDY 8

RESULT 15

US-09-104-337A-391
; Sequence 391, Application US/09104337A
; Patent No. 6492160
; GENERAL INFORMATION:

APPLICANT: Winter, Gregory Paul
Griffiths, Andrew David
Williams, Samuel Cameron
Waterhouse, Peter
Nissim, Ahuva
Johnson, Kevin Stuart
Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
binding pairs

NUMBER OF SEQUENCES: 600

CORRESPONDENCE ADDRESS:

ADDRESSEE: Audrey L. Bartnicki
STREET: Marshall, Gerstein & Borun
6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago
STATE: Illinois
COUNTRY: USA

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/104,337A
FILING DATE: 25-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/350,260
FILING DATE: 05-DEC-1994
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994

ATTORNEY/AGENT INFORMATION:

NAME: Bartnicki, Audrey L.
REGISTRATION NUMBER: 40,499
REFERENCE/DOCKET NUMBER: 28111/32372A
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 391:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 391:

US-09-104-337A-391

Query Match 46.8%; Score 22; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YGRVFPDY 8
| : ||
Db 1 YKSLSPDY 8

Search completed: December 30, 2005, 15:56:51
Job time : 45 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2005, 15:56:06 ; Search time 160 Seconds

(without alignments)
20.891 Million cell updates/sec

Title: US-10-735-916A-12

Perfect score: 47

Sequence: 1 YGRVFFDY 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 31696

Minimum DB seq length: 8

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	8	5	US-10-735-916A-12
2	28	59.6	8	3	US-09-920-174-19
3	28	59.6	8	3	US-09-920-195A-19
4	28	59.6	8	4	US-10-777-053-80
5	28	59.6	8	4	US-10-777-053-588
6	28	59.6	8	4	US-10-837-217-80
7	28	59.6	8	4	US-10-837-217-588
8	28	59.6	8	5	US-10-752-380-19
9	26	55.3	8	3	US-09-880-748-3179
10	26	55.3	8	4	US-10-293-418-3179
11	25	53.2	8	4	US-10-094-699-56
12	25	53.2	8	4	US-10-160-232-17
13	25	53.2	8	4	US-10-044-896-12
14	25	53.2	8	4	US-10-117-937-401
15	25	53.2	8	5	US-10-855-013-31
16	25	53.2	8	6	US-11-067-064-401
17	25	53.2	8	6	US-11-067-159-401
18	24	51.1	8	4	US-10-447-257-8
19	24	51.1	8	5	US-10-496-628-8
20	24	51.1	8	5	US-10-996-316-195
21	22	46.8	8	3	US-09-972-656-62
22	22	46.8	8	3	US-09-802-083-9
23	22	46.8	8	4	US-10-209-372-37
24	22	46.8	8	4	US-10-165-732A-9
25	22	46.8	8	4	US-10-172-785-9
26	22	46.8	8	4	US-10-449-566-62
27	22	46.8	8	4	US-10-275-046-33

ALIGNMENTS

RESULT 1

US-10-735-916A-12
; Sequence 12, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10735,916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-735-916A-12

Query Match 100.0%; Score 47; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRVFFDY 8
|||||||
DB 1 YGRVFFDY 8

RESULT 2

US-09-920-174-19
; Sequence 19, Application US/09920174
; Patent No. US20020150590A1
; GENERAL INFORMATION:
; APPLICANT: KHANNA, RAJIV
; APPLICANT: KERR, BEVERLEY M.
; APPLICANT: MISKO, IHOR S.

Sequence 472, App
Sequence 601, App
Sequence 473, App
Sequence 9, Appli
Sequence 9, Appli
Sequence 41, Appli
Sequence 523, App
Sequence 131, App
Sequence 581, App
Sequence 582, App
Sequence 582, App
Sequence 582, App
Sequence 60, Appl
Sequence 581, App
Sequence 16, Appl
Sequence 3, Appli
Sequence 308, App

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; APPLICANT: MOSS, DENIS J.
; APPLICANT: BURROWS, SCOTT R.
; TITLE OF INVENTION: EBV CTL EPITOPES
; FILE REFERENCE: FERC:008USC2
; CURRENT APPLICATION NUMBER: US/09/920,174
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 09/920,175
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 09/194,450
; PRIOR FILING DATE: 1998-11-23
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 19
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-920-174-19

Query Match          59.6%; Score 28; DB 3; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      4 VFPDY 8
Db      4 IFFDY 8

RESULT 3
US-09-920-195A-19
; Sequence 19, Application US/09920195A
; Publication No. US20030175300A1
; GENERAL INFORMATION:
; APPLICANT: KHANNA, RAJIV
; APPLICANT: KERR, BEVERLEY M.
; APPLICANT: MISKO, IHOR S.
; APPLICANT: MOSS, DENIS J.
; APPLICANT: BURROWS, SCOTT R.
; TITLE OF INVENTION: EBV CTL EPITOPES
; FILE REFERENCE: FERC:008USC1
; CURRENT APPLICATION NUMBER: US/09/920,195A
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 09/194,450
; PRIOR FILING DATE: 1998-11-23
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 19
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-920-195A-19

Query Match          59.6%; Score 28; DB 3; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      4 VFPDY 8
Db      4 IFFDY 8

RESULT 4
US-10-777-053-80
; Sequence 80, Application US/10777053
; Publication No. US20040132088A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
```

```
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; FILE REFERENCE: MANNK.022C1
; CURRENT APPLICATION NUMBER: US/10/777,053
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/336,968
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Epstein-Barr Virus
US-10-777-053-80

Query Match          59.6%; Score 28; DB 4; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      4 VFPDY 8
Db      4 IFFDY 8

RESULT 5
US-10-777-053-588
; Sequence 588, Application US/10777053
; Publication No. US20040132088A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; FILE REFERENCE: MANNK.022C1
; CURRENT APPLICATION NUMBER: US/10/777,053
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/336,968
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 588
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Epstein-Barr Virus (EBNA)
US-10-777-053-588

Query Match          59.6%; Score 28; DB 4; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      4 VFPDY 8
Db      4 IFFDY 8

RESULT 6
US-10-837-217-80
; Sequence 80, Application US/10837217
; Publication No. US20040203051A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
```

; TITLE OF INVENTION: TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN

; FILE REFERENCE: MANK 022C2
; CURRENT APPLICATION NUMBER: US/10/837,217
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/336,968
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Epstein-Barr Virus
US-10-837-217-80

Query Match 59.6%; Score 28; DB 4; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VFDDY 8
:||||
Db 4 IFFDY 8

RESULT 7

US-10-837-217-588

; Sequence 588, Application US/10837217
; Publication No. US20040203051A1
; GENERAL INFORMATION:

; APPLICANT: Simard, John J. L.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; APPLICANT: Diamond, David C.

; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN

; FILE REFERENCE: MANK 022C2

; CURRENT APPLICATION NUMBER: US/10/837,217

; CURRENT FILING DATE: 2004-04-30

; PRIOR APPLICATION NUMBER: 10/292,413

; PRIOR FILING DATE: 2002-11-07

; PRIOR APPLICATION NUMBER: 60/336,968

; PRIOR FILING DATE: 2001-11-07

; NUMBER OF SEQ ID NOS: 979

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 588

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Epstein-Barr Virus (EBNA)

US-10-837-217-588

Query Match 59.6%; Score 28; DB 4; Length 8;

Best Local Similarity 80.0%; Pred. No. 1.7e+06;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VFDDY 8

:||||

Db 4 IFFDY 8

RESULT 8

US-10-752-380-19

; Sequence 19, Application US/10752380

; Publication No. US20050084498A1

; GENERAL INFORMATION:

; APPLICANT: KHANNA, RAJIV

; APPLICANT: KERR, BEVERLEY M.

; APPLICANT: MISKO, THOR S.

; APPLICANT: MOSS, DENIS J.

; APPLICANT: BURROWS, SCOTT R.

; TITLE OF INVENTION: EBV CTL EPITOPES

; FILE REFERENCE: FERC:008

; CURRENT APPLICATION NUMBER: US/10/752,380

; CURRENT FILING DATE: 2004-01-06
; PRIOR APPLICATION NUMBER: US/09/194,450
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-752-380-19

Query Match 59.6%; Score 28; DB 5; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VFDDY 8
:||||
Db 4 IFFDY 8

RESULT 9

US-09-880-748-3179

; Sequence 3179, Application US/09880748

; Publication No. US20030059937A1

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

; FILE REFERENCE: PF523

; CURRENT APPLICATION NUMBER: US/09/880,748

; CURRENT FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/212,210

; PRIOR FILING DATE: 2000-06-15

; PRIOR APPLICATION NUMBER: 60/240,816

; PRIOR FILING DATE: 2000-10-17

; PRIOR APPLICATION NUMBER: 60/276,248

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/277,379

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/293,499

; PRIOR FILING DATE: 2001-05-25

; NUMBER OF SEQ ID NOS: 3239

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3179

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-880-748-3179

Query Match 55.3%; Score 26; DB 3; Length 8;

Best Local Similarity 66.7%; Pred. No. 1.7e+06;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 RVFFDY 8

:||||

Db 3 RYFFDY 8

RESULT 10

US-10-293-418-3179

; Sequence 3179, Application US/10293418

; Publication No. US2003022396A1

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

; FILE REFERENCE: PF523P2

; CURRENT APPLICATION NUMBER: US/10/293,418

; CURRENT FILING DATE: 2002-11-27

; PRIOR APPLICATION NUMBER: 60/331,469

; PRIOR FILING DATE: 2001-11-16

; PRIOR APPLICATION NUMBER: 60/340,817

; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3179
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-3179

Query Match 55.3%; Score 26; DB 4; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 RVFFDY 8
| : |||
Db 3 RYFFDY 8

RESULT 11
US-10-094-699-56
; Sequence 56, Application US/10094699
; Publication No. US20030046714A1
; GENERAL INFORMATION:
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; TITLE OF INVENTION: ANTI-NEOVASCULATURE PREPARATIONS FOR
; FILE REFERENCE: CTLIMM.015A
; CURRENT APPLICATION NUMBER: US/10/094,699
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/274,063
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-094-699-56

Query Match 53.2%; Score 25; DB 4; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRVF 5
| : |||
Db 4 YGKVP 8

RESULT 12
US-10-160-232-17
; Sequence 17, Application US/10160232
; Publication No. US20030088075A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: ITO, MIKIO
; APPLICANT: HANAI, NOBUO
; APPLICANT: KAWADA, YOKO
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: SHIBUYA, MASABUMI
; TITLE OF INVENTION: ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOCLONAL ANTIBODY
; FILE REFERENCE: 249-107

; CURRENT APPLICATION NUMBER: US/10/160,232
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US/09/453,718
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 09/315,051
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/119,014
; PRIOR FILING DATE: 1998-07-20
; PRIOR APPLICATION NUMBER: PCT/JP97/04259
; PRIOR FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
US-10-160-232-17

Query Match 53.2%; Score 25; DB 4; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GRVFFDY 8
| : |||
Db 2 GDYFFDY 8

RESULT 13
US-10-044-896-12
; Sequence 12, Application US/10044896
; Publication No. US20030166228A1
; GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Kim, Jin K.
; APPLICANT: Stewart, Timothy G.
; TITLE OF INVENTION: ANTI-INTERFERON-ALPHA ANTIBODIES
; FILE REFERENCE: GENENT.074A
; CURRENT APPLICATION NUMBER: US/10/044,896
; CURRENT FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: 60/270775
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-044-896-12

Query Match 53.2%; Score 25; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FFDY 8
| : |||
Db 5 FFDY 8

RESULT 14
US-10-117-937-401
; Sequence 401, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A

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; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 401
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-401

Query Match      53.2%; Score 25; DB 4; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YGRVP 5
Db      4 YGRVF 8
```

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RESULT 15
US-10-855-013-31
; Sequence 31, Application US/10855013
; Publication No. US20050025768A1
; GENERAL INFORMATION:
; APPLICANT: Biogen, Inc. et al.
; TITLE OF INVENTION: ANTIBODIES AGAINST MONOCYTE CHEMOTACTIC PROTEINS
; FILE REFERENCE: BGN-006PC
; CURRENT APPLICATION NUMBER: US/10/855.013
; CURRENT FILING DATE: 2004-05-27
; PRIOR APPLICATION NUMBER: US 60/343391
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/383277
; PRIOR FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 60/400469
; PRIOR FILING DATE: 2002-08-01
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-855-013-31
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Query Match      53.2%; Score 25; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 FFDY 8
Db      5 FFDY 8
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Search completed: December 30, 2005, 16:09:34
Job time : 161 secs

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OM protein - protein search, using sw model

Run on: December 30, 2005, 15:55:26 ; Search time 12 Seconds
(without alignments)

4.993 Million cell updates/sec

Title: US-10-735-916A-12

Perfect score: 47

Sequence: 1 YGRVFFDY 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 4100

Minimum DB seq length: 8

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

- 1: /cgm2_6/ptodata/1/pubpaa/US08_NEW_PUB_PEP.*
- 2: /cgm2_6/ptodata/1/pubpaa/US06_NEW_PUB_PEP.*
- 3: /cgm2_6/ptodata/1/pubpaa/US07_NEW_PUB_PEP.*
- 4: /cgm2_6/ptodata/1/pubpaa/PCT_NEW_PUB_PEP.*
- 5: /cgm2_6/ptodata/1/pubpaa/US03_NEW_PUB_PEP.*
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- 7: /cgm2_6/ptodata/1/pubpaa/US11_NEW_PUB_PEP.*
- 8: /cgm2_6/ptodata/1/pubpaa/US60_NEW_PUB_PEP.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	8	7	US-11-012-353-12
2	26	55.3	8	7	US-11-054-515-3179
3	25	53.2	8	7	US-11-073-347-56
4	25	53.2	8	7	US-11-096-046-23
5	22	46.8	8	7	US-11-152-747-37
6	22	46.8	8	7	US-11-127-677-112
7	19	40.4	8	7	US-11-016-706-76
8	19	40.4	8	7	US-11-016-706-77
9	19	40.4	8	7	US-11-054-515-3092
10	19	40.4	8	7	US-11-054-515-3111
11	19	40.4	8	7	US-11-054-515-3141
12	19	40.4	8	7	US-11-093-274-7
13	19	40.4	8	7	US-11-112-277-3
14	19	40.4	8	7	US-11-045-024-420
15	19	40.4	8	7	US-11-045-024-3592
16	19	40.4	8	7	US-11-045-024-3593
17	19	40.4	8	7	US-11-045-024-5075
18	19	40.4	8	7	US-11-045-024-5076
19	19	40.4	8	7	US-11-045-024-6906
20	19	40.4	8	7	US-11-045-024-8281
21	19	40.4	8	7	US-11-045-024-10742
22	19	40.4	8	7	US-11-045-024-10749
23	19	40.4	8	7	US-11-045-024-10751
24	19	40.4	8	7	US-11-045-024-12507
25	19	40.4	8	7	US-11-045-024-12512

ALIGNMENTS

RESULT 1

US-11-012-353-12

; Sequence 12, Application US/11012353

; Publication No. US20050249730A1

; GENERAL INFORMATION:

; APPLICANT: GOETSCH, LILIANE

; APPLICANT: CORVAIA, LATHALIE

; APPLICANT: DUFLOS, ALAIN

; APPLICANT: HAEUM, JEAN-FRANCOIS

; APPLICANT: LEGER, OLIVIER

; APPLICANT: BECK, ALAIN

; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-1 HYBRID

; FILE REFERENCE: 017753-198

; CURRENT APPLICATION NUMBER: US/11/012,353

; PRIOR FILING DATE: 2004-12-16

; PRIOR APPLICATION NUMBER: 10/735,916

; PRIOR FILING DATE: 2003-12-16

; PRIOR APPLICATION NUMBER: FR 0308538

; PRIOR FILING DATE: 2003-07-11

; PRIOR APPLICATION NUMBER: PCT/FR03/00178

; PRIOR FILING DATE: 2003-01-20

; PRIOR APPLICATION NUMBER: FR 0205753

; PRIOR FILING DATE: 2002-05-07

; PRIOR APPLICATION NUMBER: FR 0200653

; PRIOR FILING DATE: 2002-01-18

; PRIOR APPLICATION NUMBER: FR 0200654

; PRIOR FILING DATE: 2002-01-18

; NUMBER OF SEQ ID NOS: 162

; SOFTWARE: PatentIn Ver. 3.3

; SEQ ID NO 12

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Mus musculus

US-11-012-353-12

Query Match 100.0%; Score 47; DB 7; Length 8;

Best Local Similarity 100.0%; Pred. No. 4.4e+04;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRVFFDY 8

Db 1 YGRVFFDY 8

RESULT 2

US-11-054-515-3179

; Sequence 3179, Application US/11054515

Sequence 12513, A
Sequence 12862, A
Sequence 83, Appl
Sequence 89, Appl
Sequence 96, Appl
Sequence 116, Appl
Sequence 125, App
Sequence 128, App
Sequence 33, Appl
Sequence 11, Appl
Sequence 2842, Ap
Sequence 3481, Ap
Sequence 3482, Ap
Sequence 3483, Ap
Sequence 10439, A
Sequence 10447, A
Sequence 10448, A
Sequence 10449, A
Sequence 12273, A
Sequence 12281, A

26 19 40.4 8 7 US-11-045-024-12513
27 19 40.4 8 7 US-11-045-024-12862
28 19 40.4 8 7 US-11-127-677-83
29 19 40.4 8 7 US-11-127-677-89
30 19 40.4 8 7 US-11-127-677-96
31 19 40.4 8 7 US-11-127-677-116
32 19 40.4 8 7 US-11-127-677-125
33 19 40.4 8 7 US-11-127-677-128
34 18 38.3 8 6 US-10-997-066-33
35 18 38.3 8 7 US-11-176-868-11
36 18 38.3 8 7 US-11-054-515-2842
37 18 38.3 8 7 US-11-045-024-3481
38 18 38.3 8 7 US-11-045-024-3482
39 18 38.3 8 7 US-11-045-024-3483
40 18 38.3 8 7 US-11-045-024-10439
41 18 38.3 8 7 US-11-045-024-10447
42 18 38.3 8 7 US-11-045-024-10448
43 18 38.3 8 7 US-11-045-024-10449
44 18 38.3 8 7 US-11-045-024-12273
45 18 38.3 8 7 US-11-045-024-12281

oy

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; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3092
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-3092

Query Match          40.4%; Score 19; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 FDY 8
Db      6 FDY 8

RESULT 10
US-11-054-515-3111
; Sequence 3111, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3111
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-3111

Query Match          40.4%; Score 19; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 FDY 8
Db      6 FDY 8

RESULT 11
US-11-054-515-3141
; Sequence 3141, Application US/11054515
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; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3141
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-3141

Query Match          40.4%; Score 19; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 FDY 8
Db      6 FDY 8

RESULT 12
US-11-093-274-7
; Sequence 7, Application US/11093274
; Publication No. US20050266008A1
; GENERAL INFORMATION:
; APPLICANT: Graziano, Robert
; APPLICANT: Cardarelli, Josephine M.
; APPLICANT: Kempe, Thomas
; APPLICANT: Cutter, Beth
; APPLICANT: Srinivasan, Mohan
; TITLE OF INVENTION: IRTA-5 ANTIBODIES AND THEIR USES
; FILE REFERENCE: 04280/1201101-US1
; CURRENT APPLICATION NUMBER: US/11/093,274
; CURRENT FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: 60/557,741
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 7
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-093-274-7

Query Match          40.4%; Score 19; DB 7; Length 8;
Best Local Similarity 60.0%; Pred. No. 4.4e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 YGRVF 5
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```
Db      :|||
        2 WGRAP 6

RESULT 13
US-11-112-277-3
; Sequence 3, Application US/11112277
; Publication No. US20050267293A1
; GENERAL INFORMATION:
; APPLICANT: Bousquet-Gagnon, Nathalie
; APPLICANT: Quraishi, Omar
; APPLICANT: Bridon, Dominique P.
; TITLE OF INVENTION: METHOD FOR THE PURIFICATION OF ALBUMIN
; TITLE OF INVENTION: CONUGATES
; FILE REFERENCE: 50082003700
; CURRENT APPLICATION NUMBER: US/11/112,277
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/565,228
; PRIOR FILING DATE: 2004-04-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: K5 Analogue
; NAME/KEY: MOD_RES
; LOCATION: 8
; OTHER INFORMATION: Xaa is Lys linked to MPA
US-11-112-277-3

Query Match      40.4%; Score 19; DB 7; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.4e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      3 RVFFDY 8
        |||
Db      2 RKLYDY 7

RESULT 14
US-11-045-024-420
; Sequence 420, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3592
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-3592

Query Match      40.4%; Score 19; DB 7; Length 8;
Best Local Similarity 60.0%; Pred. No. 4.4e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db      4 VFIEY 8

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US-11-045-024-3592
; Sequence 3592, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
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Query Match      40.4%; Score 19; DB 7; Length 8;
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Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      4 VFFDY 8
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Db      3 VFIEY 7
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Search completed: December 30, 2005, 16:06:47
Job time : 12 secs
